

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
6 September 2002 (06.09.2002)

PCT

(10) International Publication Number
WO 02/068677 A2

(51) International Patent Classification⁷: **C12Q**

(21) International Application Number: PCT/US02/06001

(22) International Filing Date: 14 January 2002 (14.01.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/272,206 27 February 2001 (27.02.2001) US
60/281,149 2 April 2001 (02.04.2001) US
60/284,555 17 April 2001 (17.04.2001) US

(71) Applicants (for all designated States except US): **EOS BIOTECHNOLOGY, INC.** [US/US]; 225A Gateway Boulevard, South San Francisco, CA 94080-7019 (US). **CASE WESTERN RESERVE UNIVERSITY** [US/US]; 10900 Euclid Avenue, Cleveland, OH 44106 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **MACK, David, H.** [US/US]; 2076 Monterey Avenue, Menlo Park, CA 94025 (US). **MARKOWITZ, Sanford, David** [US/US]; 28950 Bolingbrook Road, Pepper Pike, OH 44124 (US).

(74) Agents: **BASTIAN, Kevin, L.** et al.; Townsend and Townsend and Crew LLP, Two Embarcadero Center, Eighth Floor, San Francisco, CA 94111-3834 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declaration under Rule 4.17:

— of inventorship (Rule 4.17(iv)) for US only

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: NOVEL METHODS OF DIAGNOSIS OF METASTATIC COLORECTAL CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF METASTATIC COLORECTAL CANCER

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of metastatic colorectal cancer. Also described herein are methods that can be used to identify modulators of metastatic colorectal cancer.



WO 02/068677 A2

NOVEL METHODS OF DIAGNOSIS OF METASTATIC COLORECTAL CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF METASTATIC COLORECTAL CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS

The present application is related to USSN 60/272,206, filed February 27, 2001, USSN 60/281,149, filed April 2, 2001, and USSN 60/284,555, filed April 17, 2001, all of which are herein incorporated by referenced in their entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in metastatic colorectal cancer; and to the use of such expression profiles and compositions in diagnosis and therapy of metastatic colorectal cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit metastatic colorectal cancer.

BACKGROUND OF THE INVENTION

Cancer of the colon and/or rectum (referred to as "colorectal cancer") are significant in Western populations and particularly in the United States. Cancers of the colon and rectum occur in both men and women most commonly after the age of 50. These develop as the result of a pathologic transformation of normal colon epithelium to an invasive cancer. There have been a number of recently characterized genetic alterations that have been implicated in colorectal cancer, including mutations in two classes of genes, tumor-suppressor genes and proto-oncogenes, with recent work suggesting that mutations in DNA repair genes may also be involved in tumorigenesis. For example, inactivating mutations of both alleles of the adenomatous polyposis coli (APC) gene, a tumor suppressor gene, appears to be one of the earliest events in colorectal cancer, and may even be the initiating event. Other genes implicated in colorectal cancer include the MCC gene, the p53 gene, the DCC (deleted in colorectal carcinoma) gene and other chromosome 18q genes, and genes in the TGF- β signaling pathway. For a review, see *Molecular Biology of Colorectal Cancer*, pp. 238-299, in *Curr. Probl. Cancer*, Sept/Oct 1997; see also Willams, *Colorectal Cancer*

(1996); Kinsella & Schofield, *Colorectal Cancer: A Scientific Perspective* (1993); *Colorectal Cancer: Molecular Mechanisms, Premalignant State and its Prevention* (Schmiegel & Scholmerich eds., 2000); *Colorectal Cancer: New Aspects of Molecular Biology and Their Clinical Applications* (Hanski *et al.*, eds 2000); McArdle *et al.*, *Colorectal Cancer* (2000); Wanebo, *Colorectal Cancer* (1993); Levin, *The American Cancer Society: Colorectal Cancer* (1999); *Treatment of Hepatic Metastases of Colorectal Cancer* (Nordlinger & Jaeck eds., 1993); *Management of Colorectal Cancer* (Dunitz *et al.*, eds. 1998); *Cancer: Principles and Practice of Oncology* (Devita *et al.*, eds. 2001); *Surgical Oncology: Contemporary Principles and Practice* (Kirby *et al.*, eds. 2001); Offit, *Clinical Cancer Genetics: Risk Counseling and Management* (1997); *Radioimmunotherapy of Cancer* (Abrams & Fritzberg eds. 2000); Fleming, *AJCC Cancer Staging Handbook* (1998); *Textbook of Radiation Oncology* (Leibel & Phillips eds. 2000); and *Clinical Oncology* (Abeloff *et al.*, eds. 2000).

Imaging of colorectal cancer for diagnosis has been problematic and limited. In addition, metastasis of the tumor to the lumen, and metastasis of tumor cells to regional lymph nodes are important prognostic factors (*see, e.g., PET in Oncology: Basics and Clinical Application* (Ruhlmann *et al.* eds. 1999). For example, five year survival rates drop from 80 percent in patients with no lymph node metastases to 45 to 50 percent in those patients who do have lymph node metastases. A recent report showed that micrometastases can be detected from lymph nodes using reverse transcriptase-PCR methods based on the presence of mRNA for carcinoembryonic antigen, which has previously been shown to be present in the vast majority of colorectal cancers but not in normal tissues. Liefers *et al.*, *New England J. of Med.* 339(4):223 (1998). In addition, colorectal cancers often metastasize to the liver. However, the lack of information about the gene expression exhibited by these cancers limits the ability to effectively diagnose and treat the disease.

Thus, methods for diagnosis and prognosis of metastatic colorectal cancer and effective treatment of colorectal cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of metastatic colorectal cancer. Further provided are methods that can be used to screen candidate therapeutic agents for the ability to modulate, e.g., treat, colorectal cancer. Additionally, provided herein are molecular targets and compositions for therapeutic intervention in metastatic colorectal disease and other metastatic cancers.

SUMMARY OF THE INVENTION

The present invention therefore provides nucleotide sequences of genes that are up- and down-regulated in metastatic colorectal cancer cells. Such genes and the proteins they

encode are useful for diagnostic and prognostic purposes, and also as targets for screening for therapeutic compounds that modulate metastatic colorectal cancer, such as antibodies. The methods of detecting nucleic acids of the invention or their encoded proteins can be used for a number of purposes. Examples include, early detection of colon cancers, monitoring and early detection of relapse following treatment of colon cancers, monitoring response to therapy of colon cancers, determining prognosis of colon cancers, directing therapy of colon cancers, selecting patients for postoperative chemotherapy or radiation therapy, selecting therapy, determining tumor prognosis, treatment, or response to treatment, and early detection of precancerous colon adenomas. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a metastatic colorectal cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-26. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1-26.

In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

In one embodiment, the polynucleotide is immobilized on a solid surface.

In one embodiment, the patient is undergoing a therapeutic regimen to treat metastatic colorectal cancer. In another embodiment, the patient is suspected of having metastatic colorectal cancer.

In one embodiment, the patient is a human.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides methods of detecting polypeptide encoded by a metastatic colorectal cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with an antibody that specifically binds a polypeptide encoded by a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of metastatic colorectal cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a metastatic colorectal cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26., thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the metastatic colorectal cancer-associated transcript to a level of the metastatic colorectal cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of metastatic colorectal cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a metastatic colorectal cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26, wherein the polypeptide specifically binds to the metastatic colorectal cancer-associated antibody, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the metastatic colorectal cancer-associated antibody to a level of the metastatic colorectal cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of metastatic colorectal cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a metastatic colorectal cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the metastatic colorectal cancer-associated polypeptide to a level of the metastatic

colorectal cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-26.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting a metastatic colorectal cancer cell in a biological sample from a patient, the method comprising contacting the biological sample with an antibody as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to metastatic colorectal cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1-26.

In another aspect, the present invention provides a method for identifying a compound that modulates a metastatic colorectal cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a metastatic colorectal cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant.

In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation of a metastatic colorectal cancer-associated cell to treat colorectal cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having colorectal cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26. in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of colorectal cancer.

In one embodiment, the control is a mammal with colorectal cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal.

In another aspect, the present invention provides a method for treating a mammal having colorectal cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having colorectal cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of colon and/or rectal cancer (e.g., colorectal cancer), including metastatic colorectal cancers, as well as methods for screening for compositions which modulate colorectal cancer. By "metastatic colorectal cancer" herein is meant a colon and/or rectal tumor or cancer that is classified as Dukes stage C or D (see, e.g., Cohen *et al.*, *Cancer of the Colon*, in *Cancer: Principles and Practice of Oncology*, pp. 1144-1197 (Devita *et al.*, eds., 5th ed. 1997); see also *Harrison's Principles of Internal Medicine*, pp. 1289-129 (Wilson *et al.*, eds., 12th ed., 1991). "Treatment, monitoring, detection or modulation of metastatic colorectal cancer" includes treatment, monitoring, detection, or modulation of metastatic colorectal disease in those patients who have metastatic colorectal

disease (Dukes stage C or D). In Dukes stage A, the tumor has penetrated into, but not through, the bowel wall. In Dukes stage B, the tumor has penetrated through the bowel wall but there is not yet any lymph involvement. In Dukes stage C, the cancer involves regional lymph nodes. In Dukes stage D, there is distant metastasis, e.g., liver, lung, etc.

Tables 1-26 provide UniGene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in metastasizing colorectal cancer samples. Tables 1-26 also provide an exemplar accession number that provides a nucleotide sequence that is part of the UniGene cluster. In Tables 1-26, the ratio provided represents primary tumor samples from known Dukes B stage survivors vs. liver metastasis samples from patients with metastatic colorectal cancer. In these samples, the identified genes are underexpressed in the metastatic samples, as the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. In Tables 1-26, the ratio provided represents liver metastasis samples from patients with known metastatic colorectal cancer vs. known primary tumor samples from Dukes B stage survivors. In these samples, the identified genes are overexpressed in the metastatic samples, as the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. In Tables 1-26, the ratio provided represents primary tumor samples from known Dukes B stage survivors vs. liver metastasis samples from patients with metastatic colorectal cancer. In these samples, the identified genes are overexpressed in the metastatic samples, as the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less. Survivors are subjects who have been disease free for five years or longer.

In Tables 1-26, the ratio provided represents liver metastasis samples from patients with known metastatic disease vs. tissue samples from normal colon tissue. In these samples, the identified genes are overexpressed in the metastatic samples, as the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. In Tables 1-26, the ratio represents liver metastasis samples from patients with known metastatic disease vs. tissue samples from normal colon tissue. In these samples, the identified genes are underexpressed in the metastatic samples, as the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

One of skill will recognize that although the sequences identified in Tables 1-26 exhibited increased or decreased expression in metastasizing colorectal cancer samples, the sequences of the invention, and their encoded proteins, can be used to diagnose, treat or prevent cancers in patients with Dukes stage A or B colorectal cancers. Alteration of gene

expression for a gene in Tables 1-26 may be more likely or less likely to indicate that the subject will progress to metastatic disease. The sequences can also be used to diagnose, treat or prevent precancerous or benign conditions such as precancerous colon adenomas.

Alteration of gene expression for a gene in Tables 1-26 may or may not indicate that the subject is more likely to progress to cancer or to metastatic disease. Thus, although the specification focuses primarily on metastasizing colorectal cancer, the methods described below can also be applied to non-metastasizing colorectal cancers (*e.g.*, Dukes stages A and B) and precancerous or benign conditions (*e.g.*, precancerous adenomas) as well.

Definitions

The term “metastatic colorectal cancer protein” or “metastatic colorectal cancer polynucleotide” or “metastatic colorectal cancer-associated transcript” refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a UniGene cluster of Tables 1-26; (2) bind to antibodies, *e.g.*, polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a UniGene cluster of Tables 1-26, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-26 and conservatively modified variants thereof or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a UniGene cluster of Tables 1-26. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, *e.g.*, human; rodent, *e.g.*, rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A “metastatic colorectal cancer polypeptide” and a “metastatic colorectal cancer polynucleotide,” include both naturally occurring or recombinant.

A “full length” metastatic colorectal cancer protein or nucleic acid refers to a metastatic colorectal cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type metastatic colorectal cancer polynucleotide or polypeptide sequences. The “full length” may be prior to, or after, various stages of post-translation processing or splicing, including alternative splicing.

“Biological sample” as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a metastatic colorectal cancer protein, polynucleotide or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; fish.

“Providing a biological sample” means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention *in vivo*. Archival tissues, having treatment or outcome history, will be particularly useful.

The terms “identical” or percent “identity,” in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (*see, e.g.*, NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be “substantially identical.” This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions

and/or additions, as well as those that have substitutions, as well as naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., *Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1997) and Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990). BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short

words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W , T , and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, $M=5$, $N=-4$ and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, $M=5$, $N=-4$, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5877 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ($P(N)$), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules

or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (*see, e.g.*, the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogenous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine,

norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions similarly to a naturally occurring amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

“Conservatively modified variants” applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are “silent variations,” which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. One of skill will recognize that in certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, often silent variations of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a “conservatively modified variant” where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention.

The following eight groups each contain amino acids that are typically conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (*see, e.g., Creighton, Proteins (1984)*).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, *see, e.g., Alberts et al., Molecular Biology of the Cell (3rd ed., 1994) and Cantor & Schimmel, Biophysical Chemistry Part I: The Conformation of Biological Macromolecules (1980)*.

“Primary structure” refers to the amino acid sequence of a particular peptide. “Secondary structure” refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. “Tertiary structure” refers to the complete three dimensional structure of a polypeptide monomer. “Quaternary structure” refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

“Nucleic acid” or “oligonucleotide” or “polynucleotide” or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, *e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc.* A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have alternate backbones, comprising, *e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press); and peptide nucleic acid backbones and linkages.* Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, *Carbohydrate Modifications in Antisense Research*, Sanghui &

Cook, eds.. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g. to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g. the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical means. For example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins

or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide.

An “effector” or “effector moiety” or “effector component” is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The “effector” can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting “hard” e.g., beta radiation.

A “labeled nucleic acid probe or oligonucleotide” is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a “nucleic acid probe or oligonucleotide” is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term “recombinant” when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g.,

recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the *in vivo* cellular machinery of the host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence,

wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1% SDS at 65°C. For PCR, a temperature of about 36°C is typical for low stringency amplification,

although annealing temperatures may vary between about 32°C and 48°C depending on primer length. For high stringency PCR amplification, a temperature of about 62°C is typical, although high stringency annealing temperatures can range from about 50°C to about 65°C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90°C - 95°C for 30 sec - 2 min., an annealing phase lasting 30 sec. - 2 min., and an extension phase of about 72°C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis *et al.*, *PCR Protocols, A Guide to Methods and Applications* (1990).

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1X SSC at 45°C. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., and *Current Protocols in Molecular Biology*, ed. Ausubel, *et al.*

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a metastatic colorectal cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the metastatic colorectal cancer protein or nucleic acid, e.g., an enzymatic, functional, physical, or chemical effect, such as the ability to decrease metastatic colorectal cancer. It includes ligand binding activity; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of metastatic colorectal cancer cells. "Functional effects" include *in vitro*, *in vivo*, and *ex vivo* activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a metastatic colorectal cancer protein sequence, e.g., functional, enzymatic, physical and

chemical effects. Such functional effects can be measured by any means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the metastatic colorectal cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on metastatic colorectal cancer can also be performed using metastatic colorectal cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of metastatic colorectal cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for metastatic colorectal cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

“Inhibitors”, “activators”, and “modulators” of metastatic colorectal cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using *in vitro* and *in vivo* assays of metastatic colorectal cancer polynucleotide and polypeptide sequences of the invention. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of metastatic colorectal cancer proteins of the invention, e.g., antagonists. Antisense nucleic acids may seem to inhibit expression and subsequent function of the protein. “Activators” are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate metastatic colorectal cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of metastatic colorectal cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the metastatic colorectal cancer protein *in vitro*, in cells, or cell membranes, applying putative modulator compounds, and then

determining the functional effects on activity, as described above. Activators and inhibitors of metastatic colorectal cancer can also be identified by incubating metastatic colorectal cancer cells with the test compound and determining increases or decreases in the expression of 1 or more metastatic colorectal cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more metastatic colorectal cancer proteins, such as colorectal cancer proteins encoded by the sequences set out in Tables 1-26.

Samples or assays comprising metastatic colorectal cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a metastatic colorectal cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., Freshney, *Culture of Animal Cells a Manual of Basic Technique* pp. 231-241 (3rd ed. 1994).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (see, Freshney, *Culture of Animal Cells a Manual of Basic Technique* (3rd ed. 1994)).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen.

The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, *Fundamental Immunology*.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab')_2$, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The $F(ab')_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab')_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see *Fundamental Immunology* (Paul ed., 3d ed. 1993)). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty *et al.*, *Nature* 348:552-554 (1990)).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (see, e.g., Kohler & Milstein, *Nature* 256:495-497 (1975); Kozbor *et al.*, *Immunology Today* 4:72 (1983); Cole *et al.*, pp. 77-96 in *Monoclonal Antibodies and Cancer Therapy* (1985); Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *Antibodies, A Laboratory Manual* (1988); and Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce

antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (*see, e.g., McCafferty et al., Nature* 348:552-554 (1990); Marks *et al., Biotechnology* 10:779-783 (1992)).

A "chimeric antibody" is an antibody molecule in which, e.g, (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

Identification of metastatic colorectal cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different metastatic colorectal cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.

The identification of sequences that are differentially expressed in metastatic colorectal cancer versus non-metastatic colorectal cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate metastatic colorectal cancer, and thus tumor growth or recurrence, in a particular patient. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Metastatic tissue can also be analyzed to determine the stage of metastatic colorectal cancer in the tissue. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a

particular expression profile; e.g., screening can be done for drugs that suppress the metastatic colorectal cancer expression profile. This may be done by making biochips comprising sets of the important metastatic colorectal cancer genes, which can then be used in these screens. PCR methods may be applied with selected primer pairs, and analysis may be of RNA or of genomic sequences. These methods can also be done on the protein basis; that is, protein expression levels of the metastatic colorectal cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the metastatic colorectal cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the metastatic colorectal cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA vaccines.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in metastatic colorectal cancer, herein termed "metastatic colorectal cancer sequences." As outlined below, metastatic colorectal cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in metastatic colorectal cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the metastatic colorectal cancer sequences are from humans; however, as will be appreciated by those in the art, metastatic colorectal cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other metastatic colorectal cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (dogs, cats, etc.). Metastatic colorectal cancer sequences from other organisms may be obtained using the techniques outlined below.

Metastatic colorectal cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, metastatic colorectal cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the metastatic colorectal cancer sequences can be generated.

A metastatic colorectal cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the metastatic colorectal cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid

or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying metastatic colorectal cancer-associated sequences, the metastatic colorectal cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue, or tumor tissue samples from patients who have been diagnosed with Dukes stage A or B cancer but have survived vs. metastatic tissue. Other suitable tissue comparisons include comparing metastatic colorectal cancer samples with metastatic cancer samples from other cancers, such as lung, breast, other gastrointestinal cancers, prostate, ovarian, etc. Samples of, e.g., Dukes stage B survivor tissue and tissue undergoing metastasis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal colon, but also including, and not limited to lung, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone and placenta. In a preferred embodiment, those genes identified during the metastatic colorectal cancer screen that are expressed in significant amounts in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is usually preferable that the target be disease specific, to minimize possible side effects.

In a preferred embodiment, metastatic colorectal cancer sequences are those that are up-regulated in metastatic colorectal cancer; that is, the expression of these genes is higher in the metastatic tissue as compared to non-metastatic cancerous tissue or normal colon tissue (*see, e.g.*, Tables 1-26). "Up-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. All UniGene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, *see, e.g.*, Benson, DA, *et al.*, Nucleic Acids Research 26:1-7 (1998) and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ).

In another preferred embodiment, metastatic colorectal cancer sequences are those that are down-regulated in the metastatic colorectal cancer; that is, the expression of these genes is lower in metastatic tissue as compared to non-metastatic cancerous tissue or normal colon tissue (*see, e.g.*, Tables 1-26). "Down-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

Informatics

The ability to identify genes that are over or under expressed in metastatic colorectal cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with metastatic colorectal cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (*see Anderson, Pharmaceutical Proteomics: Targets, Mechanism, and Function*, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (*see U.S. Patent No. 5,811,231*). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (*e.g.*, nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, *e.g.*, using array analysis either singly or in a library format. The database can be in substantially any form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing metastatic colorectal cancer, i.e., the identification of metastatic colorectal cancer-associated sequences described herein, provide an abundance of information, which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, prior data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount *et al.*, *Bioinformatics* (2001); *Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids* (Durbin *et al.*, eds., 1999); *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins* (Baxeavanis & Oeullette eds., 1998)); Rashidi & Buehler, *Bioinformatics: Basic Applications in Biological*

Science and Medicine (1999); *Introduction to Computational Molecular Biology* (Setubal et al., eds 1997); *Bioinformatics: Methods and Protocols* (Misener & Krawetz, eds, 2000); *Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach* (Higgins & Taylor, eds., 2000); Brown, *Bioinformatics: A Biologist's Guide to Biocomputing and the Internet* (2001); Han & Kamber, *Data Mining: Concepts and Techniques* (2000); and Waterman, *Introduction to Computational Biology: Maps, Sequences, and Genomes* (1995).

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for metastatic colorectal cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The

comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example,

a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of metastatic colorectal cancer-associated proteins

Metastatic colorectal cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the metastatic colorectal cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus and/or in the organelles. Proteins containing one or more transmembrane domains that exclusively reside in organelles are also considered intracellular proteins. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or dysregulated cellular processes (*see, e.g., Molecular Biology of the Cell* (Alberts, ed., 3rd ed., 1994)). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein

interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (*see, e.g., Bateman et al., Nuc. Acids Res.* 28:263-266 (2000); Sonnhammer *et al., Proteins* 28:405-420 (1997); Bateman *et al., Nuc. Acids Res.* 27:260-262 (1999); and Sonnhammer *et al., Nuc. Acids Res.* 26:320-322- (1998)).

In another embodiment, the metastatic colorectal cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 20 consecutive

hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (*see, e.g.* PSORT web site <http://psort.nibb.ac.jp/>).

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Metastatic colorectal cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins *in situ* or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeabilized to provide access to intracellular proteins.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the metastatic colorectal cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they often serve to transmit signals to various other cell types. The secreted protein may

function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. Metastatic colorectal cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests.

Use of metastatic colorectal cancer nucleic acids

As described above, metastatic colorectal cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the metastatic colorectal cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The metastatic colorectal cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-26, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the metastatic colorectal cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, *et al.*, *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/unigene/>).

Once the metastatic colorectal cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire metastatic colorectal cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant metastatic colorectal cancer nucleic acid can be further-used as a probe to identify and isolate other metastatic colorectal cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant metastatic colorectal cancer nucleic acids and proteins.

The metastatic colorectal cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the metastatic colorectal

cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, and/or antisense applications. Alternatively, the metastatic colorectal cancer nucleic acids that include coding regions of metastatic colorectal cancer proteins can be put into expression vectors for the expression of metastatic colorectal cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to metastatic colorectal cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the metastatic colorectal cancer nucleic acids, i.e. the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under appropriate reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical

equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in copending application entitled Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize

sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (*see* 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of metastatic colorectal cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a metastatic colorectal cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of metastatic colorectal

cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis *et al.*, *PCR Protocols, A Guide to Methods and Applications* (1990).

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (*see, e.g.*, literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (*see* Wu & Wallace, *Genomics* 4:560 (1989), Landegren *et al.*, *Science* 241:1077 (1988), and Barringer *et al.*, *Gene* 89:117 (1990)), transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173 (1989)), self-sustained sequence replication (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA* 87:1874 (1990)), dot PCR, and linker adapter PCR, etc.

Expression of metastatic colorectal cancer proteins from nucleic acids

In a preferred embodiment, metastatic colorectal cancer nucleic acids, e.g., encoding metastatic colorectal cancer proteins, are used to make a variety of expression vectors to express metastatic colorectal cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (*see, e.g.*, Ausubel, *supra*, and *Gene Expression Systems* (Fernandez & Hoeffler, eds, 1999)) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the metastatic colorectal cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the metastatic colorectal cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez & Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The metastatic colorectal cancer proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a metastatic colorectal cancer protein, under the appropriate conditions to induce or cause expression of the metastatic colorectal cancer protein. Conditions appropriate for metastatic colorectal cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the metastatic colorectal cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (*see, e.g., Fernandez & Hoeffler, supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation,

polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, metastatic colorectal cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the *tac* promoter is a hybrid of the *trp* and *lac* promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the metastatic colorectal cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez & Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, metastatic colorectal cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, metastatic colorectal cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The metastatic colorectal cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies,

if the desired epitope is small, the metastatic colorectal cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the metastatic colorectal cancer protein may be made as a fusion protein to increase expression for affinity purification purposes, or for other reasons. For example, when the metastatic colorectal cancer protein is a metastatic colorectal cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the metastatic colorectal cancer protein is purified or isolated after expression. Metastatic colorectal cancer proteins may be isolated or purified in a variety of appropriate ways. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the metastatic colorectal cancer protein may be purified using a standard anti-metastatic colorectal cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, *Protein Purification* (1982). The degree of purification necessary will vary depending on the use of the metastatic colorectal cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the metastatic colorectal cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

Variants of metastatic colorectal cancer proteins

In one embodiment, the metastatic colorectal cancer proteins are derivative or variant metastatic colorectal cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative metastatic colorectal cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at a particular residue within the metastatic colorectal cancer peptide.

Also included within one embodiment of metastatic colorectal cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the metastatic colorectal cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell

culture as outlined above. However, variant metastatic colorectal cancer protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the metastatic colorectal cancer protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed metastatic colorectal cancer variants screened for the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of metastatic colorectal cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be occasionally tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of a metastatic colorectal cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

Variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the metastatic colorectal cancer proteins as needed. Alternatively, the variant may be designed or reorganized such that the biological activity of the metastatic colorectal cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of metastatic colorectal cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a metastatic colorectal cancer polypeptide with an

organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a metastatic colorectal cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking metastatic colorectal cancer polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-metastatic colorectal cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutamyl and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the γ -amino groups of lysine, arginine, and histidine side chains (Creighton, *Proteins: Structure and Molecular Properties*, pp. 79-86 (1983)), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the metastatic colorectal cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence metastatic colorectal cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express metastatic colorectal cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to metastatic colorectal cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence metastatic colorectal cancer polypeptide (for O-linked glycosylation sites). The metastatic colorectal cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the metastatic colorectal cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the metastatic colorectal cancer polypeptide is by chemical or enzymatic coupling of glycosides

to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin & Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

Removal of carbohydrate moieties present on the metastatic colorectal cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, *et al.*, *Arch. Biochem. Biophys.*, 259:52 (1987) and by Edge *et al.*, *Anal. Biochem.*, 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura *et al.*, *Meth. Enzymol.*, 138:350 (1987).

Another type of covalent modification of metastatic colorectal cancer comprises linking the metastatic colorectal cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

Metastatic colorectal cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a metastatic colorectal cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a metastatic colorectal cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the metastatic colorectal cancer polypeptide. The presence of such epitope-tagged forms of a metastatic colorectal cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the metastatic colorectal cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a metastatic colorectal cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field *et al.*, *Mol. Cell. Biol.* 8:2159-2165 (1988)); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto (Evan *et al.*, *Molecular and Cellular Biology* 5:3610-3616 (1985));

and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (*Paborsky et al., Protein Engineering* 3(6):547-553 (1990)). Other tag polypeptides include the Flag-peptide (*Hopp et al., BioTechnology* 6:1204-1210 (1988)); the KT3 epitope peptide (*Martin et al., Science* 255:192-194 (1992)); tubulin epitope peptide (*Skinner et al., J. Biol. Chem.* 266:15163-15166 (1991)); and the T7 gene 10 protein peptide tag (*Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA* 87:6393-6397 (1990)).

Also included are other metastatic colorectal cancer proteins of the metastatic colorectal cancer family, and metastatic colorectal cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related metastatic colorectal cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the metastatic colorectal cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction conditions are well known in the art (e.g., Innis, PCR Protocols, *supra*).

Antibodies to metastatic colorectal cancer proteins

In a preferred embodiment, when a metastatic colorectal cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the metastatic colorectal cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller metastatic colorectal cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, *supra*; and Harlow & Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1-26 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal

being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g., Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler & Milstein, *Nature* 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1-26, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, pp. 59-103 (1986)). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and primate origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of Tables 1-26 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to metastatic colorectal cancer protein are capable of reducing or eliminating a biological function of a metastatic colorectal cancer protein, as is described below. That is, the addition of anti-metastatic colorectal cancer protein antibodies (either polyclonal or preferably monoclonal) to metastatic colorectal cancer tissue (or cells containing metastatic colorectal cancer) may reduce or eliminate the metastatic colorectal cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the metastatic colorectal cancer proteins are humanized antibodies (e.g., Xenex Biosciences, Mederex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992)). Humanization can be essentially performed following the method of Winter and co-workers (Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-327 (1988); Verhoeyen *et al.*, *Science* 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact

human variable domain has been substituted by the corresponding sequence from a non-human species.

Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom & Winter, *J. Mol. Biol.* 227:381 (1991); Marks *et al.*, *J. Mol. Biol.* 222:581 (1991)). The techniques of Cole *et al.* and Boerner *et al.* are also available for the preparation of human monoclonal antibodies (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, p. 77 (1985) and Boerner *et al.*, *J. Immunol.* 147(1):86-95 (1991)). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in virtually all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, *Bio/Technology* 10:779-783 (1992); Lonberg *et al.*, *Nature* 368:856-859 (1994); Morrison, *Nature* 368:812-13 (1994); Fishwild *et al.*, *Nature Biotechnology* 14:845-51 (1996); Neuberger, *Nature Biotechnology* 14:826 (1996); Lonberg & Huszar, *Intern. Rev. Immunol.* 13:65-93 (1995).

By immunotherapy is meant treatment of metastatic colorectal cancer with an antibody raised against a metastatic colorectal cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the metastatic colorectal cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted metastatic colorectal cancer protein.

In another preferred embodiment, the metastatic colorectal cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory,

antibodies used for this treatment typically bind the extracellular domain of the metastatic colorectal cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane metastatic colorectal cancer protein. The antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the metastatic colorectal cancer protein. The antibody may be an antagonist of the metastatic colorectal cancer protein or may prevent activation of the transmembrane metastatic colorectal cancer protein. In some embodiments, when the antibody prevents the binding of other molecules to the metastatic colorectal cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, metastatic colorectal cancer is treated by administering to a patient antibodies directed against the transmembrane metastatic colorectal cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be any number of molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the metastatic colorectal cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the metastatic colorectal cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase activity associated with metastatic colorectal cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to metastatic colorectal cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with metastatic colorectal cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like.

Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against metastatic colorectal cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane metastatic colorectal cancer proteins not only serves to increase the local concentration of therapeutic moiety in the metastatic colorectal cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the metastatic colorectal cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the metastatic colorectal cancer protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

The metastatic colorectal cancer antibodies of the invention specifically bind to metastatic colorectal cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding is also important.

Detection of metastatic colorectal cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the metastatic colorectal cancer phenotype. Expression levels of genes in normal tissue (i.e., not undergoing metastatic colorectal cancer) and in metastatic colorectal cancer tissue (and in some cases, for varying severities of metastatic colorectal cancer that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state. While two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may

be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

“Differential expression,” or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus metastatic colorectal cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, *Nature Biotechnology* 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the metastatic colorectal cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to metastatic colorectal cancer genes, i.e., those identified as being important in a metastatic colorectal cancer phenotype, can be evaluated in a metastatic colorectal cancer diagnostic test.

In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

The metastatic colorectal cancer nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of metastatic colorectal cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In a preferred embodiment nucleic acids encoding the metastatic colorectal cancer protein are detected. Although DNA or RNA encoding the metastatic colorectal cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a metastatic colorectal cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a metastatic colorectal cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The metastatic colorectal cancer proteins, antibodies, nucleic acids, modified proteins and cells containing metastatic colorectal cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, metastatic colorectal cancer proteins, including intracellular, transmembrane or secreted proteins, find use as markers of metastatic colorectal cancer. Detection of these proteins in putative metastatic colorectal cancer tissue

allows for detection or diagnosis of metastatic colorectal cancer. In one embodiment, antibodies are used to detect metastatic colorectal cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the metastatic colorectal cancer protein is detected, e.g., by immunoblotting with antibodies raised against the metastatic colorectal cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the metastatic colorectal cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993)). In this method cells are contacted with from one to many antibodies to the metastatic colorectal cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the metastatic colorectal cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of metastatic colorectal cancer proteins. Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing metastatic colorectal cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of metastatic colorectal cancer proteins. Antibodies can be used to detect a metastatic colorectal cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous metastatic colorectal cancer protein or vaccine.

In a preferred embodiment, *in situ* hybridization of labeled metastatic colorectal cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue

samples, including metastatic colorectal cancer tissue and/or normal tissue, are made. *In situ* hybridization (*see, e.g., Ausubel, supra*) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the metastatic colorectal cancer proteins, antibodies, nucleic acids, modified proteins and cells containing metastatic colorectal cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to metastatic colorectal cancer, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, metastatic colorectal cancer probes may be attached to biochips for the detection and quantification of metastatic colorectal cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment members of the three classes of proteins as described herein are used in drug screening assays. The metastatic colorectal cancer proteins, antibodies, nucleic acids, modified proteins and cells containing metastatic colorectal cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (*e.g., Zlokarnik, et al., Science 279:84-8 (1998); Heid, Genome Res 6:986-94, 1996*).

In a preferred embodiment, the metastatic colorectal cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified metastatic colorectal cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the metastatic colorectal cancer phenotype or an identified physiological function of a metastatic colorectal cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput

screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

Having identified the differentially expressed genes herein, a variety of assays may be applied. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in metastatic colorectal cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the metastatic colorectal cancer protein. "Modulation" thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing metastatic colorectal cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in metastatic colorectal cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in metastatic colorectal cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the metastatic colorectal cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the metastatic colorectal cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of metastatic colorectal cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more metastatic colorectal cancer-associated sequences, e.g., a polynucleotide sequence set out in Tables 1-26. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate metastatic colorectal cancer, modulate metastatic colorectal

cancer proteins, bind to a metastatic colorectal cancer protein, or interfere with the binding of a metastatic colorectal cancer protein and an antibody, substrate, or other binding partner.

The term “test compound” or “drug candidate” or “modulator” or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the metastatic colorectal cancer phenotype or the expression of a metastatic colorectal cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a metastatic colorectal cancer phenotype, e.g., to a normal tissue fingerprint. In another embodiment, a modulator induces a metastatic colorectal cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a modulator will neutralize the effect of a metastatic colorectal cancer protein. By “neutralize” is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a metastatic colorectal cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a “lead compound”) with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such “combinatorial chemical libraries” are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional “lead compounds” or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical “building blocks” such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of

chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop *et al.*, *J. Med. Chem.* 37(9):1233-1251 (1994)).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.*, U.S. Patent No. 5,010,175, Furka, *Pept. Prot. Res.* 37:487-493 (1991), Houghton *et al.*, *Nature*, 354:84-88 (1991)), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *Proc. Nat. Acad. Sci. USA* 90:6909-6913 (1993)), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.* 114:6568 (1992)), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.* 114:9217-9218 (1992)), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.* 116:2661 (1994)), oligocarbamates (Cho, *et al.*, *Science* 261:1303 (1993)), and/or peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.* 59:658 (1994)). *See, generally*, Gordon *et al.*, *J. Med. Chem.* 37:1385 (1994), nucleic acid libraries (*see, e.g.*, Strategene, Corp.), peptide nucleic acid libraries (*see, e.g.*, U.S. Patent 5,539,083), antibody libraries (*see, e.g.*, Vaughn *et al.*, *Nature Biotechnology* 14(3):309-314 (1996), and PCT/US96/10287), carbohydrate libraries (*see, e.g.*, Liang *et al.*, *Science* 274:1520-1522 (1996), and U.S. Patent No. 5,593,853), and small organic molecule libraries (*see, e.g.*, benzodiazepines, Baum, C&EN, Jan 18, page 33 (1993); isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.*, 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual

synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the present invention. In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.*, ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect modulation of metastatic colorectal cancer gene transcription, polypeptide expression, and polypeptide activity.

High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, *e.g.*, U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (*i.e.*, in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (*see, e.g.*, Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, *e.g.*, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, *e.g.*, cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, *e.g.*, substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that the nucleic acid or peptide consists of essentially random sequences of nucleotides and amino acids, respectively. Since these random peptides (or nucleic acids, discussed below) are often chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc.

Modulators of metastatic colorectal cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After a candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence is analyzed. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

Nucleic acid assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the

assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the metastatic colorectal cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

Genes can be screened for those that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a metastatic colorectal cancer expression pattern leading to a normal expression pattern, or to modulate a single metastatic colorectal cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated metastatic colorectal cancer tissue reveals genes that are not expressed in normal tissue or metastatic colorectal cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for metastatic colorectal cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated metastatic colorectal cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of metastatic colorectal cancer cells, that have an associated metastatic colorectal cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral

construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., metastatic colorectal cancer tissue may be screened for agents that modulate, e.g., induce or suppress the metastatic colorectal cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on metastatic colorectal cancer activity. By defining such a signature for the metastatic colorectal cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

Measure of metastatic colorectal cancer polypeptide activity, or of metastatic colorectal cancer or the metastatic colorectal cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of metastatic colorectal cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian metastatic colorectal cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a colorectal cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the metastatic colorectal cancer polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively

binds to the metastatic colorectal cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using the metastatic colorectal cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "metastatic colorectal cancer proteins." The metastatic colorectal cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the metastatic colorectal cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a metastatic colorectal cancer protein and a candidate compound, and determining the binding of the compound to the metastatic colorectal cancer protein. Preferred embodiments utilize

the human metastatic colorectal cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative metastatic colorectal cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the metastatic colorectal cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the metastatic colorectal cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the metastatic colorectal cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the metastatic colorectal cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all

or a portion of the metastatic colorectal cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophore for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (i.e., a metastatic colorectal cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the metastatic colorectal cancer protein and thus is capable of binding to, and potentially modulating, the activity of the metastatic colorectal cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the metastatic colorectal cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the metastatic colorectal cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the metastatic colorectal cancer proteins. In this embodiment, the methods comprise combining a metastatic colorectal cancer protein and a competitor in a first sample. A second sample comprises a test compound, a metastatic colorectal cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the metastatic colorectal cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the metastatic colorectal cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native metastatic colorectal cancer protein, but cannot bind to modified metastatic colorectal cancer proteins. The structure of the metastatic colorectal cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a metastatic colorectal cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a metastatic colorectal cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising metastatic colorectal cancer proteins. Preferred cell types include almost any cell. The cells contain a

recombinant nucleic acid that encodes a metastatic colorectal cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate metastatic colorectal cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the metastatic colorectal cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting metastatic colorectal cancer cell division is provided. The method comprises administration of a metastatic colorectal cancer inhibitor. In another embodiment, a method of inhibiting metastatic colorectal cancer is provided. The method comprises administration of a metastatic colorectal cancer inhibitor. In a further embodiment, methods of treating cells or individuals with metastatic colorectal cancer are provided. The method comprises administration of a metastatic colorectal cancer inhibitor.

A variety of cell growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of metastatic colorectal cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney, *Culture of Animal Cells a Manual of Basic Technique* (3rd ed., 1994),

herein incorporated by reference. *See also*, the methods section of Garkavtsev *et al.* (1996), *supra*, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. *See* Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a metastatic colorectal cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. *See*, Freshney (1994), *supra*.

Growth factor or serum dependence

Transformed cells have a lower serum dependence than their normal counterparts (*see, e.g.,* Temin, *J. Natl. Cancer Inst.* 37:167-175 (1966); Eagle *et al.*, *J. Exp. Med.* 131:836-879 (1970)); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (*see, e.g.,* Gullino, *Angiogenesis, tumor vascularization, and potential interference with tumor growth*, in *Biological Responses in Cancer*, pp. 178-184 (Mihich (ed.) 1985)). Similarly, Tumor

angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. *See, e.g., Folkman, Angiogenesis and Cancer, Sem Cancer Biol. (1992)).*

Various techniques which measure the release of these factors are described in Freshney (1994), *supra*. Also, *see, Unkless et al., J. Biol. Chem. 249:4295-4305 (1974); Strickland & Beers, J. Biol. Chem. 251:5694-5702 (1976); Whur et al., Br. J. Cancer 42:305-312 (1980); Gullino, Angiogenesis, tumor vascularization, and potential interference with tumor growth. in Biological Responses in Cancer, pp. 178-184 (Mihich (ed.) 1985); Freshney Anticancer Res. 5:111-130 (1985).*

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate metastatic colorectal cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. *See, e.g., Freshney (1984), supra.*

Tumor growth in vivo

Effects of metastatic colorectal cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the metastatic colorectal cancer gene is disrupted or in which a metastatic colorectal cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous metastatic colorectal cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous metastatic colorectal cancer gene with a mutated version of the metastatic colorectal cancer gene, or by mutating the endogenous metastatic colorectal cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (*see, e.g., Capecchi et al., Science* 244:1288 (1989)). Chimeric targeted mice can be derived according to Hogan *et al., Manipulating the Mouse Embryo: A Laboratory Manual*, Cold Spring Harbor Laboratory (1988) and *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, Robertson, ed., IRL Press, Washington, D.C., (1987).

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (*see, e.g., Giovanella et al., J. Natl. Cancer Inst.* 52:921 (1974)), a SCID mouse, a thymectomized mouse, or an irradiated mouse (*see, e.g., Bradley et al., Br. J. Cancer* 38:263 (1978); Selby *et al., Br. J. Cancer* 41:52 (1980)) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a metastatic colorectal cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (*e.g., by volume or by its two largest dimensions*) and compared to the control. Tumors that have statistically significant reduction (using, *e.g., Student's T test*) are said to have inhibited growth. Additionally, human tumor cells expressing the genes of the invention may be injected into immune compromised animals. Growth of these tumors, or xenografts, is compared to growth of similar human tumor cell that do not express the genes of the invention. These animals may also be used to binding assays and efficacy studies for therapeutic compounds that modulate metastatic colorectal cancer, such as antibodies or small molecules.

Polynucleotide modulators of metastatic colorectal cancer

Antisense Polynucleotides

In certain embodiments, the activity of a metastatic colorectal cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense polynucleotide, *i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a metastatic colorectal cancer*

protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the metastatic colorectal cancer protein mRNA. *See, e.g.*, Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, *e.g.*, be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for metastatic colorectal cancer molecules. A preferred antisense molecule is for a metastatic colorectal cancer sequence in Tables 1-26, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, *e.g.*, Stein & Cohen (*Cancer Res.* 48:2659 (1988) and van der Krol *et al.* (*BioTechniques* 6:958 (1988)).

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of metastatic colorectal cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (*see, e.g.*, Castanotto *et al.*,

Adv. in Pharmacology 25: 289-317 (1994) for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel *et al.*, *Nucl. Acids Res.* 18:299-304 (1990); European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (*see, e.g.*, WO 94/26877; Ojwang *et al.*, *Proc. Natl. Acad. Sci. USA* 90:6340-6344 (1993); Yamada *et al.*, *Human Gene Therapy* 1:39-45 (1994); Leavitt *et al.*, *Proc. Natl. Acad. Sci. USA* 92:699-703 (1995); Leavitt *et al.*, *Human Gene Therapy* 5:1151-120 (1994); and Yamada *et al.*, *Virology* 205: 121-126 (1994)).

Polynucleotide modulators of metastatic colorectal cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of metastatic colorectal cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating metastatic colorectal cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-metastatic colorectal cancer antibody that reduces or eliminates the biological activity of an endogenous metastatic colorectal cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a metastatic colorectal cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the metastatic colorectal cancer sequence is down-regulated in metastatic colorectal cancer, such state may be reversed by increasing the amount of metastatic colorectal cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous metastatic colorectal cancer gene or administering a gene encoding the metastatic colorectal cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the

incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety.

Alternatively, e.g., when the metastatic colorectal cancer sequence is up-regulated in metastatic colorectal cancer, the activity of the endogenous metastatic colorectal cancer gene is decreased, e.g., by the administration of a metastatic colorectal cancer antisense nucleic acid.

In one embodiment, the metastatic colorectal cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to metastatic colorectal cancer proteins. Similarly, the metastatic colorectal cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify metastatic colorectal cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a metastatic colorectal cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The metastatic colorectal cancer antibodies may be coupled to standard affinity chromatography columns and used to purify metastatic colorectal cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the metastatic colorectal cancer protein.

Methods of identifying variant metastatic colorectal cancer-associated sequences

Without being bound by theory, expression of various metastatic colorectal cancer sequences is correlated with metastatic colorectal cancer. Accordingly, disorders based on mutant or variant metastatic colorectal cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant metastatic colorectal cancer genes, e.g., determining all or part of the sequence of at least one endogenous metastatic colorectal cancer genes in a cell. This may be accomplished using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the metastatic colorectal cancer genotype of an individual, e.g., determining all or part of the sequence of at least one metastatic colorectal cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced metastatic colorectal cancer gene to a known metastatic colorectal cancer gene, i.e., a wild-type gene.

The sequence of all or part of the metastatic colorectal cancer gene can then be compared to the sequence of a known metastatic colorectal cancer gene to determine if any

differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the metastatic colorectal cancer gene of the patient and the known metastatic colorectal cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the metastatic colorectal cancer genes are used as probes to determine the number of copies of the metastatic colorectal cancer gene in the genome.

In another preferred embodiment, the metastatic colorectal cancer genes are used as probes to determine the chromosomal localization of the metastatic colorectal cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the metastatic colorectal cancer gene locus.

Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a metastatic colorectal cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel *et al.*, *Pharmaceutical Dosage Forms and Drug Delivery*; Lieberman, *Pharmaceutical Dosage Forms* (vols. 1-3, 1992), Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd, *The Art, Science and Technology of Pharmaceutical Compounding* (1999); and Pickar, *Dosage Calculations* (1999)). As is known in the art, adjustments for metastatic colorectal cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the metastatic colorectal cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above,

including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the metastatic colorectal cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a metastatic colorectal cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that metastatic colorectal cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. It is also recognized that, after delivery to other

sites in the body (e.g., circulatory system, lymphatic system, or the tumor site) the metastatic colorectal cancer modulators of the invention may need to be protected from excretion, hydrolysis, proteolytic digestion or modification, or detoxification by the liver. In all these cases, protection is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier or by modifying the molecular size, weight, and/or charge of the modulator. Means of protecting agents from digestion degradation, and excretion are well known in the art.

The compositions for administration will commonly comprise a metastatic colorectal cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., *Remington's Pharmaceutical Science* (15th ed., 1980) and Goodman & Gillman, *The Pharmacological Basis of Therapeutics* (Hardman *et al.*, eds., 1996)).

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, e.g., *Remington's Pharmaceutical Science* and Goodman and Gillman, *The Pharmacological Basis of Therapeutics*, *supra*.

The compositions containing modulators of metastatic colorectal cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its

complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer.

It will be appreciated that the present metastatic colorectal cancer protein-modulating compounds can be administered alone or in combination with additional metastatic colorectal cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in Tables 1-26, such as antisense polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of metastatic colorectal cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo* or *in vivo* (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.,* Berger & Kimmel, *Guide to Molecular Cloning Techniques, Methods in Enzymology* volume 152 (Berger), Ausubel *et al.*, eds., *Current Protocols* (supplemented through 1999), and Sambrook *et al.*, *Molecular Cloning - A Laboratory Manual* (2nd ed., Vol. 1-3, 1989).

In a preferred embodiment, metastatic colorectal cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above.

Similarly, metastatic colorectal cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the metastatic colorectal cancer coding regions) can be administered in a gene therapy application. These metastatic colorectal cancer genes can include antisense applications, either as gene therapy (i.e., for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

Metastatic colorectal cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (*see, e.g., Vitiello, et al., J. Clin. Invest.* 95:341 (1995)), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (*see, e.g., Eldridge, et al., Molec. Immunol.* 28:287-294, (1991); Alonso *et al., Vaccine* 12:299-306 (1994); Jones *et al., Vaccine* 13:675-681 (1995)), peptide compositions contained in immune stimulating complexes (ISCOMS) (*see, e.g., Takahashi et al., Nature* 344:873-875 (1990); Hu *et al., Clin Exp Immunol.* 113:235-243 (1998)), multiple antigen peptide systems (MAPs) (*see, e.g., Tam, Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413 (1988); Tam, *J. Immunol. Methods* 196:17-32 (1996)), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, *et al., In: Concepts in vaccine development* (Kaufmann, ed., p. 379, 1996); Chakrabarti, *et al., Nature* 320:535 (1986); Hu *et al., Nature* 320:537 (1986); Kieny, *et al., AIDS Bio/Technology* 4:790 (1986); Top *et al., J. Infect. Dis.* 124:148 (1971); Chanda *et al., Virology* 175:535 (1990)), particles of viral or synthetic origin (*see, e.g., Kofler et al., J. Immunol. Methods.* 192:25 (1996); Eldridge *et al., Sem. Hematol.* 30:16 (1993); Falo *et al., Nature Med.* 7:649 (1995)), adjuvants (Warren *et al., Annu. Rev. Immunol.* 4:369 (1986); Gupta *et al., Vaccine* 11:293 (1993)), liposomes (Reddy *et al., J. Immunol.* 148:1585 (1992); Rock, *Immunol. Today* 17:131 (1996)), or, naked or particle absorbed cDNA (Ulmer, *et al., Science* 259:1745 (1993); Robinson *et al., Vaccine* 11:957 (1993); Shiver *et al., In: Concepts in vaccine development* (Kaufmann, ed., p. 423, 1996); Cease & Berzofsky, *Annu. Rev. Immunol.* 12:923 (1994) and Eldridge *et al., Sem. Hematol.* 30:16 (1993)). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit,

MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff *et al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, *e.g.*, as a vector to express nucleotide sequences that encode metastatic colorectal cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization *e.g.*, adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein (*see, e.g.*, Shata *et al.*, *Mol Med Today* 6:66-71 (2000); Shedlock *et al.*, *J Leukoc Biol* 68:793-806 (2000); Hipp *et al.*, *In Vivo* 14:571-85 (2000)).

Methods for the use of genes as DNA vaccines are well known, and include placing a metastatic colorectal cancer gene or portion of a metastatic colorectal cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a metastatic colorectal cancer patient. The metastatic colorectal cancer gene used for DNA vaccines can encode full-length metastatic colorectal cancer proteins, but more preferably

encodes portions of the metastatic colorectal cancer proteins including peptides derived from the metastatic colorectal cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a metastatic colorectal cancer gene. For example, metastatic colorectal cancer-associated genes or sequence encoding subfragments of a metastatic colorectal cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the metastatic colorectal cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment metastatic colorectal cancer genes find use in generating animal models of metastatic colorectal cancer. When the metastatic colorectal cancer gene identified is repressed or diminished in metastatic tissue, gene therapy technology, e.g., wherein antisense RNA directed to the metastatic colorectal cancer gene will also diminish or repress expression of the gene. Animal models of metastatic colorectal cancer find use in screening for modulators of a metastatic colorectal cancer-associated sequence or modulators of metastatic colorectal cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the metastatic colorectal cancer protein. When desired, tissue-specific expression or knockout of the metastatic colorectal cancer protein may be necessary.

It is also possible that the metastatic colorectal cancer protein is overexpressed in metastatic colorectal cancer. As such, transgenic animals can be generated that overexpress the metastatic colorectal cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of metastatic colorectal cancer and are additionally useful in screening for modulators to treat metastatic colorectal cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include any or all of the following: assay reagents, buffers, metastatic colorectal cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative metastatic colorectal cancer polypeptides or polynucleotides, small molecules inhibitors of metastatic colorectal cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (i.e., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. Any medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of metastatic colorectal cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a metastatic colorectal cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing metastatic colorectal cancer-associated activity. Optionally, the kit contains biologically active metastatic colorectal cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

Table 1

Pkey: Unique Eos probeset identifier number ExAccn: Exemplar Accession number, Genbank accession number UnigeneID: Unigene number Unigene Title: Unigene gene title					
Pkey	ExAccn	UnigeneID	Unigene Title	Ratio BS_Mets	Top 3 expressing cell lines
103989	AA314779	Hs.105484	ESTs; Weakly similar to LITHOSTATHINE 1	15.77	EB_cells, HT29_cells, HMEC
101169	L15533	Hs.423	pancreatitis-associated protein	11.98	HMEC (total RNA), Fibroblasts 2, Fibroblasts 2
101880	M97925	Hs.72887	defensin; alpha 5; Paneth cell-specific	9.24	Fibroblasts 2, MB231_cells, MB-MDA-453
129462	D84239	Hs.111732	IgG Fc binding protein	8.57	EB_cells, OVCAR_cells, HS578T_cells
131676	C20785	Hs.30514	ESTs	7.43	HMEC (total RNA), HMEC, Fibroblasts 2
131861	D11925	Hs.184245	KIAA0929 protein Msx2 interacting nuclea	7.15	HMEC, HMEC (total RNA), Fibroblasts 2
118823	N79237	Hs.50813	ESTs; Weakly similar to long chain fatty	6.72	HMEC, HMEC (total RNA), Lu_AD_H23
101107	L08010	Hs.4158	regenerating islet-derived 1 beta (pancr	6.33	BT474_cells, Fibroblasts 2, MB231_cells
103466	Y00339	Hs.155097	carbonic anhydrase II	6.18	OVCAR_cells, MCF7, 293T_cells
102306	U33317	Hs.711	defensin; alpha 6; Paneth cell-specific	5.67	Fibroblasts 2, HMEC, HT29_cells
126419	AA451775	Hs.129084	H sapiens chromosome 19; cosmid F22162	5.14	HS578T_cells, HMEC (total RNA), HMEC
101198	L21998	Hs.315	mucin 2; intestinal/tracheal	5.1	EB_cells, HT29_cells, MB231_cells
107652	AA010195	Hs.52642	ESTs; Weakly similar to IIII ALU CLASS F	4.94	HMEC (total RNA), HMEC, EB_cells
128145	AI498467	Hs.166669	ESTs; Weakly similar to sodium bicarbona	4.77	HS578T_cells, HMEC, Lu_SQ_H520
110660	H82117	Hs.28043	ESTs	4.54	HMEC, HS578T_cells, BT474_cells
111669	R19305	Hs.110347	H sapiens mRNA for alpha Integrin bindin	4.52	HMEC, HS578T_cells, Caco2
124867	R68971	Hs.168500	ESTs	4.5	HMEC, HMEC (total RNA), HS578T_cells
127352	AA416577	Hs.189105	ESTs	4.41	HMEC, HMEC (total RNA), MB-MDA-435s
130736	T99385	Hs.18646	EST	4.29	HMEC, EB_cells, HMEC (total RNA)
128592	AA470056	Hs.113994	ESTs; Weakly similar to alternatively sp	4.18	HMEC (total RNA), HMEC, Fibroblasts 2
108092	AA045961	Hs.169355	ESTs; Weakly similar to TRANSCRIPTION RE	4.03	4.04 HMEC (total RNA), HMEC, Fibroblasts 2
133373	S72487	Hs.73946	endothelial cell growth factor 1 (plate)	4.03	EB_cells, HMEC, HMEC (total RNA)
100572	HG2271		Profilaggrin	4.03	HMEC (total RNA), HMEC, Fibroblasts 2
115775	AA424030	Hs.46627	ESTs	4.02	HMEC, HMEC (total RNA), EB_cells
120811	AA346854	Hs.52788	fragile X mental retardation; autosomal	4.01	HMEC (total RNA), HMEC, Fibroblasts 2
111919	R39926	Hs.21031	ESTs	3.98	EB_cells, HMEC (total RNA), HMEC
117009	H85422	Hs.108556	ESTs	3.97	HMEC (total RNA), HMEC, Fibroblasts 2
101124	L10343	Hs.112341	protease inhibitor 3; skin-derived (SKAL	3.89	PC3_cells, RPWE_2, Caco2
106151	AA424958	Hs.33735	ESTs	3.88	EB_cells, HMEC, HMEC (total RNA)
134733	U03644	Hs.89421	CBF1 interacting corepressor	3.88	EB_cells, HMEC, HMEC (total RNA)
131739	AA449749	Hs.31386	ESTs; Highly similar to secreted apoptos	3.87	HS578T_cells, MB-MDA-435s, HT29_cells
116311	AA490469	Hs.48752	ESTs	3.84	HS578T_cells, HMEC, LNCaP_cells
134174	U05259	Hs.79630	CD79A antigen (immunoglobulin-associated	3.83	DU145_cells, Lu_AD_H23, MB231_cells
106753	AA476944	Hs.7331	ESTs	3.82	LNCaP_cells, Lu_SC_H345, DU145_cells
104842	AA039854	Hs.8065	H sapiens mRNA full length insert cDNA c	3.78	HS578T_cells, A549_cells, CALU6_cells
129161	N27334	Hs.181780	ESTs	3.75	HMEC (total RNA), HMEC, BT474_cells
105675	AA284767	Hs.252808	ESTs; Highly similar to pulmonary surfac	3.75	293T_cells, PRSC_con, HT29_cells
100547	HG2149		Mucin (Gb:M57417)	3.75	HMEC (total RNA), HMEC, Fibroblasts 2
116857	H65841	Hs.186550	ESTs	3.73	HS578T_cells, 293T_cells, HMEC
113222	T59670	Hs.10615	ESTs	3.7	HMEC, HS578T_cells, Caco2
118768	N74467	Hs.94304	EST	3.68	HMEC, HS578T_cells, OVCAR_cells
114542	AA055768	Hs.122576	ESTs	3.66	EB_cells, MCF7, LNCaP_cells
101640	M58459	Hs.180911	ribosomal protein S4; Y-linked	3.62	DU145_cells, RPWE_2, A549_cells
107754	AA017462	Hs.187571	ESTs	3.6	HMEC (total RNA), Fibroblasts 2, Fibroblasts 2
104668	AA007312	Hs.183852	ESTs; Weakly similar to polymerase (H.sa	3.58	HMEC (total RNA), HMEC, Fibroblasts 2
135377	C21382	Hs.99766	H sapiens mRNA; cDNA DKFZp564J0323 (from	3.53	3.56 HMEC, HMEC (total RNA), EB_cells
127083	Z44079	Hs.91608	otoferlin	3.53	HMEC (total RNA), HMEC, Fibroblasts 2
102329	U35407	Hs.158084	peroxisome receptor 1	3.51	HMEC, HMEC (total RNA), EB_cells
117882	N50101	Hs.124724	ESTs; Weakly similar to coded for by C.	3.47	HMEC (total RNA), HMEC, EB_cells
126405	U46278	Hs.122489	ESTs	3.46	LNCaP_cells, MCF7, DU145_cells
131378	AA463886	Hs.203910	small glutamine-rich tetratricopeptide r	3.45	EB_cells, HMEC, HMEC (total RNA)
111418	R01084	Hs.19081	ESTs	3.43	HS578T_cells, EB_cells, Lu_AD_H23
135398	AA194075	Hs.99908	nuclear receptor coactivator 4	3.4	HS578T_cells, EB_cells, HMEC
108710	AA121960		zm24g9.s1 Stratagene pancreas (#93728) H mRNA seq	3.4	EB_cells, HMEC, HMEC (total RNA)
105437	AA252191	Hs.25199	ESTs; Highly similar to match to ESTs AA	3.38	EB_cells, LNCaP_cells, RPWE_2
103448	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	3.38	PC3_cells, EB_cells, HT29_cells
130436	M84526	Hs.155597	D component of complement (adipsin)	3.37	PRSC_con, EB_cells, Lu_AD_H23
112309	R55021		yj76d5.s1 Soares breast 2NbHBst H sapien	3.36	EB_cells, HMEC, HMEC (total RNA)
103211	X73079	Hs.205126	polymeric immunoglobulin receptor	3.35	MB231_cells, HT29_cells, Lu_SC_H69
109012	AA156576	Hs.191466	ESTs	3.21	EB_cells, HMEC, HMEC (total RNA)
129989	AF005887	Hs.247433	activating transcription factor 6	3.19	HMEC (total RNA), HMEC, Lu_AD_H23
113466	T86945	Hs.16304	ESTs	3.18	HMEC, MB231_cells, Caco2
103029	X54489	Hs.789	GRO1 oncogene (melanoma growth stimulat	3.16	Lu_LC_H460, PC3_cells, Fibroblasts 2

109374	AA218727	Hs.210785	ESTs; Highly similar to lbd1 [H.sapiens]	3.13	Caco2, A549_cells, MB231_cells
131403	R55750	Hs.26455	ESTs	3.13	HS578T_cells, HMEC, MB231_cells
113420	T83964	Hs.15400	ESTs	3.11	HMEC (total RNA), HMEC, EB_cells
112532	R69824	Hs.28313	ESTs	3.11	HMEC, HMEC (total RNA), EB_cells
117905	N50782	Hs.231713	EST	3.11	HMEC, HS578T_cells, Caco2
125349	T87826	Hs.164480	ESTs	3.1	HS578T_cells, EB_cells, MB-MDA-435s
107072	AA609113	Hs.177533	H sapiens mRNA; cDNA DKFZp586N0318 (from	3.1	Lu_SC_H69, MB-MDA-453, MB231_cells
118389	N64583	Hs.182385	ESTs	3.05	HMEC, HMEC, LNCaP_cells
117653	N38970	Hs.194214	ESTs	3.04	HMEC, HMEC (total RNA), Fibroblasts 2
101082	L05072	Hs.80645	interferon regulatory factor 1	3.04	EB_cells, PRSC_con, DU145_cells
126105	H75323	Hs.167614	ESTs	3.03	HS578T_cells, HMEC (total RNA), HMEC
120006	W90108	Hs.10848	KIAA0187 gene product	3.03	HMEC, HMEC (total RNA), EB_cells
127191	AA297581		EST113160 Gall bladder I H sapiens cDNA	3.02	HMEC, Lu_AD_H23, Lu_SC_H520
106899	AA490107	Hs.21753	JM5 protein	3.02	EB_cells, HMEC (total RNA), HMEC
112784	R96306	Hs.191290	ESTs	3.02	EB_cells, HMEC, Lu_AD_358
113613	T93337	Hs.17167	ESTs; Highly similar to LRR FLH intera	3.02	HMEC (total RNA), EB_cells, HMEC
107631	AA007230	Hs.95026	ESTs	3.02	Lu_SC_H345, HS578T_cells, Lu_LC_H460
101923	S75256		HNL=neutrophil lipocalin [human, ovarian	3.01	PC3_cells, EB_cells, HT29_cells
100695	HG315T		Beta-1-Glycoprotein 11, Pregnancy-Specif	3.01	Fibroblasts 2, Lu_AD_H23, MB-MDA-435s
102523	U53445	Hs.15432	downregulated in ovarian cancer 1	2.98	PRSC_con, Fibroblasts 2, HMEC
121588	AA416615	Hs.98242	ESTs	2.94	HMEC, HS578T_cells, BT474_cells
103714	AA047055	Hs.192943	ESTs	2.94	HS578T_cells, EB_cells, HMEC
104916	AA056588	Hs.16542	ESTs	2.93	HMEC (total RNA), Fibroblasts 2, HMEC
109928	H05961	Hs.26331	ESTs	2.92	HMEC, MB231_cells, HS578T_cells
104586	R78309	Hs.20787	ESTs	2.92	Caco2, Lu_AD_358, Lu_AD_358
101236	L29433	Hs.47913	coagulation factor X	2.91	HMEC, HS578T_cells, Caco2
134749	L10955	Hs.89485	carbonic anhydrase IV	2.9	BT474_cells, MCF7, HMEC (total RNA)
124703	R07294	Hs.109108	solute carrier family 22 (organic cation	2.9	HMEC, HMEC (total RNA), MB-MDA-435s
114108	Z38431	Hs.27038	ESTs; Moderately similar to X-linked ret	2.89	HMEC, HMEC (total RNA), EB_cells
107857	AA024687	Hs.61208	ESTs	2.88	HS578T_cells, MB231_cells, HMEC
111586	R10759	Hs.15177	ESTs	2.88	HS578T_cells, Lu_LC_H460, PRSC_con
127553	AA282433		H sapiens p80 katanin mRNA; complete cds	2.87	EB_cells, MB-MDA-435s, RPWE_2
129881	AA458952	Hs.197728	ESTs; Weakly similar to ZINC FINGER PROT	2.86	EB_cells, PC3_cells, HMEC
116852	H65459	Hs.38323	ESTs	2.85	HMEC, Caco2, HS578T_cells
133468	X03068	Hs.73931	major histocompatibility complex; class	2.82	MB-MDA-435s, BT474_cells, HT29_cells
130998	C00810	Hs.21970	guanine nucleotide binding protein (G pr	2.82	LNCaP_cells, Lu_SC_H345, EB_cells
124075	H05741	Hs.101643	ESTs	2.82	HMEC, HS578T_cells, HT29_cells
128108	AI247422	Hs.129966	ESTs	2.82	HS578T_cells, Lu_LC_H460, Lu_SC_H69
128096	R15413	Hs.164919	ESTs; Highly similar to PROTEIN KINASE C	2.8	MB231_cells, Lu_AD_H23, RPWE_2
126619	Z28861		HSBA7E032 STRATAGENE Human skeletal musc	2.77	HMEC, Lu_AD_H23, HMEC (total RNA)
			cDNA clone A7E03, mRNA seq.	2.77	HS578T_cells, EB_cells, MCF7
114418	AA011383	Hs.177313	ESTs	2.77	EB_cells, Fibroblasts 2, HMEC (total RNA)
120383	AA228030	Hs.120234	ESTs	2.77	Fibroblasts 2, PRSC_con, DU145_cells
126535	H73017	Hs.250723	ESTs; Weakly similar to atrophin-1 relat	2.76	EB_cells, Lu_AD_H23, Lu_SC_H69
119347	T64349		yc10d08.s1 Stratagene lung (#937210) H s	2.76	Lu_AD_H23, HMEC (total RNA), MB-MDA-435s
126219	N36368	Hs.141438	ESTs; Moderately similar to similar to C	2.76	2.75 HMEC, HMEC (total RNA), Lu_SC_H69
125426	R43963	Hs.169355	ESTs; Weakly similar to TRANSCRIPTION RE	2.74	HS578T_cells, HMEC, MB-MDA-453
103005	X52008	Hs.2700	glycine receptor; alpha 2	2.74	Fibroblasts 2, HMEC (total RNA), MB-MDA-435s
109170	AA180352	Hs.191472	ESTs	2.74	Lu_LC_H460, 293T_cells, EB_cells
101125	L10373	Hs.82749	transmembrane 4 superfamily member 2	2.73	HMEC (total RNA), HMEC, Fibroblasts 2
130656	Z20481	Hs.17411	KIAA0699 protein	2.73	HMEC, EB_cells, HMEC (total RNA)
122933	AA476728	Hs.107537	ESTs	2.72	2.71 Lu_SC_H345, Lu_SC_H69, 293T_cells
126033	AA055978	Hs.3807	ESTs; Weakly similar to PHOSPHOLEMMAN PR	2.71	EB_cells, HMEC, HMEC (total RNA)
111644	R16539	Hs.223649	EST; Moderately similar to Cd-7 Metallo	2.71	Caco2, Fibroblasts 2, MB-MDA-435s
133719	AA033790	Hs.75736	apolipoprotein D	2.71	HMEC, HS578T_cells, HMEC (total RNA)
127555	AA582324	Hs.192857	ESTs	2.7	HMEC (total RNA), Fibroblasts 2, PRSC_con
113321	T70580	Hs.13759	ESTs	2.69	MB-MDA-435s, HS578T_cells, Lu_SC_H69
109326	AA210719	Hs.86414	ESTs	2.68	HS578T_cells, EB_cells, PRSC_con
135003	H42527	Hs.92832	ESTs	2.68	HMEC, HS578T_cells, PRSC_con
103650	Z70220		H.sapiens mRNA for 5'UTR for unknown pro	2.68	HMEC (total RNA), HMEC, EB_cells
111507	R07728	Hs.191218	ESTs	2.67	HS578T_cells, HMEC, MB231_cells
117084	H93081	Hs.41829	ESTs	2.67	DU145_cells, HS578T_cells, MB-MDA-435s
103975	AA306264	Hs.176403	ESTs; Moderately similar to !!!! ALU SUB	2.67	HS578T_cells, EB_cells, 293T_cells
132850	R89741	Hs.58215	ESTs; Moderately similar to rhotekin [M.	2.66	HMEC (total RNA), HMEC, EB_cells
121599	AA416770	Hs.98255	EST	2.61	HMEC (total RNA), HMEC, Fibroblasts 2
124230	H63111	Hs.6655	ESTs	2.6	Caco2, MB-MDA-453, A549_cells
114174	Z39055	Hs.27264	ESTs; Moderately similar to !!!! ALU SUB	2.58	Lu_LC_H460, Lu_SC_H69, MB-MDA-435s
128469	T23724	Hs.258677	EST	2.57	HMEC, HMEC (total RNA), EB_cells
117399	N26480	Hs.43805	lipoma HMGIC fusion partner-like 3	2.57	HS578T_cells, EB_cells, HT29_cells
129279	AA460551	Hs.184860	ESTs; Weakly similar to EG:87B1.6 [D.mel	2.57	HMEC, HMEC (total RNA), Lu_SC_H69
119817	W74257	Hs.159690	ESTs	2.57	HMEC, HT29_cells, Lu_LC_H460
114445	AA019594	Hs.250493	ESTs; Weakly similar to KIAA0390 [H.sapi	2.56	HMEC, HMEC (total RNA), Fibroblasts 2
120651	AA287286	Hs.99657	ESTs	2.55	HMEC (total RNA), EB_cells, BT474_cells
105707	AA291012	Hs.37617	ESTs; Weakly similar to KIAA0727 protein	2.55	HMEC, HS578T_cells, MB231_cells
128483	T58588	Hs.5148	FLN29 gene product	2.54	2.54 HMEC (total RNA), HMEC, OVCAR_cells
125890	AA448739	Hs.116708	ESTs; Weakly similar to HYPOTHETICAL PRO		

134764	M74715	Hs.89560	Iduronidase; alpha-L-	2.54	BT474_cells, PRSC_con, HT29_cells
113404	T82323	Hs.70337	Immunoglobulin superfamily, member 4	2.54	Caco2, HS578T_cells, HMEC
129128	AA423854	Hs.108812	ESTs	2.54	BT474_cells, MB-MDA-435s, HMEC
101428	M19684	Hs.184929	protease inhibitor 1 (alpha-1-antitrypsin)	2.54	HMEC, HT29_cells, HMEC (total RNA)
103206	X72755	Hs.77367	monokine induced by gamma interferon	2.53	Fibroblasts 2, MB231_cells, HMEC (total RNA)
132273	AA489716	Hs.43658	DKFZP586L151 protein	2.53	EB_cells, HMEC, HMEC (total RNA)
108392	AA075124		zm86a1.s1 Stratagene ovarian cancer (#93 IMAGE:544776 3', mRNA seq	2.52	HMEC (total RNA), HMEC, HS578T_cells
119508	W37895	Hs.45519	ESTs	2.52	Lu_SC_H69, CALU6_cells, 293T_cells
109828	F13763	Hs.19827	ESTs	2.52	PRSC_log, PRSC_con, HS578T_cells
135096	N89775	Hs.132390	zinc finger protein 36 (KOX 18)	2.51	HMEC, HS578T_cells, HT29_cells
130860	U66061	Hs.241395	protease; serine; 1 (trypsin 1)	2.51	OVCAR_cells, MB231_cells, PC3_cells
105725	AA292228	Hs.199791	STAT induced STAT inhibitor 3	2.51	HS578T_cells, HT29_cells, HMEC
110427	H48579	Hs.36275	EST	2.51	HS578T_cells, Caco2, Lu_LC_H460
123762	AA610013	Hs.244553	EST	2.51	HMEC (total RNA), HMEC, Fibroblasts 2
126406	AA034096		zi06f05.r1 Soares_fetal_liver_spleen_1NF IMAGE:430017 5', mRNA seq.	2.5	Lu_AD_H23, HS578T_cells, Lu_AD_358
129751	AA346065	Hs.111286	KIAA0714 protein	2.5	HMEC, HS578T_cells, Fibroblasts 2
121704	AA418743	Hs.98306	ESTs	2.5	EB_cells, HMEC (total RNA), HMEC
112595	R77783	Hs.22404	protease; serine; 12 (neutrypsin; moto	2.5	Fibroblasts 2, EB_cells, PRSC_con
108499	AA083103		zn1b12.s1 Stratagene hNT neuron (#937233 IMAGE:5477 3', mRNA seq	2.5	LNCaP_cells, MB-MDA-453, HMEC
131968	AA151333	Hs.36029	ESTs; Highly similar to basic helix-loop	2.5	Fibroblasts 2, A549_cells, 293T_cells
112665	R85661	Hs.221447	ESTs	2.48	Lu_AD_H23, HMEC, Lu_LC_H460
115764	AA421562	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	2.48	EB_cells, Caco2, MCF7
105959	AA405540	Hs.7001	ESTs	2.48	OVCAR_cells, BT474_cells, Caco2
125804	R79519	Hs.16899	ESTs	2.48	HMEC (total RNA), EB_cells, HMEC
110102	H16681	Hs.180950	guanine nucleotide binding protein (G pr	2.46	HS578T_cells, HMEC, OVCAR_cells
104680	AA009809	Hs.37599	ESTs	2.46	HMEC, HS578T_cells, Caco2
132339	D80030	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	2.45	OVCAR_cells, 293T_cells, HMEC (total RNA)
121712	AA419116	Hs.193663	ESTs; Weakly similar to IIII ALU SUBFAMI	2.45	Lu_SC_H520, Lu_AD_H23, Lu_SC_H69
129226	M96843	Hs.180919	inhibitor of DNA binding 2; dominant neg	2.44	MB-MDA-453, 293T_cells, Caco2
128731	AF005271	Hs.104555	neuropeptide FF-amide peptide precursor	2.43	HMEC, HMEC (total RNA), EB_cells
106670	AA461174	Hs.5943	ESTs	2.43	EB_cells, HS578T_cells, Lu_SC_H69
119306	T26914	Hs.132785	EAP30 subunit of ELL complex	2.43	EB_cells, HMEC (total RNA), HMEC
133507	X74295	Hs.74369	integrin; alpha 7	2.42	Fibroblasts 2, Caco2, EB_cells
125713	AA367905	Hs.77356	transferrin receptor (p90; CD71)	2.41	HS578T_cells, Fibroblasts 2, Lu_AD_H23
107438	W27841	Hs.17118	ESTs; Weakly similar to B0025.2 [C.elega	2.41	HMEC, HS578T_cells, MB231_cells
101784	M83186	Hs.114346	cytochrome c oxidase subunit VIIa polype	2.41	Fibroblasts 2, PRSC_con, PRSC_log
134578	AA194724	Hs.182418	endonuclease G	2.4	EB_cells, HMEC, Lu_AD_H23
125105	T95642	Hs.189759	ESTs	2.4	EB_cells, A549_cells, HS578T_cells
127087	AA380418	Hs.88012	SHP2 interacting transmembrane adaptor	2.4	HMEC, HMEC (total RNA), EB_cells
113118	T47906	Hs.220512	ESTs	2.39	MB-MDA-435s, HS578T_cells, HMEC
104791	AA029046	Hs.30377	ESTs; Moderately similar to cAMP inducib	2.39	LNCaP_cells, OVCAR_cells, PC3_cells
115833	AA428269	Hs.125035	ESTs	2.38	Caco2, LNCaP_cells, CALU6_cells
132223	R77451	Hs.4245	ESTs; Weakly similar to similar to S. ce	2.38	HMEC, HMEC (total RNA), EB_cells
115836	AA428863	Hs.89388	ESTs	2.38	HS578T_cells, HMEC, PRSC_con
101891	S45630	Hs.1940	crystallin; alpha B	2.38	HS578T_cells, OVCAR_cells, Lu_LC_H460
132894	D82422	Hs.5944	ESTs	2.37	Caco2, MB-MDA-453, HT29_cells
106939	AA496048	Hs.26570	ESTs	2.35	LNCaP_cells, 293T_cells, EB_cells
131104	W27770	Hs.258721	ESTs	2.35	HMEC (total RNA), HMEC, HT29_cells
122355	AA443789	Hs.189324	ESTs	2.34	HMEC (total RNA), HMEC, EB_cells
119343	T62873		yc3d2.s1 Stratagene lung (#93721) H sapi	2.34	HS578T_cells, Lu_SC_H69, HT29_cells
			to contains Alu repetitive element; mR	2.34	Lu_AD_H23, HMEC (total RNA), BT474_cells
115442	AA284722	Hs.89121	H sapiens mRNA; chromosome 1 specific tr	2.33	HMEC, HMEC (total RNA), MB231_cells
134286	T69384	Hs.68398	period (Drosophila) homolog 1	2.33	HMEC (total RNA), EB_cells, HMEC
125465	A1375276	Hs.158732	ESTs	2.33	Lu_AD_H23, HMEC (total RNA), HMEC
127449	A1421866	Hs.75722	ribophorin II	2.33	HS578T_cells, HMEC, Lu_LC_H460
110225	H23927	Hs.222381	ESTs	2.33	HMEC, HMEC (total RNA), EB_cells
119930	W86471	Hs.151624	hypocretin (orexin) receptor 2	2.32	MB231_cells, HMEC (total RNA), HMEC
125958	A1073357	Hs.12311	H sapiens clone 23570 mRNA seq	2.32	2.32 HMEC, HS578T_cells, MB231_cells
119746	W70279	Hs.221189	ESTs; Weakly similar to 15-HYDROXYPROSTA		
108874	AA134112	Hs.107187	H sapiens DNA seq from cosmid ICK0721Q o		
			L12 LIKE protein in an intron of the HS	2.32	Caco2, PRSC_con, LNCaP_cells
127368	AA434362	Hs.193326	ESTs	2.32	HMEC (total RNA), HS578T_cells, HMEC
120437	AA243427	Hs.104311	ESTs	2.32	HMEC (total RNA), HMEC, MB-MDA-435s
119867	W80852	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.32	Fibroblasts 2, HS578T_cells, MB-MDA-435s
131205	J02947	Hs.2420	superoxide dismutase 3; extracellular	2.32	PRSC_con, EB_cells, Lu_AD_358
133710	X76057	Hs.75694	mannose phosphate isomerase	2.31	293T_cells, LNCaP_cells, RPWE_2
104834	AA039331	Hs.16323	ESTs; Weakly similar to GAGE-7 [H.sapien	2.31	Caco2, HS578T_cells, HMEC
113186	T56048	Hs.189674	ESTs	2.31	HMEC, Fibroblasts 2, HMEC (total RNA)
113462	T86826	Hs.142528	ESTs	2.31	PC3_cells, HS578T_cells, HMEC
104743	AA021157	Hs.33619	ESTs	2.3	HMEC (total RNA), HMEC, OVCAR_cells
129667	Y00097	Hs.118796	annexin A6	2.3	PRSC_log, PRSC_con, HS578T_cells
111573	R10305	Hs.185683	ESTs	2.3	HMEC, HMEC (total RNA), EB_cells
117523	N32626	Hs.145532	ESTs; Weakly similar to Gag polypeptide	2.29	EB_cells, Fibroblasts 2, HS578T_cells

115540	AA349954	Hs.56281	ESTs; Weakly similar to ASB-1 protein [H	2.29	Fibroblasts 2, BT474_cells, MB231_cells
101622	M55621	Hs.151513	mannosyl (alpha-1;3-)glycoprotein beta-	2.29	PRSC_con, RPWE_2, PRSC_log
103535	Y13620	Hs.122607	B-cell CLL/lymphoma 9	2.28	Lu_SC_H69, Lu_AD_358, Lu_AD_H23
127482	AI337294	Hs.155014	ESTs	2.28	HS578T_cells, 293T_cells, CALU6_cells
104297	D31111	Hs.106005	ESTs; Highly similar to NY-REN-50 antige	2.27	EB_cells, DU145_cells, HT29_cells
112318	R55470	Hs.11067	ESTs	2.27	MB-MDA-453, LNCaP_cells, OVCAR_cells
101877	M97496	Hs.778	guanylate cyclase activator 1B (retina)	2.27	HT29_cells, BT474_cells, Caco2
100760	HG3576		Major Histocompatibility Complex, Class	2.26	MB-MDA-435s, MB231_cells, BT474_cells
102362	U39412	Hs.75932	N-ethylmaleimide-sensitive factor attach	2.26	LNCaP_cells, MB-MDA-453, Caco2
106142	AA424590	Hs.239631	Golgi transport complex protein (90 kDa)	2.26	HMEC, HS578T_cells, Caco2
101461	M22430	Hs.76422	phospholipase A2; group IIA (platelets;	2.26	LNCaP_cells, BT474_cells, Caco2
119336	T55340	Hs.208238	ESTs	2.26	HS578T_cells, EB_cells, HMEC
127619	AA627122	Hs.163787	ESTs	2.25	Lu_SC_H520, Lu_SC_H460, Lu_SC_H69
104113	AA427510	Hs.181202	ESTs; Weakly similar to Wiscott-Aldrich	2.25	MB-MDA-435s, Fibroblasts 2, HMEC (total RNA)
131219	C00476	Hs.24395	small inducible cytokine subfamily B (Cy	2.25	Lu_SC_H520, BT474_cells, Fibroblasts 2
118915	N91481	Hs.54713	ESTs	2.25	HMEC (total RNA), HMEC, MCF7
127556	AA679831	Hs.190228	ESTs	2.24	HS578T_cells, EB_cells, HMEC
128700	U59286	Hs.103982	small inducible cytokine subfamily B (Cy	2.24	HMEC, HS578T_cells, Fibroblasts 2
113674	T96374	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2	2.24	A549_cells, DU145_cells, Lu_AD_358
133085	M73720	Hs.646	carboxypeptidase A3 (mast cell)	2.24	HS578T_cells, Fibroblasts 2, HT29_cells
106017	AA411882	Hs.26268	ESTs	2.24	MB-MDA-453, OVCAR_cells, 293T_cells
100582	HG2348		Peptide Yy	2.24	HMEC, HS578T_cells, HMEC (total RNA)
134811	N66357	Hs.89761	ATP synthase; H+ transporting; mitochond	2.23	Lu_SC_H520, LNCaP_cells, Lu_AD_H23
102543	U57627	Hs.234776	oculocerebrorenal syndrome of Lowe	2.23	293T_cells, EB_cells, LNCaP_cells
127357	AA452788		zx39g11.r1 Soares_total_fetus_Nb2HF8_9w	2.23	
			IMAGE:788900 5', mRNA seq.	2.23	HS578T_cells, RPWE_2, HMEC (total RNA)
135288	AA402930	Hs.97876	ESTs	2.23	HS578T_cells, 293T_cells, OVCAR_cells
105581	AA278850	Hs.28891	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.23	BT474_cells, BT474_cells, MB231_cells
103812	AA137107	Hs.124094	ESTs; Weakly similar to NFAT1-A [M.muscu	2.23	Lu_SC_H345, Lu_AD_H23, PRSC_con
117016	H87171	Hs.52170	ESTs	2.22	Fibroblasts 2, Lu_SC_H460, HMEC (total RNA)
114607	AA079342	Hs.129057	breast carcinoma amplified seq 1	2.22	BT474_cells, HT29_cells, HT29_cells
134000	U29091	Hs.7833	selenium binding protein 1	2.22	LNCaP_cells, MB-MDA-453, BT474_cells
111069	N58461	Hs.22036	ESTs	2.22	HMEC, Lu_SC_H345, HS578T_cells
129048	L27670	Hs.108287	intercellular adhesion molecule 4; Lands	2.21	Lu_AD_H23, HS578T_cells, Lu_SC_H520
124995	T52700	Hs.110044	ESTs	2.2	Caco2, MB-MDA-453, HT29_cells
116678	F05063	Hs.251736	ESTs	2.2	HS578T_cells, BT474_cells, 293T_cells
118222	N62263	Hs.48501	EST	2.2	HS578T_cells, BT474_cells, MB231_cells
127888	AI149662	Hs.143590	ESTs	2.19	BT474_cells, CALU6_cells, MB231_cells
113790	W33178	Hs.26912	ESTs	2.19	HMEC, HMEC (total RNA), Fibroblasts 2
100097	AF002224		H sapiens Angelman Syndrome Gene, E6-AP		
			from promoter P1, 5'UTR	2.19	HS578T_cells, CALU6_cells, 293T_cells
109151	AA176800	Hs.73452	ESTs	2.19	CALU6_cells, Lu_AD_H23, Lu_SC_H69
135368	AA086057	Hs.9964	ribosomal protein; mitochondrial; S12	2.19	OVCAR_cells, A549_cells, Lu_AD_H23
109016	AA156936	Hs.58069	ESTs; Highly similar to type II cAMP-dep	2.19	HS578T_cells, BT474_cells, A549_cells
124300	H92575	Hs.105959	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.18	Lu_AD_358, Lu_SC_H69, Lu_SC_H345
123450	AA598913	Hs.111207	ESTs	2.18	HMEC (total RNA), HMEC, MB-MDA-435s
117435	N27628		yw50b08.s1 Weizmann Olfactory Epithelium	2.18	LNCaP_cells, DU145_cells, Lu_SC_H520
119860	W80709	Hs.58485	ESTs	2.18	HS578T_cells, MB231_cells, Caco2
123833	AA620717	Hs.112889	ESTs	2.18	Lu_AD_H23, Lu_SC_H520, Lu_AD_358
107938	AA029446	Hs.53115	ESTs	2.17	Caco2, 293T_cells, 293T_cells
119380	T83659	Hs.184407	ESTs	2.16	Lu_AD_H23, Lu_AD_358, PRSC_con
114066	Z38152	Hs.26920	ESTs	2.15	HMEC (total RNA), HMEC, EB_cells
128748	T59001	Hs.10475	ESTs	2.15	HMEC, HT29_cells, MB231_cells
130414	M21121	Hs.241392	small inducible cytokine A5 (RANTES)	2.15	HS578T_cells, PC3_cells, A549_cells
123490	AA599723		TAP binding protein (tapasin)	2.15	HS578T_cells, EB_cells, Lu_SC_H69
112588	R77302	Hs.20226	ESTs	2.14	HMEC (total RNA), HMEC, Fibroblasts 2
110548	H58715	Hs.14706	ESTs	2.14	HMEC, HMEC (total RNA), HT29_cells
101581	M34996	Hs.198253	major histocompatibility complex; class	2.14	MB-MDA-435s, HMEC, HMEC
115248	AA278887	Hs.194530	ESTs; Weakly similar to unknown [H.sapie	2.14	HT29_cells, BT474_cells, CALU6_cells
105619	AA280810	Hs.24003	ESTs; Moderately similar to LEYDIG CELL	2.14	Lu_SC_H520, MB-MDA-435s, LNCaP_cells
128058	AI126617	Hs.132449	ESTs	2.14	HS578T_cells, EB_cells, HMEC (total RNA)
134573	AA442125	Hs.171873	ESTs; Weakly similar to PUTATIVE STEROID	2.14	EB_cells, MB231_cells, Caco2
134863	AA353903	Hs.183373	ATX1 (antioxidant protein 1; yeast) homo	2.14	Lu_SC_H345, HT29_cells, BT474_cells
128811	H17317	Hs.169100	ESTs; Weakly similar to HPBR11-7 protein	2.13	Caco2, Lu_SC_H345, EB_cells
112368	R59371	Hs.26653	EST	2.13	HMEC, HMEC (total RNA), Lu_SC_H520
108395	AA075144		zm86f6.s1 Stratagene ovarian cancer (#93		
			gb:X1664 TRANSLATIONALLY CONTROLLED TUM	2.13	HMEC (total RNA), HMEC, OVCAR_cells
129611	D45680	Hs.11614	ESTs	2.13	HMEC, HS578T_cells, Caco2
101253	L34355	Hs.99931	sarcoglycan; alpha (50kD dystrophin-asso	2.12	HS578T_cells, OVCAR_cells, CALU6_cells
126701	AA515212	Hs.202590	ESTs; Weakly similar to mucin glycoprote	2.12	EB_cells, Lu_AD_H23, Lu_AD_H23
111628	R15825	Hs.4014	KIAA0946 protein; Huntingtin interacting	2.12	A549_cells, BT474_cells, MB-MDA-435s
108675	AA115240	Hs.61816	ESTs	2.12	Lu_AD_H23, MB-MDA-453, PRSC_con
127131	Z44658	Hs.105460	DKFZP564O0823 protein	2.12	EB_cells, Lu_SC_H69, Lu_SC_H69
109590	F02465	Hs.27281	ESTs	2.12	HMEC, HS578T_cells, HMEC (total RNA)
116539	D12124	Hs.242890	EST	2.12	Lu_AD_H23, Caco2, BT474_cells
112117	R45402	Hs.23789	ESTs	2.12	EB_cells, Lu_AD_H23, Lu_SC_H520

126367	AA477929	Hs.25584	ESTs	2.12	Lu_SC_H69, Lu_AD_H23, Lu_AD_358
135252	U62966	Hs.97207	solute carrier family 28 (sodium-coupled	2.11	MB-MDA-435s, 293T_cells, CALU6_cells
117565	N34301	Hs.248426	EST	2.11	HMEC, HS578T_cells, MB231_cells
129430	AA258842	Hs.197877	H sapiens clone 23777 putative transmembr	2.11	HS578T_cells, Lu_AD_358, MB-MDA-435s
120256	AA169801		sema domain; immunoglobulin domain (Ig);	2.11	HMEC, HMEC (total RNA), EB_cells
134169	D20342	Hs.178137	transducer of ERBB2; 1 (TOB1)	2.11	HMEC (total RNA), 293T_cells, OVCAR_cells
130397	AA487452	Hs.155344	DNA fragmentation factor, 45 kD; alpha s	2.11	293T_cells, Caco2, Lu_AD_H23
132859	D20925	Hs.5842	ESTs	2.11	HMEC (total RNA), Fibroblasts 2, HMEC
117633	N36404	Hs.44807	ESTs	2.11	HMEC, Caco2, HS578T_cells
125003	T59442	Hs.100445	ESTs	2.11	MB-MDA-435s, HMEC (total RNA), HT29_cells
125329	AA825437	Hs.58875	ESTs	2.11	HS578T_cells, PRSC_con, PRSC_log
114065	Z38149	Hs.134015	uronyl 2-sulfotransferase	2.11	MB-MDA-435s, 293T_cells, PRSC_con
120718	AA292747	Hs.97296	ESTs	2.11	HT29_cells, Lu_AD_H23, Lu_SC_H69
133869	T49444	Hs.77031	Sp2 transcription factor	2.1	Lu_LC_H460, Lu_AD_358, RPWE_2
135351	AA430179	Hs.9933	putative Ac-like transposon	2.1	HS578T_cells, EB_cells, HMEC
110973	N51529	Hs.118047	ESTs	2.09	EB_cells, HS578T_cells, MCF7
131879	AA017161	Hs.33792	ESTs	2.09	HMEC (total RNA), MB231_cells, BT474_cells
116656	F03935	Hs.241640	EST	2.09	HS578T_cells, Lu_LC_H460, Lu_SC_H69
120311	AA194074	Hs.193401	ESTs	2.09	OVCAR_cells, HMEC (total RNA), HMEC
108024	AA040433	Hs.61898	DKFZP586N2124 protein	2.09	HMEC (total RNA), BT474_cells, HT29_cells
105871	AA399633	Hs.24872	ESTs	2.09	Fibroblasts 2, A549_cells, HS578T_cells
120206	Z40805	Hs.91668	ESTs	2.09	BT474_cells, MB-MDA-453, EB_cells
112333	R56222	Hs.26514	ESTs	2.09	Lu_AD_H23, Fibroblasts 2, Lu_LC_H460
116746	H04811	Hs.79027	ESTs	2.08	MB-MDA-435s, HMEC (total RNA), Lu_SC_H345
121529	AA412257	Hs.98121	ESTs	2.08	HMEC, HMEC (total RNA), HS578T_cells
105592	AA279337	Hs.180549	ESTs; Highly similar to R26660_1; partia	2.08	LNCaP_cells, PRSC_log, PRSC_log
108582	AA088231	Hs.91732	ESTs	2.08	HS578T_cells, Lu_SC_H345, Lu_SC_H69
123197	AA489250	Hs.59403	serine palmitoyltransferase; subunit II	2.08	EB_cells, Lu_SC_H69, Lu_SC_H345
134965	J05480	Hs.92	protein phosphatase 3 (formerly 2B); cat	2.08	LNCaP_cells, MB-MDA-435s, HMEC
123856	AA620814	Hs.144959	ESTs	2.08	HS578T_cells, BT474_cells, BT474_cells
132058	AA251737	Hs.172818	Apg12 (autophagy 12; S. cerevisiae)-like	2.07	HS578T_cells, MCF7, HMEC
126476	R94666	Hs.195155	ESTs; Weakly similar to transporter prot	2.07	PRSC_log, Lu_LC_H460, RPWE_2
106087	AA418740	Hs.21111	ESTs	2.07	OVCAR_cells, A549_cells, Lu_AD_H23
103802	AA122003	Hs.62954	ferritin; heavy polypeptide 1	2.07	HMEC, HMEC (total RNA), HS578T_cells
125633	AA908225	Hs.126841	ESTs	2.07	EB_cells, Fibroblasts 2, Lu_SC_H69
112817	R98491	Hs.14584	ESTs	2.07	HMEC, HMEC (total RNA), Fibroblasts 2
111050	N56984	Hs.74335	heat shock 90kD protein 1; beta	2.07	LNCaP_cells, DU145_cells, 293T_cells
133072	AA425294	Hs.64322	ESTs; Weakly similar to Closely related	2.07	LNCaP_cells, MB-MDA-453, Caco2
118270	N62868	Hs.48653	ESTs	2.07	HMEC (total RNA), HMEC, EB_cells
105035	AA128486	Hs.8859	ESTs	2.07	LNCaP_cells, PC3_cells, EB_cells
102337	U36922		Human fork head domain protein (FKHR) mR	2.07	293T_cells, HMEC, HT29_cells
109687	F09380	Hs.182859	lifeguard	2.06	BT474_cells, BT474_cells, Lu_AD_H23
109802	F10789	Hs.12439	ESTs	2.06	EB_cells, EB_cells, Caco2
128103	AA905960	Hs.48516	ESTs	2.06	HT29_cells, HMEC (total RNA), HMEC
128278	AI018343	Hs.131275	ESTs	2.06	PRSC_con, Lu_SC_H345, HS578T_cells
131873	H39997	Hs.33716	ESTs	2.06	HMEC (total RNA), HMEC, EB_cells
122683	AA455528	Hs.96772	ESTs	2.05	LNCaP_cells, Lu_AD_H23, HS578T_cells
128066	AA884838	Hs.189171	ESTs	2.05	HMEC, HMEC (total RNA), Fibroblasts 2
131451	N28028	Hs.26968	H sapiens mRNA from chromosome 5q21-22;	2.05	MB-MDA-435s, Lu_LC_H460, Lu_SC_H520
120887	AA365644	Hs.97043	ESTs	2.05	HS578T_cells, PRSC_con, HMEC
103966	AA303166	Hs.127270	ESTs	2.05	HMEC (total RNA), LNCaP_cells, PC3_cells
105861	AA399260	Hs.28454	ESTs	2.05	Fibroblasts 2, HMEC (total RNA), EB_cells
104627	AA001976	Hs.19603	ESTs	2.05	HS578T_cells, HMEC, BT474_cells
108794	AA129468	Hs.203392	ESTs	2.04	HS578T_cells, HMEC, A549_cells
111896	R38936	Hs.24894	H sapiens clone 25248 mRNA seq	2.04	HS578T_cells, PC3_cells, 293T_cells
101849	M94167	Hs.172816	neuregulin 1	2.04	HMEC, HS578T_cells, HMEC (total RNA)
119913	W85931	Hs.58785	ESTs	2.04	HMEC, BT474_cells, MB231_cells
130785	AA242826	Hs.19405	caspase recruitment domain 4	2.04	HMEC, HS578T_cells, BT474_cells
124702	R06984	Hs.7745	ESTs; Weakly similar to TESTIS-SPECIFIC	2.03	Fibroblasts 2, PRSC_con, HMEC
106769	AA478001	Hs.225935	diacylglycerol O-acyltransferase (mouse)	2.03	PC3_cells, EB_cells, HS578T_cells
132219	N48682	Hs.172971	ESTs	2.03	HT29_cells, PC3_cells, A549_cells
122033	AA431334	Hs.109297	ESTs	2.03	OVCAR_cells, A549_cells, Caco2
120461	AA251301		zs10b02.s1 NCI_CGAP_GCB1 H sapiens cDNA		
			contains Alu repetitive element; mRNA	2.03	HS578T_cells, EB_cells, EB_cells
134959	U90550	Hs.91813	butyrophilin; subfamily 2; member A2	2.03	HMEC, Fibroblasts 2, EB_cells
104909	AA055892	Hs.14543	ESTs	2.03	Lu_SC_H345, PC3_cells, DU145_cells
101950	S79219	Hs.80741	propionyl Coenzyme A carboxylase; alpha	2.03	Lu_SC_H69, EB_cells, CALU6_cells
133878	D78947	Hs.7718	ESTs; Weakly similar to weak similarity	2.02	EB_cells, MCF7, MB231_cells
103459	X99894	Hs.32938	Insulin promoter factor 1; homeodomain t	2.02	EB_cells, Lu_AD_H23, Lu_AD_358
125507	AI436377	Hs.258590	tetraspanin TM4-B	2.02	A549_cells, Lu_SC_H520, Lu_AD_H23
116657	F04014	Hs.65996	ESTs	2.01	HS578T_cells, HMEC, MB231_cells
112920	T10234	Hs.4275	ESTs	2.01	HS578T_cells, EB_cells, PRSC_con
105533	AA258572	Hs.6418	ESTs; Moderately similar to seven transm	2.01	HS578T_cells, HMEC, EB_cells
126762	AA064671		zm13b04.r1 Stratagene pancreas (#937208)		
			similar to TR:G413842 G413842 NONCLASSI		
128999	R37808	Hs.107765	ESTs	2.01	2.01 RPWE_2, Lu_AD_H23, Lu_AD_358
					HS578T_cells, OVCAR_cells, EB_cells

133902 AA114858 Hs.7745 ESTs; Weakly similar to TESTIS-SPECIFIC 2

Fibroblasts 2, PRSC_con, DU145_cells

Table 2

Pkey: Unique Eos probeset identifier number ExAccn: Exemplar Accession number, Genbank accession number UnigeneID: Unigene number Unigene Title: Unigene gene title					
Pkey	Ex Accn	UniG_ID	Complete_Title	Ratio Mets/BS	Top 3 expressing cell lines
101447	M21305	Hs.247946	Human alpha satellite and satellite 3 ju	110.98	EB_cells, Fibroblasts 2, A549_cells
105039	AA130349	Hs.36475	ESTs	9.13	EB_cells, OVCAR_cells, Lu_SC_H345
106094	AA419461	Hs.18127	ESTs	8.51	HT29_cells, MB-MDA-453, HS578T_cells
105777	AA348412	Hs.23096	ESTs	8.4	293T_cells, OVCAR_cells, EB_cells
129818	N54841	Hs.172572	ESTs	7.2	Lu_SC_H69, EB_cells, Lu_SC_H345
118475	N66845	Hs.165411	ESTs; Weakly similar to IIII ALU CLASS B	7	DU145_cells, EB_cells, Caco2
112170	R48744	Hs.192878	ESTs	6.91	293T_cells, DU145_cells, HT29_cells
114918	AA236813	Hs.72324	ESTs; Highly similar to unknown [H.sapie	6.6	EB_cells, 293T_cells, DU145_cells
104590	R79750	Hs.83623	nuclear receptor subfamily 1; group I; m	6.58	293T_cells, OVCAR_cells, HMEC
120625	AA285053	Hs.107168	ESTs	6.55	CALU6_cells, OVCAR_cells, EB_cells
115650	AA404564	Hs.47094	ESTs	6.43	EB_cells, LNCaP_cells, Lu_SC_H345
124568	N67086	Hs.102000	ESTs	6.35	PC3_cells, A549_cells, DU145_cells
134238	R81509	Hs.184571	splicing factor; arginine/serine-rich 11	6.32	293T_cells, Lu_SC_H345, HMEC
114721	AA131450	Hs.103822	ESTs	6.13	Caco2, MB-MDA-435s, PRSC_log
106145	AA424791	Hs.5734	KIAA0679 protein	6	OVCAR_cells, EB_cells, 293T_cells
114610	AA081079		zn32h9.s1 Stratagene endothelial cell 93 IMAGE:549185 3', mRNA seq	5.97	PRSC_con, DU145_cells, HS578T_cells
130281	R12777	Hs.15395	ESTs; Weakly similar to ARGINYL-TRNA SYN	5.94	PRSC_con, HT29_cells, EB_cells
124690	R05818	Hs.173830	ESTs	5.92	LNCaP_cells, EB_cells, OVCAR_cells
113490	T88700	Hs.173374	ESTs	5.81	DU145_cells, PC3_cells, HMEC (total RNA)
104425	H88496	Hs.40583	ESTs	5.77	OVCAR_cells, HS578T_cells, A549_cells
118828	N79496	Hs.50824	EST	5.45	LNCaP_cells, OVCAR_cells, DU145_cells
129076	AA262179	Hs.169343	ESTs	5.35	293T_cells, BT474_cells, MCF7
109684	F09317	Hs.140885	ESTs; Weakly similar to LINE-1 REVERSE T	5.34	Fibroblasts 2, Lu_SC_H69, DU145_cells
104558	R56678	Hs.88959	Human DNA seq from clone 967N21 on chr 2 part of KIAA0172; the gene for a novel	5.32	EB_cells, PC3_cells, Lu_SC_H345
109032	AA158234	Hs.72222	ESTs	5.23	HT29_cells, PC3_cells, Lu_AD_358
129350	U50535	Hs.110630	Human BRCA2 region; mRNA seq CG006	5.2	293T_cells, EB_cells, DU145_cells
112662	R85436	Hs.193150	ESTs	5.2	MB-MDA-435s, PRSC_con, MB-MDA-453
132902	AA490969	Hs.168147	ESTs	5.18	PC3_cells, LNCaP_cells, CALU6_cells
126872	AA136653		ESTs	5.04	EB_cells, Fibroblasts 2, A549_cells
122528	AA449804	Hs.250992	EST	5.04	Lu_SC_H345, PRSC_con, LNCaP_cells
102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	5.02	Lu_SC_H460, A549_cells, MB-MDA-435s
121332	AA404384	Hs.97921	ESTs	5.01	EB_cells, Lu_SC_H69, DU145_cells
135357	AA235803	Hs.79572	cathepsin D (lysosomal aspartyl protease	4.96	EB_cells, MCF7, DU145_cells
109141	AA176428	Hs.193380	ESTs	4.86	DU145_cells, PC3_cells, PRSC_log
135324	AA082041	Hs.9873	ESTs	4.83	EB_cells, Lu_SC_H345, HS578T_cells
124875	R70506	Hs.207693	ESTs; Weakly similar to IIII ALU SUBFAMI	4.75	DU145_cells, OVCAR_cells, LNCaP_cells
102380	U40434	Hs.155981	mesothelin	4.71	OVCAR_cells, Lu_AD_H23, RPWE_2
127956	AA826117	Hs.194013	ESTs	4.69	EB_cells, HS578T_cells, DU145_cells
125038	T78089	Hs.168887	ESTs	4.58	OVCAR_cells, 293T_cells, DU145_cells
102515	U52696		Human adrenal Creb-rp hmlg (Creb-rp), com	4.57	Lu_SC_H345, Lu_SC_H69, HT29_cells
109027	AA157818	Hs.238380	Human endogenous retroviral protease mRN	4.57	PC3_cells, EB_cells, Lu_SC_H520
115096	AA255991	Hs.175319	ESTs	4.57	OVCAR_cells, 293T_cells, PC3_cells
123470	AA599106	Hs.194208	ESTs	4.55	LNCaP_cells, Lu_SC_H69, 293T_cells
113219	T59257	Hs.194407	ESTs	4.55	A549_cells, 293T_cells, 293T_cells
123433	AA598661	Hs.112478	ESTs	4.55	EB_cells, OVCAR_cells, HT29_cells
135182	M28170	Hs.96023	CD19 antigen	4.53	OVCAR_cells, DU145_cells, EB_cells
121721	AA419470	Hs.199961	ESTs	4.51	DU145_cells, LNCaP_cells, EB_cells
129126	H88486	Hs.108806	ESTs	4.45	LNCaP_cells, Caco2, EB_cells
135232	AA342457	Hs.96800	ESTs; Moderately similar to IIII ALU SUB	4.43	LNCaP_cells, DU145_cells, OVCAR_cells
124847	R60044	Hs.106706	ESTs; Highly similar to BETA-CATENIN [H.	4.42	OVCAR_cells, CALU6_cells, CALU6_cells
110349	H40988		ESTs; Weakly similar to IIII ALU SUBFAMI	4.39	DU145_cells, OVCAR_cells, LNCaP_cells
134402	U25165	Hs.82712	fragile X mental retardation; autosomal	4.38	HS578T_cells, OVCAR_cells, DU145_cells
115494	AA290603	Hs.256517	ESTs	4.36	Lu_SC_H345, OVCAR_cells, PC3_cells
119174	R71234		yi54c08.s1 Soares placenta Nb2HP H sapie transcript, (rRNA); gb:S41458 ROD CGMP- BETA-SUBUNIT (HUMAN);contain	4.33	DU145_cells, OVCAR_cells, LNCaP_cells
121943	AA429265	Hs.126759	ESTs	4.3	EB_cells, HT29_cells, Lu_SC_H69
110856	N33063	Hs.23291	ESTs; Weakly similar to S164 [H.sapiens]	4.28	OVCAR_cells, EB_cells, Lu_SC_H69
102474	U49973		Human Tigger1 transposable element, comp	4.28	DU145_cells, LNCaP_cells, OVCAR_cells
123458	AA598963	Hs.112499	KIAA0612 protein	4.27	A549_cells, A549_cells, BT474_cells
116459	AA621399	Hs.64193	ESTs	4.22	Caco2, HS578T_cells, MB-MDA-435s
126301	N62371	Hs.100043	ESTs; Weakly similar to Similar to cutic	4.22	PC3_cells, DU145_cells, Lu_SC_H345
123461	AA598990	Hs.251119	EST	4.22	Lu_SC_H345, Lu_SC_H69, OVCAR_cells

130588	AA287735	Hs.16411	Human DNA seq from clone 1189B24 on chro MLRQ subunit (EC 1.6.5.3; EC 1.6.99.3; Tyrosine-protein Kinase FER (EC 2.7.1.1	4.2	EB_cells, LNCaP_cells, MCF7
125756	W25498	Hs.81634	ATP synthase; H ⁺ transporting; mitochond	4.2	HMEC, EB_cells, DU145_cells
135009	AA040507	Hs.251865	ESTs	4.19	293T_cells, EB_cells, DU145_cells
107001	AA598589	Hs.24492	ESTs	4.18	293T_cells, DU145_cells, EB_cells
124896	R82063	Hs.101594	EST	4.16	OVCAR_cells, Lu_SC_H345, HMEC (total RNA)
119404	T92950		ye27c10.s1 Stratagene lung (#937210) H s	4.15	DU145_cells, PC3_cells, Fibroblasts 2
125090	T91518		ye20f05.s1 Stratagene lung (#937210) H s contains Alu repetitive element; contain	4.14	LNCaP_cells, DU145_cells, OVCAR_cells
117348	N24157	Hs.139615	ESTs	4.1	Lu_SC_H345, Lu_SC_H69, PRSC_log
111389	N95837	Hs.169111	ESTs; Weakly similar to L82A [D.melanoga	4.1	DU145_cells, MCF7, LNCaP_cells
134977	AA464698	Hs.19390	ESTs; Weakly similar to bullous pemphigo	4.09	OVCAR_cells, Fibroblasts 2, Lu_SC_H69
124696	R06273	Hs.186467	ESTs; Moderately similar to IIII ALU SUB	4.09	OVCAR_cells, Lu_SC_H345, PRSC_con
124090	H09570	Hs.143032	ESTs; Weakly similar to neuronal thread	3.98	DU145_cells, OVCAR_cells, Lu_SC_H345
133992	R46354	Hs.169832	zinc finger protein 42 (myeloid-specific	3.98	HT29_cells, MB231_cells, BT474_cells
126009	H51652	Hs.242985	hemoglobin; gamma G	3.96	Lu_SC_H69, OVCAR_cells, EB_cells
114161	Z38904	Hs.22385	ESTs; Weakly similar to KIAA0970 protein	3.94	HS578T_cells, EB_cells, PRSC_con
109171	AA180356	Hs.73700	EST	3.94	293T_cells, MB-MDA-435s, A549_cells
122007	AA430629	Hs.98564	ESTs	3.93	PC3_cells, A549_cells, OVCAR_cells
131936	AA094865	Hs.179972	interferon; alpha-inducible protein (clo	3.9	CALU6_cells, EB_cells, Lu_SC_H69
128668	AA194849	Hs.103422	ESTs	3.9	Lu_AD_H23, EB_cells, Lu_SC_H69
124977	T33859	Hs.190452	KIAA0365 gene product	3.89	293T_cells, DU145_cells, EB_cells
107048	AA600012	Hs.10669	ESTs; Moderately similar to KIAA0400 [H.	3.89	PC3_cells, HS578T_cells, DU145_cells
105358	AA236034	Hs.25362	ESTs	3.89	Caco2, EB_cells, CALU6_cells
135106	AA599037	Hs.9456	SWI/SNF related; matrix assocd; actin de	3.86	EB_cells, LNCaP_cells, Caco2
106686	AA463215	Hs.29896	ESTs; Weakly similar to proline-rich pro	3.85	OVCAR_cells, DU145_cells, EB_cells
132093	AA400091	Hs.39421	ESTs	3.85	OVCAR_cells, OVCAR_cells, LNCaP_cells
128651	AA446990	Hs.103135	ESTs	3.84	EB_cells, LNCaP_cells, OVCAR_cells
102459	U48936		Human amiloride-sensitive epithelial sod	3.84	HT29_cells, BT474_cells, Lu_SC_H69
113732	T98288	Hs.193295	ESTs; Weakly similar to IIII ALU SUBFAMI	3.82	DU145_cells, OVCAR_cells, LNCaP_cells
116000	AA448710	Hs.41327	ESTs	3.82	DU145_cells, MB-MDA-453, Lu_SC_H69
120748	AA303153	Hs.237994	EST; Weakly similar to IIII ALU SUBFAMIL	3.82	DU145_cells, DU145_cells, Lu_SC_H345
116318	AA490830	Hs.58570	deleted in cancer 1; RNA helicase HDB/DI	3.79	MB-MDA-453, CALU6_cells, EB_cells
114366	Z41747	Hs.469	succinate dehydrogenase complex; subunit	3.78	DU145_cells, Fibroblasts 2, Caco2
107248	D59894	Hs.34782	ESTs	3.75	LNCaP_cells, DU145_cells, EB_cells
132713	AA286906	Hs.55335	ESTs	3.75	OVCAR_cells, EB_cells, Lu_SC_H345
102222	U24683	Hs.159386	Immunoglobulin heavy variable 4-4	3.73	EB_cells, OVCAR_cells, 293T_cells
108201	AA057518	Hs.63394	ESTs	3.72	293T_cells, DU145_cells, EB_cells
119940	W86779	Hs.171807	DKFZP586B0319 protein	3.71	EB_cells, Caco2, DU145_cells
106508	AA452590	Hs.30348	ESTs	3.67	EB_cells, LNCaP_cells, 293T_cells
114360	Z41592	Hs.22129	hypothetical protein	3.67	HT29_cells, Lu_SC_H520, Lu_SC_H520
100991	J03764	Hs.82085	plasminogen activator inhibitor; type I	3.67	Fibroblasts 2, HS578T_cells, MB231_cells
107580	AA002091	Hs.175476	ESTs; Weakly similar to IIII ALU SUBFAMI	3.67	OVCAR_cells, LNCaP_cells, Lu_SC_H345
111685	R21408	Hs.106095	ESTs	3.66	OVCAR_cells, A549_cells, 293T_cells
128336	AJ242720	Hs.146043	ESTs; Weakly similar to alternatively sp	3.66	Lu_SC_H345, Caco2, OVCAR_cells
130868	AA004900	Hs.171917	ESTs; Weakly smlr to smlr to glycerophos	3.61	EB_cells, HS578T_cells, LNCaP_cells
116802	H44061	Hs.194026	ESTs	3.6	Lu_SC_H345, OVCAR_cells, DU145_cells
130753	Z46632	Hs.189	phosphodiesterase 4C; cAMP-specific (dun	3.6	Lu_SC_H69, Lu_AD_H23, Lu_SC_H345
123074	AA485117	Hs.105653	ESTs	3.6	293T_cells, MB231_cells, Fibroblasts 2
114317	Z41038	Hs.469	succinate dehydrogenase complex; subunit	3.6	DU145_cells, HS578T_cells, CALU6_cells
134194	AA233231	Hs.79828	ESTs	3.59	BT474_cells, MB231_cells, HT29_cells
127752	AA808388	Hs.211167	ESTs	3.59	Lu_SC_H520, MB-MDA-435s, DU145_cells
123526	AA608657		ESTs; Moderately similar to IIII ALU SUB	3.59	DU145_cells, OVCAR_cells, LNCaP_cells
127917	AA211895	Hs.118831	EST; Highly similar to dJ1163J1.2.1 [H.s	3.58	Lu_SC_H345, OVCAR_cells, PRSC_con
105941	AA404427	Hs.10669	ESTs; Moderately similar to KIAA0400 [H.	3.58	PC3_cells, DU145_cells, HS578T_cells
124694	R06108	Hs.135258	ESTs	3.56	Lu_AD_H23, Lu_SC_H520, Lu_AD_358
105656	AA282571	Hs.203772	FSHD region gene 1	3.56	DU145_cells, EB_cells, A549_cells
111168	N66951	Hs.238380	Human endogenous retroviral protease mRN	3.55	PC3_cells, EB_cells, MB231_cells
133254	AA156670	Hs.180780	H sapiens agrin precursor mRNA; partial	3.54	OVCAR_cells, DU145_cells, PC3_cells
132640	U33821		Tax1 (human T-cell leukemia virus type I	3.53	MB231_cells, CALU6_cells, BT474_cells
116562	D25807	Hs.90145	ESTs	3.52	MB231_cells, BT474_cells, Lu_SC_H345
126045	N80361	Hs.14248	ESTs	3.51	DU145_cells, Lu_SC_H345, OVCAR_cells
122878	AA465341	Hs.99640	ESTs	3.47	HT29_cells, OVCAR_cells, HMEC
105220	AA210695	Hs.17212	ESTs	3.47	MB-MDA-435s, HT29_cells, HT29_cells
127001	AA731636	Hs.59319	ESTs; Weakly similar to IIII ALU SUBFAMI	3.45	LNCaP_cells, DU145_cells, Lu_SC_H345
112693	R88741	Hs.91065	ESTs; Moderately similar to proliferatio	3.44	EB_cells, LNCaP_cells, DU145_cells
104935	AA063280	Hs.35552	ESTs	3.43	LNCaP_cells, CALU6_cells, 293T_cells
128710	J04813	Hs.104117	cytochrome P450; subfamily IIIA (niphedi	3.41	HT29_cells, A549_cells, Fibroblasts 2
131996	D86956	Hs.36927	heat shock 105kD	3.4	EB_cells, PC3_cells, Lu_SC_H345
119229	T03229		H sapiens (clone 104) retinoblastoma 1 g	3.4	DU145_cells, Lu_SC_H345, EB_cells
128046	AA873285	Hs.137947	ESTs	3.39	EB_cells, LNCaP_cells, DU145_cells
105175	AA186804	Hs.25740	ESTs; Weakly similar to ubiquitous TPR m	3.39	PC3_cells, MCF7, DU145_cells
132349	Y00705	Hs.181286	serine protease inhibitor; Kazal type 1	3.38	Caco2, EB_cells, Lu_SC_H69
101559	M32053		Human H19 RNA gene, complete cds	3.37	Lu_SC_H69, MCF7, OVCAR_cells
116389	AA599011		tropoin T1; skeletal; slow	3.36	DU145_cells, LNCaP_cells, OVCAR_cells

130641	AA182001	Hs.17155	ESTs	3.36	DU145_cells, MB-MDA-435s, HS578T_cells
109362	AA214615	Hs.194348	ESTs	3.33	HT29_cells, Fibroblasts 2, BT474_cells
106278	AA432292	Hs.23388	ESTs; Moderately similar to IIII ALU SUB	3.33	EB_cells, Fibroblasts 2, BT474_cells
127241	AA321849	Hs.248340	H sapiens mRNA; cDNA DKFZp564J2116 (from		3.32 LNCaP_cells, DU145_cells, EB_cells
133339	N64588	Hs.71252	ESTs	3.32	DU145_cells, EB_cells, Caco2
113260	T64896	Hs.237992	ESTs	3.32	Lu_SC_H345, LNCaP_cells, Lu_SC_H69
133349	N75791	Hs.7153	L-3-hydroxyacyl-Coenzyme A dehydrogenase	3.31	Caco2, EB_cells, OVCAR_cells
107149	AA621159	Hs.23284	ESTs	3.29	HS578T_cells, DU145_cells, PRSC_con
133195	AA350744	Hs.181409	KIAA1007 protein	3.29	EB_cells, Lu_AD_H23, Lu_AD_358
111302	N73838	Hs.15049	ESTs	3.29	DU145_cells, EB_cells, HS578T_cells
106414	AA447971	Hs.28827	ESTs	3.28	A549_cells, OVCAR_cells, PC3_cells
121768	AA421561	Hs.251664	insulin-like growth factor 2 (somatomedi	3.28	Caco2, PRSC_con, PRSC_log
117176	H98670	Hs.49753	ESTs; Weakly similar to hypothetical pro	3.28	PRSC_log, CALU6_cells, OVCAR_cells
131320	AA171948	Hs.145696	splicing factor (CC1.3)	3.28	EB_cells, LNCaP_cells, DU145_cells
100700	HG3227-H		Guanine Nucleotide-Binding Protein Hsr1	3.27	EB_cells, RPWE_2, Lu_AD_H23
134275	AA132328	Hs.3688	acid-inducible phosphoprotein	3.26	EB_cells, DU145_cells, LNCaP_cells
117667	N39214	Hs.44708	Ser-Thr protein kinase related to the my	3.26	LNCaP_cells, DU145_cells, MB-MDA-453
124889	R78604	Hs.101570	ESTs	3.25	Lu_AD_H23, Lu_SC_H69, Lu_SC_H345
126631	W95117	Hs.193337	ESTs	3.25	Lu_SC_H345, OVCAR_cells, Lu_SC_H69
105643	AA282069	Hs.173802	KIAA0603 gene product	3.24	Caco2, EB_cells, 293T_cells
132718	AA056731	Hs.554	Sjogren syndrome antigen A2 (60kD; ribon	3.24	CALU6_cells, OVCAR_cells, A549_cells
116417	AA609309	Hs.239302	ESTs; Weakly similar to IIII ALU SUBFAMI	3.24	A549_cells, CALU6_cells, 293T_cells
108039	AA041341	Hs.46670	ESTs	3.24	293T_cells, EB_cells, Caco2
114116	Z38496	Hs.103283	KIAA0594 protein	3.23	DU145_cells, OVCAR_cells, EB_cells
124514	N58045	Hs.142737	ESTs	3.22	EB_cells, Caco2, Lu_SQ_H520
110802	N26651	Hs.252748	ESTs	3.22	LNCaP_cells, MB-MDA-435s, MB-MDA-453
106920	AA490899	Hs.24462	ESTs	3.22	DU145_cells, EB_cells, OVCAR_cells
123523	AA608588	Hs.193634	ESTs	3.21	DU145_cells, LNCaP_cells, OVCAR_cells
131564	AA491465	Hs.28792	ESTs	3.2	HS578T_cells, HMEC (total RNA), HMEC
119423	T99544	Hs.173734	ESTs; Weakly similar to IIII ALU CLASS B	3.2	EB_cells, DU145_cells, Caco2
128736	F03934	Hs.104607	ESTs	3.19	PC3_cells, Lu_SQ_H520, Lu_SC_H69
101511	M27826	Hs.238380	Human endogenous retroviral protease mRN	3.18	PC3_cells, DU145_cells, Lu_SQ_H520
114509	AA043551	Hs.95249	ESTs	3.18	EB_cells, Lu_SC_H345, DU145_cells
124196	H52617	Hs.144167	ESTs	3.17	BT474_cells, MB231_cells, HMEC
129095	L12350	Hs.108623	thrombospondin 2	3.17	Fibroblasts 2, PRSC_con, PRSC_log
116457	AA621367	Hs.119683	ESTs	3.17	293T_cells, Lu_SC_H345, CALU6_cells
117040	H89112		yw25e5.s1 Morton Fetal Cochlea H sapiens	3.16	OVCAR_cells, 293T_cells, EB_cells
129112	N32521	Hs.108738	ESTs	3.16	EB_cells, Fibroblasts 2, MB231_cells
130418	J03242	Hs.251664	insulin-like growth factor 2 (somatomedi	3.16	Caco2, PRSC_con, PRSC_log
131199	R80048	Hs.234433	ESTs; Weakly similar to transporter prot	3.15	PC3_cells, EB_cells, OVCAR_cells
110357	H41529	Hs.33549	ESTs; Highly similar to sulfonylurea rec	3.15	Lu_SC_H345, PRSC_con, Lu_AD_H23
130068	AA608903	Hs.106220	KIAA0336 gene product	3.15	OVCAR_cells, CALU6_cells, HS578T_cells
127423	T47546	Hs.119252	tumor protein; translationally-controlle	3.15	EB_cells, PRSC_con, LNCaP_cells
105028	AA126719	Hs.25282	ESTs	3.14	LNCaP_cells, PC3_cells, EB_cells
102349	U37547	Hs.75263	apoptosis inhibitor 1	3.14	DU145_cells, HS578T_cells, LNCaP_cells
105126	AA157814	Hs.36288	ESTs	3.13	EB_cells, HS578T_cells, LNCaP_cells
115465	AA286941	Hs.43691	ESTs	3.12	EB_cells, DU145_cells, 293T_cells
133246	AA086452	Hs.68731	triadin	3.12	Lu_SQ_H520, Lu_AD_H23, PRSC_log
122698	AA456112	Hs.99410	ESTs	3.12	DU145_cells, OVCAR_cells, A549_cells
123553	AA608841	Hs.111977	ESTs	3.12	EB_cells, Caco2, DU145_cells
133437	R57419	Hs.7370	ESTs	3.11	HS578T_cells, 293T_cells, Caco2
104956	AA074880	Hs.120975	ESTs; Weakly similar to hypothetical pro	3.11	OVCAR_cells, Fibroblasts 2, Caco2
116314	AA490588	Hs.43118	ESTs	3.11	EB_cells, MB-MDA-435s, HT29_cells
120562	AA280036	Hs.173912	eukaryotic translation initiation factor	3.11	LNCaP_cells, DU145_cells, EB_cells
108770	AA127845	Hs.71027	EST	3.11	Lu_LC_H460, Lu_SC_H345, Lu_AD_358
129791	F02778	Hs.173887	KIAA0876 protein	3.1	Lu_SC_H345, Lu_SC_H69, PRSC_log
115783	AA424487	Hs.72289	ESTs; Weakly similar to LIV-1 protein [H	3.09	Lu_AD_358, EB_cells, PC3_cells
107630	AA007218	Hs.60178	ESTs	3.07	Lu_SC_H345, CALU6_cells, Lu_SC_H69
124339	H99093	Hs.6179	H sapiens mRNA; cDNA DKFZp586K2322 (from		3.07 293T_cells, MB-MDA-453, Caco2
122314	AA442257	Hs.192076	ESTs	3.07	293T_cells, LNCaP_cells, PC3_cells
104589	R79299	Hs.241160	ESTs; Moderately similar to IIII ALU SUB	3.07	293T_cells, DU145_cells, EB_cells
115687	AA410508	Hs.183765	ESTs; Moderately smir to ORF derived frm	3.06	Caco2, EB_cells, MB231_cells
123796	AA620390	Hs.247444	ESTs	3.06	Lu_SC_H345, LNCaP_cells, DU145_cells
106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	3.06	OVCAR_cells, HMEC (total RNA), HMEC
133318	AA256168	Hs.70838	ESTs	3.05	OVCAR_cells, LNCaP_cells, 293T_cells
117244	N20979	Hs.1757	L1 cell adhesion molecule (hydrocephalus		
			thumbs) syndrome; spastic paraplegia 1)	3.05	MB231_cells, MCF7, CALU6_cells
130797	AA430050	Hs.180948	KIAA0729 protein	3.05	EB_cells, DU145_cells, DU145_cells
128959	D79791	Hs.107381	ESTs; Weakly similar to F38A5.1 [C.elega	3.05	LNCaP_cells, HS578T_cells, Lu_SQ_H520
120481	AA252703	Hs.191754	ESTs	3.04	EB_cells, Fibroblasts 2, PRSC_con
126649	AA856990	Hs.125058	ESTs	3.03	OVCAR_cells, LNCaP_cells, 293T_cells
106970	AA504835	Hs.24252	ESTs	3.03	EB_cells, OVCAR_cells, 293T_cells
126488	N34935	Hs.25633	ESTs; Highly similar to ARF GTPase-activ	3.03	Lu_AD_358, MCF7, MB231_cells
119498	W37226	Hs.55573	ESTs	3.01	293T_cells, HS578T_cells, CALU6_cells
129967	H99653	Hs.138618	ESTs	3.01	Lu_SC_H345, Lu_SC_H69, PRSC_log
130698	AA037357	Hs.188212	ESTs	3.01	OVCAR_cells, LNCaP_cells, DU145_cells

111018	N54067	Hs.3628	mitogen-activated protein kinase kinase	3.01	PC3_cells, Caco2, Fibroblasts 2
123196	AA489250	Hs.59403	serine palmitoyltransferase; subunit II	3	Lu_SC_H345, BT474_cells, Lu_SC_H69
133229	AA203433	Hs.6834	KIAA1014 protein	3	OVCAR_cells, 293T_cells, EB_cells
130405	H88359	Hs.155396	nuclear factor (erythroid-derived 2)-lik	3	PRSC_con, EB_cells, DU145_cells
107881	AA025567	Hs.61273	H sapiens chromosome 19; cosmid R32611	3	Lu_SQ_H520, MCF7, Lu_AD_358
116589	D59570	Hs.17132	ESTs	3	EB_cells, A549_cells, HS578T_cells
105479	AA255546	Hs.23467	ESTs	2.99	Lu_SC_H345, PC3_cells, OVCAR_cells
115560	AA393812	Hs.50575	ESTs; Moderately similar to IIII ALU SUB	2.99	EB_cells, Lu_SC_H69, Fibroblasts 2
130166	AA350690	Hs.151411	KIAA0916 protein	2.98	LNCaP_cells, EB_cells, 293T_cells
123355	AA504773	Hs.160657	ESTs	2.98	PRSC_con, PRSC_log, PRSC_log
109546	F01449	Hs.26954	ESTs	2.97	Lu_SC_H345, HT29_cells, BT474_cells
129001	AA448946	Hs.107812	ESTs; Weakly similar to proline-rich pro	2.97	EB_cells, Lu_AD_H23, Lu_AD_358
102259	U28369	Hs.82222	sema domain; immunoglobulin domain (Ig);	2.97	EB_cells, MB231_cells, OVCAR_cells
105583	AA278907	Hs.24549	ESTs	2.96	EB_cells, DU145_cells, 293T_cells
131859	M90657	Hs.3337	transmembrane 4 superfamily member 1	2.96	A549_cells, PC3_cells, DU145_cells
114533	AA053401	Hs.177526	ESTs	2.96	293T_cells, Lu_LC_H460, PC3_cells
110220	H23543	Hs.27090	ESTs	2.95	PRSC_log, Lu_SC_H345, MB231_cells
124917	R91241	Hs.75470	hypothetical protein; expressed in osteo	2.95	Lu_SC_H345, Lu_SC_H69, PRSC_log
127111	AA805726	Hs.220509	ESTs	2.94	HS578T_cells, 293T_cells, 293T_cells
134882	N73762	Hs.90638	ESTs	2.94	EB_cells, MB-MDA-453, Fibroblasts 2
121788	AA423968	Hs.178113	ESTs; Moderately similar to kinesin like	2.94	HT29_cells, CALU6_cells, HMEC
128530	AA504343	Hs.183475	H sapiens clone 25061 mRNA seq	2.94	DU145_cells, Lu_SC_H345, Caco2
128435	AI301201	Hs.147112	ESTs	2.93	EB_cells, Lu_SQ_H520, PRSC_con
113782	W15580	Hs.15342	phosphate cytidyltransferase 1; cholin	2.93	EB_cells, Lu_AD_H23, PRSC_log
127569	AA588536	Hs.191783	ESTs	2.93	EB_cells, HS578T_cells, Lu_AD_358
109642	F04465	Hs.22394	ESTs; Weakly similar to weak similarity		
			protein US)1 [C.elegans]	2.92	PC3_cells, EB_cells, OVCAR_cells
114615	AA083812	Hs.159456	DKFZP566F123 protein	2.92	A549_cells, HS578T_cells, PRSC_con
126808	AA086320		zn52d12.s1 Stratagene muscle 937209 H sa	2.92	Lu_SC_H69, Lu_SC_H345, EB_cells
113947	W84768	Hs.141742	ESTs	2.92	DU145_cells, Fibroblasts 2, MCF7
129455	W27301	Hs.187991	DKFZP564A122 protein	2.91	OVCAR_cells, DU145_cells, CALU6_cells
107772	AA018587	Hs.40515	ESTs; Weakly similar to IIII ALU SUBFAM	2.91	OVCAR_cells, EB_cells, PC3_cells
127159	AA284097	Hs.237955	RAB7; member RAS oncogene family	2.91	293T_cells, OVCAR_cells, PC3_cells
124792	R44357	Hs.132784	ESTs; Weakly similar to cDNA EST EMBL:TO	2.91	DU145_cells, DU145_cells, CALU6_cells
109751	F10210	Hs.6679	H sapiens mRNA; cDNA DKFZp586A0424 (from		2.91 EB_cells, Lu_SC_H69, 293T_cells
128926	AA481403	Hs.107213	ESTs; Highly similar to NY-REN-6 antigen	2.9	CALU6_cells, EB_cells, OVCAR_cells
106637	AA459961	Hs.250824	ESTs	2.9	EB_cells, Caco2, MB-MDA-435s
132164	U84573	Hs.41270	procollagen-lysine; 2-oxoglutarate 5-dio	2.9	DU145_cells, HS578T_cells, A549_cells
128099	AA905327		ESTs	2.9	MCF7, HMEC (total RNA), 293T_cells
104818	AA034947	Hs.24831	ESTs	2.9	EB_cells, Lu_LC_H460, 293T_cells
126050	H27267	Hs.75860	hydroxyacyl-Coenzyme A dehydrogenase/3-k		
			-Coenzyme A hydratase (trifunctional pro	2.89	
116696	F09780	Hs.66124	EST	2.89	LNCaP_cells, DU145_cells, OVCAR_cells
135204	AA421146	Hs.183418	cell division cycle 2-like 1 (PITSLRE pr	2.89	CALU6_cells, 293T_cells, 293T_cells
134946	AA406534	Hs.193053	ESTs; Weakly similar to hiwi [H.sapiens]	2.88	PC3_cells, EB_cells, LNCaP_cells
114975	AA250850	Hs.13944	adrenergic; beta; receptor kinase 2	2.88	EB_cells, LNCaP_cells, Caco2
113792	W35212	Hs.17691	ESTs; Weakly similar to env protein [H.s	2.88	EB_cells, EB_cells, EB_cells
102322	U34962	Hs.54473	cardiac-specific homeo box	2.88	MB-MDA-435s, Lu_SC_H69, CALU6_cells
125642	AI096849	Hs.25274	ESTs; Moderately similar to putative sev	2.88	293T_cells, HT29_cells, Lu_AD_H23
100288	D43951	Hs.153834	Human mRNA for KIAA0099 gene; complete	2.88	PC3_cells, CALU6_cells, 293T_cells
105878	AA400184	Hs.24656	KIAA0907 protein	2.88	293T_cells, LNCaP_cells, EB_cells
125262	W88755	Hs.108514	ESTs; Highly similar to Trio [H.sapiens]	2.88	OVCAR_cells, DU145_cells, 293T_cells
114419	AA011448	Hs.106532	ESTs; Weakly similar to transposon LRE2	2.88	DU145_cells, HS578T_cells, MB231_cells
130639	D59711	Hs.17132	ESTs	2.87	EB_cells, Lu_AD_H23, Fibroblasts 2
130972	AA370302	Hs.21739	H sapiens mRNA; cDNA DKFZp586I1518 (from		EB_cells, A549_cells, OVCAR_cells
126906	H66949	Hs.168069	ESTs; Highly similar to CALCIUM-BINDING	2.87	2.87 293T_cells, A549_cells, Lu_LC_H460
121807	AA424507	Hs.247478	H sapiens Mut S homolog 5 gene; partial		Lu_SC_H345, Lu_SC_H69, LNCaP_cells
			1C7; LST-1; lymphotoxin beta; tumor necr	2.87	
105474	AA255440	Hs.219614	F-box protein FBL11	2.87	Lu_SC_H69, HT29_cells, RPWE_2
122348	AA443695	Hs.231476	ESTs	2.87	Lu_AD_H23, Caco2, EB_cells
116368	AA521186	Hs.94217	ESTs	2.86	HT29_cells, Lu_SC_H69, BT474_cells
135143	AA102644	Hs.69559	KIAA1096 protein	2.86	MB-MDA-453, OVCAR_cells, Lu_SC_H69
106711	AA464741	Hs.143187	Human DNA from chromosome 19-specific co	2.86	PC3_cells, EB_cells, 293T_cells
128583	L32832	Hs.101842	AT-binding transcription factor 1	2.85	EB_cells, Lu_AD_H23, Lu_LC_H460
132139	AA213410	Hs.111554	ADP-ribosylation factor-like 7	2.85	LNCaP_cells, Caco2, EB_cells
114484	AA034378	Hs.252351	HERV-H LTR-associating 2	2.85	A549_cells, HS578T_cells, Caco2
124620	N74051	Hs.194092	ESTs; Weakly similar to IIII ALU SUBFAM	2.85	PC3_cells, Lu_SQ_H520, MB231_cells
100403	D85527		H sapiens mRNA for LIM domain, partial c	2.84	Lu_SC_H345, MB231_cells, Fibroblasts 2
129795	AA448627	Hs.125163	ESTs; Weakly similar to IIII ALU SUBFAM	2.84	Lu_AD_358, Lu_AD_358, MB231_cells
128258	T70214	Hs.183548	ESTs	2.84	Lu_SC_H345, OVCAR_cells, PC3_cells
102662	U70321	Hs.130227	tumor necrosis factor receptor superfam	2.84	DU145_cells, DU145_cells, OVCAR_cells
132232	AA252030	Hs.42640	ESTs	2.84	EB_cells, Lu_AD_H23, Fibroblasts 2
106111	AA421638	Hs.6451	ESTs	2.83	EB_cells, OVCAR_cells, Lu_SC_H345
123963	C13961	Hs.210115	EST	2.83	EB_cells, Lu_LC_H460, OVCAR_cells
122783	AA459895	Hs.98988	ESTs	2.83	DU145_cells, LNCaP_cells, Lu_SC_H345
112788	R96586	Hs.163630	ESTs	2.82	EB_cells, MCF7, Lu_SC_H69
					DU145_cells, Lu_SC_H345, EB_cells

120823	AA347546	Hs.185780	ESTs	2.82	HT29_cells, HMEC (total RNA), BT474_cells
100378	D80009	Hs.10848	KIAA0187 gene product	2.82	Caco2, PC3_cells, OVCAR_cells
114677	AA114163	Hs.188877	ESTs	2.81	DU145_cells, MCF7, EB_cells
108085	AA045602	Hs.62863	ESTs; Moderately similar to serine/threo	2.81	EB_cells, Lu_AD_H23, HT29_cells
104938	AA064627	Hs.18341	ESTs; Highly similar to CGI-72 protein [2.81	PC3_cells, HS578T_cells, OVCAR_cells
128743	AA237013	Hs.2730	heterogeneous nuclear ribonucleoprotein	2.8	OVCAR_cells, LNCaP_cells, Caco2
124314	H94877	Hs.215766	GTP-binding protein	2.8	LNCaP_cells, DU145_cells, Caco2
134227	D79986	Hs.80338	KIAA0164 gene product	2.8	LNCaP_cells, A549_cells, EB_cells
122922	AA476268		zw44h1.s1 Soares_total_fetus_Nb2HF8_9w H		
			contains Alu repetitive element;contain	2.79	Lu_SC_H345, OVCAR_cells, Lu_SC_H69
126096	H42968	Hs.155606	paired mesoderm homeo box 1	2.78	Lu_AD_H23, Lu_SC_H69, Lu_LC_H460
129295	AA424782	Hs.110121	SEC7 homolog	2.78	Lu_AD_H23, EB_cells, Lu_SC_H345
116155	AA460957	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.78	EB_cells, OVCAR_cells, 293T_cells
105911	AA401809	Hs.189910	ESTs	2.77	293T_cells, HS578T_cells, DU145_cells
119232	T03475	Hs.258624	EST	2.77	EB_cells, Lu_AD_H23, Lu_AD_358
131168	AA482007	Hs.23788	ESTs; Weakly similar to homology with is	2.77	EB_cells, Lu_LC_H460, MCF7
106048	AA416697	Hs.15330	ESTs	2.76	OVCAR_cells, Lu_SC_H345, 293T_cells
124352	N21626	Hs.102406	ESTs	2.76	MCF7, MB-MDA-453, CALU6_cells
129349	D86974	Hs.110613	KIAA0220 protein	2.76	DU145_cells, HT29_cells, Lu_SC_H69
106120	AA423808	Hs.8765	RNA helicase-related protein	2.76	OVCAR_cells, EB_cells, 293T_cells
100643	HG2755-H		T-Plastin	2.75	293T_cells, PC3_cells, HS578T_cells
128500	U60521	Hs.100641	caspase 9; apoptosis-related cysteine pr	2.75	Lu_AD_358, Lu_SC_H69, Lu_SC_H345
126090	R44789	Hs.119486	ESTs; Weakly similar to rostral cerebell	2.75	Lu_SC_H69, Lu_SC_H345, BT474_cells
127064	Z43709		HSC1JA091 normalized infant brain cDNA H	2.75	Caco2, A549_cells, HT29_cells
132989	AA480074	Hs.394	adrenomedullin	2.75	EB_cells, OVCAR_cells, DU145_cells
108888	AA135606	Hs.189384	ESTs; Weakly similar to IIII ALU SUBFAMI	2.75	OVCAR_cells, LNCaP_cells, DU145_cells
119579	W42429	Hs.150607	ESTs	2.74	293T_cells, DU145_cells, PC3_cells
100387	D83777	Hs.75137	KIAA0193 gene product	2.74	CALU6_cells, DU145_cells, Caco2
114744	AA135407	Hs.252351	HERV-H LTR-associating 2	2.74	PC3_cells, Lu_SC_H520, RPWE_2
129092	AA011243	Hs.63525	poly(rC)-binding protein 2	2.74	EB_cells, MCF7, DU145_cells
125360	AA677978	Hs.189741	ESTs	2.74	Lu_AD_358, Lu_AD_358, PRSC_log
107874	AA025305	Hs.25218	ESTs; Weakly similar to reverse transcri	2.74	Lu_SC_H345, Lu_LC_H460, HT29_cells
114086	Z38266	Hs.12770	H sapiens PAC clone DJ0777023 from 7p14-	2.74	EB_cells, LNCaP_cells, BT474_cells
116180	AA463902	Hs.94964	ESTs	2.73	Lu_SC_H69, PRSC_con, Lu_AD_H23
126027	M61982		ESTs	2.73	LNCaP_cells, DU145_cells, A549_cells
116339	AA496257	Hs.72165	ESTs; Weakly similar to R26984_1 [H.sapi	2.73	EB_cells, DU145_cells, OVCAR_cells
105387	AA236951	Hs.108636	chromosome 1 open reading frame 9	2.72	PC3_cells, EB_cells, Caco2
111359	N91273	Hs.27179	ESTs	2.72	EB_cells, LNCaP_cells, 293T_cells
106680	AA461458	Hs.24789	ESTs	2.72	PC3_cells, Lu_SC_H345, Caco2
118598	N69136	Hs.214343	ESTs	2.72	MB-MDA-453, 293T_cells, BT474_cells
107913	AA027161	Hs.59523	ESTs; Highly similar to G1 TO S PHASE TR	2.71	EB_cells, MCF7, Lu_SC_H345
134315	AA136269	Hs.81648	ESTs; Weakly similar to S164 [H.sapiens]	2.71	EB_cells, DU145_cells, HMEC
135233	AA127463	Hs.9683	protein-kinase; interferon-inducible dou	2.71	EB_cells, OVCAR_cells, Caco2
112932	T15470	Hs.189810	ESTs	2.7	293T_cells, Lu_AD_H23, PC3_cells
119053	R11501		yf28f1.s1 Soares fetal liver spleen 1NFL		
			contains Alu repetitive element; mRNA	2.7	Lu_SC_H345, Lu_SC_H69, DU145_cells
131206	AA044078	Hs.24210	ESTs	2.7	Caco2, Lu_SC_H345, HS578T_cells
126759	AA063642		ESTs; Highly similar to (define not ava	2.7	LNCaP_cells, Lu_SC_H345, Lu_SC_H69
131060	AA160890	Hs.22564	myosin VI	2.7	LNCaP_cells, MCF7, HT29_cells
132135	N69101	Hs.40730	ESTs	2.7	EB_cells, 293T_cells, OVCAR_cells
120835	AA348446	Hs.96906	ESTs	2.7	Fibroblasts 2, CALU6_cells, RPWE_2
113815	W45311	Hs.14756	ESTs	2.7	EB_cells, PC3_cells, DU145_cells
133234	T90092	Hs.6853	ESTs; Weakly similar to IIII ALU SUBFAMI	2.69	Lu_SC_H345, OVCAR_cells, DU145_cells
126819	AA305536	Hs.161489	ESTs	2.69	EB_cells, DU145_cells, Caco2
125198	W69474	Hs.225550	ESTs	2.69	Lu_SC_H345, Lu_AD_H23, Lu_AD_H23
108394	AA075144		zm86f6.s1 Stratagene ovarian cancer (#93		
			gb:X1664 TRANSLATIONALLY CONTROLLED TUM		
134456	X59405	Hs.83532	membrane cofactor protein (CD46; trophob	2.69	2.69 HMEC, HMEC (total RNA), Fibroblasts 2
111720	R23739	Hs.23585	KIAA1078 protein	2.68	EB_cells, LNCaP_cells, DU145_cells
114617	AA084148	Hs.110659	ESTs	2.68	PC3_cells, HMEC (total RNA), OVCAR_cells
127787	AA731764		ESTs; Weakly similar to IIII ALU CLASS C	2.68	DU145_cells, LNCaP_cells, OVCAR_cells
101437	M20681	Hs.7594	solute carrier family 2 (facilitated glu	2.68	HT29_cells, Lu_SC_H345, MB231_cells
133761	AA477223	Hs.75922	brain protein I3	2.68	Caco2, Lu_LC_H460, Fibroblasts 2
105869	AA399574	Hs.19086	ESTs	2.68	EB_cells, Lu_AD_H23, Lu_SC_H345
125191	W67257	Hs.138871	ESTs; Weakly similar to IIII ALU CLASS B	2.68	PC3_cells, MCF7, MB231_cells
116238	AA479362	Hs.47144	DKFZP586N0819 protein	2.67	OVCAR_cells, DU145_cells, LNCaP_cells
124770	R40555	Hs.120429	ESTs	2.67	OVCAR_cells, DU145_cells, LNCaP_cells
101764	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium		Lu_AD_H23, Lu_SC_H69, PRSC_con
			murine placental homolog)	2.67	
130897	AA063428	Hs.21022	adaptor-related protein complex 3; beta	2.67	A549_cells, MB231_cells, OVCAR_cells
133303	H61046	Hs.237352	EST	2.66	EB_cells, Lu_AD_H23, HMEC
124724	R12405	Hs.112423	H sapiens mRNA; cDNA DKFZp586i1420 (from		Lu_SC_H345, Lu_SC_H69, PRSC_con
123697	AA609601	Hs.221224	ESTs	2.66	2.66 Lu_SC_H345, BT474_cells, OVCAR_cells
111548	R09170	Hs.258707	ESTs	2.66	OVCAR_cells, 293T_cells, Lu_SC_H69
107005	AA598679	Hs.194215	ESTs	2.66	293T_cells, CALU6_cells, A549_cells
105569	AA278399	Hs.20596	ESTs	2.65	Lu_SC_H345, OVCAR_cells, Lu_AD_H23
					MCF7, HT29_cells, BT474_cells

132687	AB002301	Hs.54985	KIAA0303 protein	2.65	HMEC (total RNA), HMEC, LNCaP_cells
104105	AA422123	Hs.42457	ESTs	2.65	Lu_SC_H345, Lu_SC_H69, DU145_cells
121335	AA404418	Hs.144953	ESTs	2.65	EB_cells, Fibroblasts 2, DU145_cells
124853	R61693	Hs.172330	ESTs; Weakly similar to Wiskott-Aldrich	2.64	Lu_SC_H69, 293T_cells, EB_cells
124253	H69742	Hs.102201	ESTs	2.64	DU145_cells, OVCAR_cells, Lu_SC_H345
123044	AA481549	Hs.165694	ESTs	2.64	EB_cells, Lu_SC_H69, Lu_SC_H345
129535	AA608852	Hs.112603	EST	2.64	EB_cells, Lu_AD_H23, Fibroblasts 2
131397	AB002336	Hs.26395	erythrocyte membrane protein band 4.1-li	2.64	EB_cells, DU145_cells, Caco2
130175	X75593	Hs.151536	RAB13; member RAS oncogene family	2.64	Fibroblasts 2, PRSC_con, HS578T_cells
127507	AI188445	Hs.152618	ESTs	2.63	EB_cells, Lu_AD_H23, Lu_SC_H460
105377	AA236702	Hs.24371	ESTs	2.63	Caco2, EB_cells, CALU6_cells
114671	AA112679	Hs.252291	ESTs; Weakly similar to IIII ALU SUBFAMI	2.63	EB_cells, DU145_cells, Caco2
133726	W19983	Hs.75761	SFRS protein kinase 1	2.63	EB_cells, Lu_AD_H23, Lu_SC_H69
132380	H68018		yr76h05.r1 Soares fetal liver spleen 1NF IMAGE:211257 5', mRNA seq.	2.62	EB_cells, Lu_AD_H23, Lu_SC_H69
127986	AI370418	Hs.192050	ESTs; Weakly similar to IIII ALU CLASS A	2.62	DU145_cells, OVCAR_cells, LNCaP_cells
116208	AA476333	Hs.42532	ESTs	2.61	DU145_cells, PRSC_con, Fibroblasts 2
130946	AA069456	Hs.21490	KIAA0438 gene product	2.6	LNCaP_cells, DU145_cells, HS578T_cells
106687	AA463234	Hs.119387	KIAA0792 gene product	2.59	EB_cells, MB-MDA-453, Caco2
101551	M31606	Hs.196177	phosphorylase kinase; gamma 2 (testis)	2.59	LNCaP_cells, EB_cells, MB-MDA-453
114479	AA032084	Hs.124841	ESTs; Moderately similar to transformati	2.59	DU145_cells, Caco2, OVCAR_cells
111863	R37495	Hs.23578	ESTs	2.59	HT29_cells, MB231_cells, Lu_SC_H520
129018	AA029973	Hs.107979	small membrane protein 1	2.59	A549_cells, EB_cells, HS578T_cells
107058	AA600357	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	2.58	DU145_cells, Lu_SC_H345, EB_cells
126175	AA056181	Hs.17311	DKFZP434N161 protein	2.58	Lu_SC_H345, DU145_cells, LNCaP_cells
131979	D52154	Hs.172458	iduronate 2-sulfatase (Hunter syndrome)	2.58	DU145_cells, PC3_cells, A549_cells
126122	H80181		ESTs	2.58	DU145_cells, OVCAR_cells, LNCaP_cells
106961	AA504110	Hs.18063	ESTs	2.58	HMEC, DU145_cells, DU145_cells
114730	AA133527	Hs.126925	ESTs; Weakly similar to The KIAA0138 gen	2.58	DU145_cells, LNCaP_cells, MCF7
117342	N24020	Hs.132913	ESTs	2.58	HS578T_cells, DU145_cells, LNCaP_cells
131622	AA424813	Hs.29692	ESTs	2.57	PRSC_con, PRSC_log, HS578T_cells
104904	AA055560	Hs.13179	ESTs; Moderately similar to IIII ALU SUB	2.57	Lu_SC_H345, Lu_SC_H69, BT474_cells
117359	N24848	Hs.114062	ESTs; Weakly similar to T15B7.2 [C.elega	2.57	HS578T_cells, PRSC_con, EB_cells
123331	AA497013	Hs.188740	ESTs; Weakly similar to IIII ALU SUBFAMI	2.57	Lu_SC_H69, Caco2, PRSC_con
125324	R07785		yf15c06.r1 Soares fetal liver spleen 1NF contains Alu repetitive element; contain	2.57	EB_cells, Lu_AD_H23, Fibroblasts 2
129813	T33462	Hs.12600	ESTs	2.57	Lu_SC_H345, 293T_cells, Lu_SC_H69
100265	D38521	Hs.75935	KIAA0077 protein	2.57	EB_cells, LNCaP_cells, PC3_cells
134890	T40902	Hs.90786	ATP-binding cassette; sub-family C (CFTR	2.57	A549_cells, DU145_cells, EB_cells
133582	AA421874	Hs.75087	Fas-activated serine/threonine kinase	2.56	EB_cells, Lu_AD_H23, Lu_AD_358
135011	H73161	Hs.92991	ESTs; Weakly similar to C13F10.4 [C.eleg	2.56	EB_cells, LNCaP_cells, MB-MDA-453
107226	D58185	Hs.21945	ESTs	2.56	Lu_SC_H345, Lu_SC_H69, HMEC (total RNA)
126042	H62441	Hs.157082	H sapiens PAC clone DJ0988G15 from 7q33-	2.56	HMEC (total RNA), HMEC, RPWE_2
114472	AA028924	Hs.177407	ESTs; Weakly similar to IIII ALU SUBFAMI	2.56	Lu_SC_H345, Lu_SC_H69, DU145_cells
126291	N42090		yy05b07.r1 Soares melanocyte 2NbHM H sap	2.56	HMEC, HMEC (total RNA), PC3_cells
113349	T79021	Hs.14438	ESTs; Moderately similar to histamine N-	2.56	HT29_cells, PRSC_log, Lu_SC_H345
105769	AA347485	Hs.25477	ESTs; Moderately similar to rig-1 protei	2.56	Lu_AD_H23, RPWE_2, Lu_SC_H520
110918	N46423	Hs.24283	ESTs	2.56	EB_cells, CALU6_cells, DU145_cells
117170	H98153	Hs.42500	ADP-ribosylation factor-like 5	2.56	OVCAR_cells, EB_cells, LNCaP_cells
105159	AA173981	Hs.30490	CD2-associated protein	2.55	LNCaP_cells, EB_cells, DU145_cells
105726	AA292328	Hs.9754	activating transcription factor 5	2.55	MCF7, EB_cells, MB-MDA-453
132079	H67964	Hs.38694	ESTs	2.55	EB_cells, DU145_cells, HS578T_cells
131813	X51757	Hs.3268	heat shock 70kD protein 6 (HSP70B)	2.55	Lu_AD_H23, MB231_cells, Fibroblasts 2
133538	L14837	Hs.74614	tight junction protein 1 (zona occludens	2.54	DU145_cells, Caco2, A549_cells
124981	T40849	Hs.114034	maternal G10 transcript	2.54	EB_cells, Caco2, LNCaP_cells
122028	AA431306	Hs.98722	ESTs	2.54	Fibroblasts 2, BT474_cells, HMEC (total RNA)
122487	AA448332	Hs.80598	transcription elongation factor A (SII);	2.54	Lu_SC_H345, MCF7, MB-MDA-453
119315	T41152	Hs.90485	ESTs	2.54	Lu_SC_H345, MB-MDA-435s, PRSC_con
107957	AA031948	Hs.57548	ESTs	2.54	A549_cells, RPWE_2, DU145_cells
122457	AA447780	Hs.96418	ESTs	2.54	DU145_cells, EB_cells, A549_cells
103572	Z25749	Hs.75538	ribosomal protein S7	2.54	EB_cells, CALU6_cells, DU145_cells
124395	N29963	Hs.193977	ESTs	2.54	HMEC (total RNA), HMEC, RPWE_2
116024	AA451748	Hs.83883	Human DNA seq from clone 718J7 on chromo phosphoenolpyruvate carboxykinase 1; ES	2.53	LNCaP_cells, RPWE_2, MB-MDA-453
134361	D43682	Hs.82208	acyl-Coenzyme A dehydrogenase; very long	2.53	LNCaP_cells, CALU6_cells, DU145_cells
130420	U60975		Human hybrid receptor gp25 precursor mRN	2.53	EB_cells, HMEC (total RNA), Caco2
100336	D63478	Hs.8127	KIAA0144 gene product	2.53	BT474_cells, HT29_cells, Lu_AD_358
105519	AA258063	Hs.23438	ESTs	2.53	EB_cells, Caco2, MB-MDA-435s
124684	R02401	Hs.221078	ESTs	2.53	Lu_SC_H345, OVCAR_cells, Lu_SC_H69
105852	AA398933	Hs.172613	solute carrier family 12 (potassium/chlo	2.52	LNCaP_cells, DU145_cells, EB_cells
105012	AA116036	Hs.9329	chromosome 20 open reading frame 1	2.52	CALU6_cells, Caco2, DU145_cells
126534	W39128	Hs.247901	Human DNA seq from clone 8B1 on chromoso -CELL MEMBRANE GLYCOPROTEIN PC-1; the ge	2.52	2.52 BT474_cells, LNCaP_cells, Lu_AD_H23
135334	AA053134	Hs.241558	ariadne-2 (D. melanogaster) homolog (all	2.52	293T_cells, CALU6_cells, DU145_cells
128538	R44214	Hs.101189	ESTs	2.52	EB_cells, Lu_AD_H23, Lu_SC_H345
109865	H02566	Hs.191268	H sapiens mRNA; cDNA DKFZp434N174 (from	2.52	2.52 DU145_cells, LNCaP_cells, OVCAR_cells

118579	N68905		small inducible cytokine A5 (RANTES)	2.51	Lu_SC_H345, LNCaP_cells, Lu_SC_H69
117590	N34904		ESTs; Moderately similar to IIII ALU SUB	2.51	Lu_SC_H345, DU145_cells, Lu_SC_H69
104340	F15201		ESTs	2.51	Lu_SC_H345, PRSC_con, PRSC_log
122455	AA447744	Hs.99141	EST	2.51	Caco2, Lu_SC_H69, 293T_cells
109339	AA211901	Hs.86430	ESTs	2.51	EB_cells, DU145_cells, CALU6_cells
123258	AA490929	Hs.105274	ESTs	2.51	EB_cells, Lu_AD_H23, Lu_SC_H69
118467	N66763	Hs.43080	ESTs	2.51	CALU6_cells, HS578T_cells, OVCAR_cells
106044	AA416546	Hs.149436	kinesin family member 5B	2.51	EB_cells, Caco2, DU145_cells
107480	W58057	Hs.74304	periplakin	2.5	Caco2, OVCAR_cells, HMEC (total RNA)
111760	R26892	Hs.221434	ESTs	2.5	Lu_AD_H23, EB_cells, Lu_AD_358
132474	N68018	Hs.180930	TBP-associated factor 172	2.5	LNCaP_cells, EB_cells, DU145_cells
103423	X97249	Hs.123122	FSH primary response (LRPR1; rat) homolo	2.5	HS578T_cells, Lu_SC_H345, PC3_cells
123488	AA599708	Hs.187764	ESTs; Weakly similar to IIII ALU SUBFAMI	2.49	OVCAR_cells, Lu_SC_H345, DU145_cells
100475	D90276	Hs.12	carcinoembryonic antigen-related cell ad	2.49	MB-MDA-453, 293T_cells, CALU6_cells
112003	R42547	Hs.172551	ESTs	2.49	EB_cells, Lu_AD_H23, Lu_SC_H345
114315	Z41027	Hs.26297	ESTs	2.49	Lu_SC_H69, OVCAR_cells, Lu_AD_H23
105291	AA233311	Hs.28752	ESTs	2.49	EB_cells, CALU6_cells, DU145_cells
135354	AA188934	Hs.99367	ESTs	2.49	MB-MDA-453, Lu_SC_H69, 293T_cells
107521	X78262		H.sapiens mRNA for TRE5	2.49	Lu_SC_H345, Lu_SC_H69, PRSC_con
108373	AA074393	Hs.61950	ESTs; Weakly similar to nuclear protein	2.49	MCF7, MB-MDA-453, Lu_SC_H345
108836	AA132061	Hs.222727	ESTs; Weakly similar to ubiquitous TPR m	2.48	DU145_cells, Lu_SC_H345, Lu_SC_H345
110386	H45516	Hs.33268	ESTs	2.48	PC3_cells, OVCAR_cells, Lu_SC_H520
129658	M22348	Hs.131255	ubiquinol-cytochrome c reductase binding	2.48	LNCaP_cells, CALU6_cells, PC3_cells
134283	H12661	Hs.8107	H sapiens mRNA; cDNA DKFZp586B0918 (from	2.48	HMEC (total RNA), HS578T_cells, HMEC
101844	M93425	Hs.62	protein tyrosine phosphatase; non-recept	2.48	DU145_cells, EB_cells, CALU6_cells
133461	M33318	Hs.183584	cytochrome P450; subfamily IIA (phenobar	2.48	EB_cells, Lu_AD_H23, Lu_AD_358
103545	Z14000	Hs.35384	ring finger protein 1	2.47	HT29_cells, Lu_SC_H520, BT474_cells
128440	N76763		ESTs	2.47	EB_cells, Lu_AD_H23, Lu_AD_358
134992	H05625	Hs.92414	ESTs	2.47	Lu_SC_H345, CALU6_cells, Lu_SC_H69
116295	AA489016	Hs.91216	ESTs; Highly similar to partial CDS; hum	2.47	MB-MDA-453, 293T_cells, MB-MDA-435s
107004	AA598675	Hs.239475	ESTs	2.47	LNCaP_cells, Caco2, OVCAR_cells
132137	AA282312	Hs.4076	CTD (carboxy-terminal domain; RNA polyme	2.46	Lu_SC_H69, HMEC, EB_cells
126390	W28286	Hs.100090	tetraspan 3	2.46	EB_cells, DU145_cells, LNCaP_cells
113050	T26366	Hs.22711	EST; Weakly similar to 60S RIBOSOMAL PRO	2.46	Lu_SC_H460, EB_cells, Lu_AD_358
101667	M60858	Hs.79110	nucleolin	2.46	PC3_cells, 293T_cells, A549_cells
108569	AA085398		zn7e3.s1 Stratagene hNT neuron (#937233)		
			IMAGE:546748 3', mRNA seq	2.45	HT29_cells, BT474_cells, Lu_SC_H520
117186	H98988	Hs.42612	ESTs	2.45	EB_cells, Lu_AD_H23, Lu_AD_358
129091	AA044622	Hs.183755	Human Chromosome 16 BAC clone CIT987SK-A	2.45	EB_cells, Lu_AD_H23, Lu_AD_H23
128468	T23625	Hs.258674	EST	2.45	Lu_AD_H23, EB_cells, Lu_SC_H69
117498	N31726	Hs.44268	ESTs; Highly similar to myelin gene expr	2.45	Lu_SC_H69, DU145_cells, OVCAR_cells
105407	AA243478	Hs.5206	ESTs	2.45	EB_cells, 293T_cells, PC3_cells
128941	R55763	Hs.107287	ESTs	2.44	EB_cells, LNCaP_cells, A549_cells
116486	C14128	Hs.251980	EST	2.44	MB-MDA-435s, HS578T_cells, 293T_cells
134869	T35288	Hs.90421	ESTs; Moderately similar to IIII ALU SUB	2.44	EB_cells, Lu_AD_H23, Lu_AD_358
130664	R09049	Hs.17625	ESTs	2.44	PC3_cells, EB_cells, A549_cells
107985	AA035638	Hs.71968	H sapiens mRNA; cDNA DKFZp564F053 (from	2.44	PRSC_con, PRSC_log, Caco2
110300	H37820	Hs.124147	ESTs	2.44	MB-MDA-453, Caco2, OVCAR_cells
113471	T87174	Hs.16341	ESTs; Moderately similar to IIII ALU SUB	2.44	Caco2, OVCAR_cells, LNCaP_cells
131474	U28749	Hs.2726	high-mobility group (nonhistone chromoso	2.44	CALU6_cells, OVCAR_cells, 293T_cells
120791	AA342802	Hs.194031	ESTs	2.44	Lu_AD_H23, Lu_SC_H520, PRSC_con
133733	AA416973	Hs.75798	Human DNA seq from clone 1183I21 on chro		
			to predicted fly and worm proteins. Con	2.43	EB_cells, Caco2, DU145_cells
119977	W88579	Hs.124744	ESTs	2.43	HT29_cells, HMEC (total RNA), HMEC
134921	W60186	Hs.169487	Kreisler (mouse) maf-related leucine zip	2.43	LNCaP_cells, HS578T_cells, MB-MDA-453
132295	H66351	Hs.181042	Dmx-like 1	2.43	Lu_SC_H69, BT474_cells, Lu_SC_H520
133395	AA491296	Hs.72805	ESTs	2.43	EB_cells, LNCaP_cells, OVCAR_cells
106728	AA465355	Hs.153768	U3 snoRNP-associated 55-kDa protein	2.43	EB_cells, Lu_AD_H23, PC3_cells
116370	AA521256	Hs.236204	ESTs; Moderately similar to NUCLEAR PORE	2.43	EB_cells, A549_cells, 293T_cells
113936	W81552	Hs.83623	nuclear receptor subfamily 1; group I; m	2.43	293T_cells, OVCAR_cells, Fibroblasts 2
128862	R61297	Hs.108673	eukaryotic translation initiation factor	2.43	EB_cells, DU145_cells, DU145_cells
111614	R12581	Hs.191146	ESTs	2.43	HMEC (total RNA), Fibroblasts 2, MB-MDA-435s
111993	R42241	Hs.106359	ESTs	2.43	A549_cells, DU145_cells, CALU6_cells
131554	AA100026	Hs.28669	ESTs; Weakly similar to PROTEIN-TYROSINE	2.43	EB_cells, LNCaP_cells, Caco2
130983	N71215	Hs.21862	NCK-associated protein 1	2.42	EB_cells, Caco2, A549_cells
131654	AA497050	Hs.30204	ESTs	2.42	MCF7, MB-MDA-435s, Lu_SC_H345
105014	AA121123	Hs.191374	ESTs	2.42	EB_cells, Lu_AD_H23, Lu_SC_H460
106300	AA435840	Hs.19114	high-mobility group (nonhistone chromoso	2.42	EB_cells, Lu_SC_H345, A549_cells
102386	U40998	Hs.81728	unc119 (C.elegans) homolog	2.42	OVCAR_cells, EB_cells, DU145_cells
112517	R68589	Hs.23721	ESTs	2.42	Caco2, MCF7, DU145_cells
125375	H72971		KIAA0277 gene product	2.42	Lu_SC_H345, OVCAR_cells, Lu_SC_H69
123808	AA620552	Hs.25682	ESTs; Weakly similar to PHOSPHATIDYLETHA	2.42	EB_cells, Lu_AD_H23, Lu_SC_H69
114950	AA243503	Hs.11801	adenosine A2b receptor pseudogene	2.42	MB-MDA-453, HT29_cells, Lu_SC_H460
129906	H39216	Hs.239970	ESTs; Weakly similar to ZNF91L [H.sapien	2.41	Lu_SC_H345, Fibroblasts 2, DU145_cells
103408	X95876	Hs.198252	G protein-coupled receptor 9	2.41	RPWE_2, PRSC_log, Lu_SC_H345
129703	AA401348	Hs.179999	ESTs	2.41	EB_cells, 293T_cells, DU145_cells

105693	AA287104	Hs.181368	U5 snRNP-specific protein (220 kD); orth	2.41	293T_cells, CALU6_cells, A549_cells
106532	AA453628	Hs.37443	ESTs	2.41	EB_cells, OVCAR_cells, Caco2
132132	AA010933	Hs.4055	core promoter element binding protein	2.41	HMEC, HMEC (total RNA), EB_cells
111409	R00311	Hs.18798	EST; Weakly similar to IIII ALU SUBFAMIL	2.41	Lu_SC_H345, Lu_SC_H69, PRSC_con
133813	M26657	Hs.250711	dipeptidyl carboxypeptidase 1 (angiotens	2.41	HT29_cells, BT474_cells, MB231_cells
127240	AA888387	Hs.243845	ESTs; Moderately similar to IIII ALU SUB	2.41	Lu_SC_H345, DU145_cells, LNCaP_cells
104975	AA086071	Hs.50758	chromosome-associated polypeptide C	2.41	OVCAR_cells, DU145_cells, PC3_cells
118078	N54321	Hs.47790	EST	2.41	EB_cells, Fibroblasts 2, HMEC (total RNA)
115840	AA429253	Hs.58103	A kinase (PRKA) anchor protein 9	2.41	OVCAR_cells, EB_cells, PC3_cells
101186	L20298	Hs.179881	core-binding factor; beta subunit	2.4	EB_cells, DU145_cells, CALU6_cells
113098	T40936	Hs.8349	ESTs	2.4	Caco2, HT29_cells, EB_cells
115185	AA259140	Hs.60238	ESTs	2.4	Lu_SC_H69, EB_cells, Caco2
113778	W15263	Hs.5422	ESTs	2.4	Caco2, MB-MDA-435s, LNCaP_cells
128261	A1061213	Hs.13179	ESTs; Moderately similar to IIII ALU SUB	2.4	DU145_cells, LNCaP_cells, OVCAR_cells
132210	AA235013	Hs.42322	A kinase (PRKA) anchor protein 2	2.4	Caco2, DU145_cells, PRSC_log
112561	R72427	Hs.129873	ESTs; Weakly similar to CYTOCHROME P450	2.4	2.4 Lu_SC_H520, Lu_AD_H23, EB_cells
127598	AA610677	Hs.168851	ESTs	2.4	LNCaP_cells, DU145_cells, OVCAR_cells
106664	AA460969	Hs.7510	mitogen-activated protein kinase kinase	2.4	OVCAR_cells, 293T_cells, A549_cells
131367	AA456687	Hs.26057	ESTs	2.4	EB_cells, MB-MDA-453, 293T_cells
103163	X67683		H.sapiens mRNA for keratin 4	2.39	EB_cells, Lu_AD_H23, Lu_AD_358
109639	F04444	Hs.6217	ESTs; Weakly similar to IIII ALU SUBFAMIL	2.39	EB_cells, Lu_SC_H345, Lu_SC_H69
112007	R42671	Hs.140853	EST; Weakly similar to IIII ALU SUBFAMIL	2.39	MB-MDA-435s, Lu_SC_H345, Lu_AD_H23
100023			AFFX control: BioC-3	2.39	Caco2, Lu_AD_358, LNCaP_cells
119923	W86214	Hs.184642	ESTs	2.39	EB_cells, HS578T_cells, DU145_cells
127705	AJ003307		AJ003307 Selected chr 21 cDNA library H	2.39	Lu_AD_H23, Lu_SC_H345, Lu_LC_H460
130362	AA182658	Hs.179817	DKFZP586F0222 protein	2.39	EB_cells, DU145_cells, PC3_cells
100168	D14874	Hs.394	adrenomedullin	2.39	Fibroblasts 2, Caco2, HS578T_cells
134261	AA227678	Hs.8084	Human DNA seq from clone 465N24 on chr 1		
			Contains two novel genes; ESTs; GSSs an	2.39	
103392	X94563		H.sapiens dbi/acbp gene exon 1 & 2	2.38	PRSC_con, MB-MDA-453, LNCaP_cells
129888	U81001	Hs.131891	Human SNRPN mRNA; 3' UTR; partial seq	2.38	EB_cells, Lu_AD_H23, Lu_SC_H69
130119	T12649	Hs.251653	tubulin; beta; 2	2.38	LNCaP_cells, Lu_SC_H69, Lu_LC_H460
118136	N57710	Hs.233952	proteasome (prosome; macropain) subunit;	2.38	Lu_AD_H23, Lu_LC_H460, Lu_LC_H460
131163	H80107	Hs.23754	ESTs	2.38	293T_cells, OVCAR_cells, HS578T_cells
115964	AA446622	Hs.74313	ESTs	2.38	Lu_AD_H23, Lu_SC_H69, Lu_SC_H345
135026	H59730	Hs.93231	ESTs	2.37	EB_cells, LNCaP_cells, DU145_cells
133300	D51401	Hs.70333	ESTs	2.37	EB_cells, 293T_cells, Lu_SC_H69
129948	H69281	Hs.13643	ESTs	2.37	OVCAR_cells, Caco2, CALU6_cells
112505	R67923	Hs.23368	ESTs	2.37	EB_cells, Lu_AD_H23, Lu_SC_H345
130715	T98227	Hs.171952	occludin	2.37	DU145_cells, OVCAR_cells, 293T_cells
120301	AA192163	Hs.104085	EST	2.37	Caco2, LNCaP_cells, DU145_cells
128062	AA379500	Hs.193155	ESTs	2.37	Lu_AD_H23, EB_cells, PRSC_con
127154	AA789101	Hs.198860	ESTs; Weakly similar to IIII ALU SUBFAMIL	2.37	EB_cells, LNCaP_cells, DU145_cells
102814	U90716	Hs.79187	coxsackie virus and adenovirus receptor	2.37	HS578T_cells, MCF7, Lu_SC_H69
120239	Z41691	Hs.65919	ESTs	2.37	OVCAR_cells, DU145_cells, Lu_SC_H345
106829	AA481883	Hs.31236	ESTs; Weakly similar to Unknown [H.sapie	2.37	EB_cells, DU145_cells, LNCaP_cells
132681	AA435762	Hs.54894	ESTs; Highly similar to unknown [H.sapie	2.37	EB_cells, DU145_cells, OVCAR_cells
108845	AA132946	Hs.68864	ESTs	2.36	EB_cells, LNCaP_cells, PRSC_con
133226	T85327	Hs.169552	ESTs	2.36	Lu_AD_H23, Lu_AD_358, Lu_SC_H520
106789	AA478726	Hs.26373	ESTs; Moderately similar to IIII ALU SUB	2.36	Caco2, MB-MDA-453, MCF7
119236	T10166	Hs.237297	ESTs	2.36	MB-MDA-453, Caco2, OVCAR_cells
106619	AA459255	Hs.23956	ESTs	2.36	EB_cells, 293T_cells, LNCaP_cells
109178	AA181600	Hs.62741	ESTs	2.36	LNCaP_cells, A549_cells, Caco2
112724	R91753	Hs.17757	ESTs	2.36	Lu_SC_H345, LNCaP_cells, EB_cells
112655	R85069	Hs.141139	ESTs	2.36	Caco2, EB_cells, DU145_cells
132820	AA454988	Hs.57621	ESTs	2.36	Fibroblasts 2, Lu_AD_H23, Lu_LC_H460
106155	AA425309	Hs.33287	nuclear factor I/B	2.36	EB_cells, OVCAR_cells, HS578T_cells
114632	AA084742	Hs.194380	ESTs; Weakly similar to IIII ALU SUBFAMIL	2.35	OVCAR_cells, Lu_SC_H345, MB-MDA-453
134776	J05582	Hs.89603	mucin 1; transmembrane	2.35	Lu_SC_H345, Lu_LC_H460, Lu_AD_H23
101192	L20859	Hs.78452	solute carrier family 20 (phosphate tran	2.35	DU145_cells, Lu_AD_H23, Lu_AD_358
130349	W16686	Hs.171825	basic helix-loop-helix domain containing	2.35	PC3_cells, CALU6_cells, MB-MDA-435s
106389	AA446949	Hs.6236	ESTs	2.35	A549_cells, DU145_cells, HT29_cells
109637	F04426	Hs.23131	kinesin family member C3	2.35	LNCaP_cells, PC3_cells, DU145_cells
101483	M24486	Hs.76768	procollagen-proline; 2-oxoglutarate 4-di	2.35	MB-MDA-435s, A549_cells, Lu_LC_H460
131751	H18335	Hs.31562	ESTs	2.35	PC3_cells, HS578T_cells, EB_cells
131050	X13967	Hs.2250	leukemia inhibitory factor (cholinergic	2.35	DU145_cells, MB231_cells, HMEC
130097	N21159	Hs.14845	forkhead box O3A	2.34	Lu_AD_H23, PC3_cells, PRSC_log
134533	AA013468	Hs.241493	natural killer-tumor recognition seq	2.34	EB_cells, LNCaP_cells, LNCaP_cells
134839	D63479	Hs.115907	diacylglycerol kinase; delta (130kD)	2.34	EB_cells, HT29_cells, HMEC
115690	AA410894	Hs.44159	ESTs	2.34	Lu_LC_H460, Caco2, DU145_cells
129079	N91011	Hs.108502	ESTs	2.34	PC3_cells, EB_cells, OVCAR_cells
123517	AA608525	Hs.243059	EST	2.34	Lu_AD_H23, Lu_SC_H69, Lu_AD_358
126239	AA527215	Hs.75879	ribosomal protein L19	2.34	Lu_SC_H345, PC3_cells, MB-MDA-435s
124440	N46435		ESTs	2.34	BT474_cells, Lu_LC_H460, Lu_AD_H23
111468	R05809	Hs.205481	ESTs	2.34	Lu_SC_H69, HT29_cells, MB-MDA-435s
129560	H18428	Hs.113613	ESTs; Moderately similar to IIII ALU SUB	2.34	Lu_AD_H23, PRSC_log, Lu_SC_H520
					Lu_SC_H69, Lu_SC_H345, LNCaP_cells

104857	AA043219	Hs.19058	ESTs	2.34	Lu_AD_H23, Lu_SC_H345, Lu_SC_H345
109647	F04587	Hs.28241	ESTs	2.34	HS578T_cells, A549_cells, CALU6_cells
117160	H97817	Hs.183302	ESTs	2.34	EB_cells, Fibroblasts 2, Lu_SC_H69
112352	R58974	Hs.167343	ESTs	2.34	EB_cells, Lu_SC_H345, HT29_cells
113653	T95745	Hs.187433	ESTs	2.34	MB-MDA-435s, MB-MDA-453, Lu_SC_H345
131606	W56804	Hs.29385	AFG3 (ATPase family gene 3; yeast)-like	2.34	OVCAR_cells, Fibroblasts 2, MB-MDA-435s
101525	M29536	Hs.12163	eukaryotic translation initiation factor	2.34	EB_cells, Caco2, DU145_cells
125921	AA775029	Hs.122591	ESTs	2.33	293T_cells, PRSC_log, Lu_SC_H345
125775	AA213555	Hs.29205	alpha Integrin binding protein 63	2.33	EB_cells, DU145_cells, LNCaP_cells
108743	AA126917	Hs.71074	ESTs	2.33	Lu_AD_H23, Lu_AD_358, Lu_LC_H460
133735	AC002045	Hs.251928	nuclear pore complex interacting protein	2.33	LNCaP_cells, Lu_SC_H69, DU145_cells
120403	AA234916	Hs.243851	ESTs	2.33	MB231_cells, Lu_SC_H345, Lu_SC_H69
134998	R02207	Hs.92679	ESTs; Weakly similar to microtubule-base	2.33	LNCaP_cells, BT474_cells, MCF7
108456	AA079326	Hs.143654	ESTs	2.33	HT29_cells, Lu_AD_H23, RPWE_2
130552	M86667	Hs.179662	nucleosome assembly protein 1-like 1	2.33	EB_cells, A549_cells, DU145_cells
111114	N63391	Hs.9238	ESTs	2.33	Caco2, EB_cells, MB-MDA-453
127767	AI269498	Hs.125543	ESTs; Moderately similar to TADA1 protei	2.33	CALU6_cells, 293T_cells, PC3_cells
106546	AA454725	Hs.21056	H sapiens mRNA from chromosome 5q21-22;	2.33	OVCAR_cells, Caco2, LNCaP_cells
122379	AA446110	Hs.250989	EST	2.33	BT474_cells, Fibroblasts 2, MB-MDA-435s
133650	D84294	Hs.118174	tetratricopeptide repeat domain 3	2.33	Lu_SC_H345, EB_cells, EB_cells
106434	AA449099	Hs.8151	ESTs; Weakly similar to atopy related au	2.33	EB_cells, LNCaP_cells, Caco2
105297	AA233451	Hs.183858	transcriptional intermediary factor 1	2.33	EB_cells, LNCaP_cells, Caco2
115976	AA447442	Hs.86327	ESTs	2.33	EB_cells, 293T_cells, Lu_SC_H69
105788	AA351031	Hs.23965	solute carrier family 22 (organic anion	2.33	EB_cells, Lu_AD_H23, Lu_SC_H345
113774	W04550	Hs.9927	H sapiens mRNA; cDNA DKFZp564D156 (from	2.32	2.32 OVCAR_cells, EB_cells, Lu_SC_H69
110617	H68772	Hs.35820	ESTs; Weakly similar to b34l8.1 [H.sapie	2.32	Lu_SC_H345, Lu_AD_H23, PRSC_con
102234	U26312	Hs.8123	chromobox homolog 3 (Drosophila HP1 gamm	2.32	CALU6_cells, LNCaP_cells, A549_cells
114777	AA151699	Hs.184519	ESTs; Weakly similar to IIII ALU SUBFAMI	2.32	HT29_cells, Fibroblasts 2, Lu_SC_H345
125518	R20148	Hs.193851	ESTs	2.32	HT29_cells, HMEC (total RNA), MB231_cells
130814	AA256695	Hs.19813	ESTs	2.32	MB-MDA-435s, Lu_SC_H69, PRSC_log
123473	AA599143		ESTs; Moderately similar to IIII ALU SUB	2.32	LNCaP_cells, DU145_cells, Lu_SC_H345
134310	AA313414	Hs.8148	H sapiens clone 24856 mRNA seq; complete	2.32	PC3_cells, LNCaP_cells, OVCAR_cells
119192	R85375	Hs.237262	EST	2.32	Lu_SC_H69, PRSC_log, PRSC_con
114391	AA004876	Hs.133100	ESTs	2.32	PC3_cells, 293T_cells, 293T_cells
119133	R49144	Hs.119756	ESTs	2.32	PRSC_log, 293T_cells, 293T_cells
109710	F09792	Hs.12929	ESTs	2.32	Lu_AD_H23, Lu_SC_H69, Lu_SC_H345
116726	F13681	Hs.42309	ESTs	2.32	MCF7, BT474_cells, MB-MDA-453
133206	R32993	Hs.6762	ESTs; Weakly similar to similar to leucy	2.31	DU145_cells, 293T_cells, EB_cells
135163	AA125988	Hs.199955	ESTs	2.31	Lu_SC_H345, LNCaP_cells, DU145_cells
111219	N68836	Hs.19247	ESTs	2.31	OVCAR_cells, LNCaP_cells, 293T_cells
110283	H29565	Hs.12271	ESTs	2.31	BT474_cells, MB231_cells, MB-MDA-453
103772	AA092473	Hs.8123	chromobox homolog 3 (Drosophila HP1 gamm	2.31	CALU6_cells, MCF7, DU145_cells
122766	AA459386	Hs.194058	ESTs; Weakly similar to atypical PKC spe	2.31	HT29_cells, BT474_cells, HMEC
120886	AA365566	Hs.132736	ESTs; Weakly similar to allograft inflam	2.31	DU145_cells, A549_cells, Lu_LC_H460
123512	AA600248	Hs.142245	HERV-H LTR-associating 3	2.31	PC3_cells, 293T_cells, DU145_cells
106644	AA460239	Hs.12680	ESTs	2.31	HS578T_cells, MB231_cells, Lu_SQ_H520
127359	H72971		KIAA0277 gene product	2.31	Lu_SC_H345, DU145_cells, OVCAR_cells
105919	AA402494	Hs.3990	ESTs	2.31	HS578T_cells, DU145_cells, LNCaP_cells
125241	W86291	Hs.121593	ESTs	2.3	HMEC, HMEC (total RNA), EB_cells
104624	AA001936	Hs.184721	ESTs	2.3	DU145_cells, PC3_cells, PRSC_log
128765	AA101767	Hs.10494	ESTs	2.3	EB_cells, HMEC (total RNA), Lu_LC_H460
108360	AA071539		zm74b6.s1 Stratagene neuroepithelium (#9		
			HYDROXYSTEROID DEHYDROGENASE/DELTA-5-DEL		
115682	AA410300	Hs.44618	ESTs	2.3	2.3 HT29_cells, RPWE_2, Lu_AD_H23
134528	M23161	Hs.84775	Human transposon-like element mRNA	2.3	HT29_cells, Lu_SQ_H520, Lu_AD_H23
111091	N59858	Hs.33032	H sapiens mRNA; cDNA DKFZp434N185 (from	2.3	EB_cells, CALU6_cells, A549_cells
134044	AA262475	Hs.78746	phosphodiesterase 8A	2.29	2.3 LNCaP_cells, DU145_cells, PRSC_log
118229	N62339	Hs.180532	heat shock 90kD protein 1; alpha	2.29	DU145_cells, A549_cells, MCF7
110188	H20522	Hs.20969	ESTs	2.29	MCF7, DU145_cells, EB_cells
125073	T87185	Hs.193638	ESTs; Weakly similar to IIII ALU CLASS C	2.29	Fibroblasts 2, MB-MDA-435s, Lu_LC_H460
111495	R07210	Hs.19913	ESTs	2.29	EB_cells, Lu_SC_H345, Lu_SC_H69
124024	F03077	Hs.106672	ESTs	2.29	CALU6_cells, EB_cells, MCF7
128230	AA984074	Hs.176757	ESTs	2.29	HS578T_cells, RPWE_2, Lu_AD_358
125471	AA477571	Hs.152601	UDP-glucose ceramide glucosyltransferase	2.29	LNCaP_cells, DU145_cells, OVCAR_cells
120734	AA299949		EST12545 Uterus tumor I H sapiens cDNA 3	2.28	DU145_cells, PRSC_con, PRSC_log
134349	AA406373	Hs.8208	ESTs	2.28	Lu_AD_H23, Lu_SC_H345, Lu_SC_H69
123412	AA521443	Hs.187763	ESTs	2.28	DU145_cells, PC3_cells, LNCaP_cells
116297	AA489042	Hs.59498	ESTs	2.28	BT474_cells, BT474_cells, Lu_SC_H69
104476	N33807	Hs.223014	protease; serine; 15	2.28	EB_cells, 293T_cells, MB-MDA-453
101004	J04101	Hs.248109	v-ets avian erythroblastosis virus E26 o	2.28	LNCaP_cells, MCF7, PC3_cells
109991	H09813	Hs.12896	KIAA1034 protein	2.28	HT29_cells, MB-MDA-435s, HMEC (total RNA)
118934	N92571	Hs.54808	ESTs	2.28	EB_cells, CALU6_cells, 293T_cells
125096	T94328	Hs.194533	ESTs	2.28	HS578T_cells, 293T_cells, A549_cells
117514	N32226	Hs.124058	ESTs	2.28	Lu_SC_H345, Lu_SC_H69, 293T_cells
132792	AA401903	Hs.242985	hemoglobin; gamma G	2.28	CALU6_cells, HMEC, Lu_AD_H23
129009	AA131421	Hs.107884	ESTs	2.28	OVCAR_cells, Lu_SC_H69, MCF7
				2.28	HS578T_cells, CALU6_cells, Caco2

111658	R16981	Hs.15276	ESTs	2.28	MB-MDA-435s, 293T_cells, A549_cells
112322	R55757	Hs.26457	EST	2.28	Lu_SC_H345, Lu_SC_H69, Lu_AD_358
133477	W69310	Hs.740	PTK2 protein tyrosine kinase 2	2.28	EB_cells, PC3_cells, DU145_cells
132149	T10822	Hs.4095	ESTs	2.28	LNCaP_cells, EB_cells, PC3_cells
115119	AA256524	Hs.46847	Human DNA seq from clone 30M3 on chromos		
			yeast and archaea bacterial genes; and	2.27	A549_cells, EB_cells, LNCaP_cells
102130	U15009	Hs.1575	small nuclear ribonucleoprotein D3 polyp	2.27	LNCaP_cells, Caco2, EB_cells
114343	Z41424	Hs.21259	ESTs	2.27	HT29_cells, OVCAR_cells, Fibroblasts 2
106746	AA476436	Hs.7991	ESTs	2.27	Lu_AD_358, RPWE_2, Lu_AD_H23
119359	T71021	Hs.93334	ESTs; Highly similar to WS basic-helix-l	2.27	Lu_SC_H69, 293T_cells, DU145_cells
106301	AA435867	Hs.168212	kinesin family member 3B	2.27	OVCAR_cells, LNCaP_cells, EB_cells
130280	L13738	Hs.153937	activated p21cdc42Hs kinase	2.27	MB-MDA-453, DU145_cells, DU145_cells
119724	W69468	Hs.47622	ESTs	2.27	PC3_cells, HT29_cells, A549_cells
108960	AA150199	Hs.49378	DKFZP586D0919 protein	2.27	EB_cells, HS578T_cells, Lu_AD_358
103489	Y08614	Hs.79090	exportin 1 (CRM1; yeast; homolog)	2.26	EB_cells, CALU6_cells, DU145_cells
107711	AA015736	Hs.220687	ESTs	2.26	EB_cells, Lu_AD_H23, Lu_AD_358
131950	W84704	Hs.35380	ESTs	2.26	HS578T_cells, OVCAR_cells, MB-MDA-435s
107093	AA609600	Hs.10018	ESTs	2.26	LNCaP_cells, OVCAR_cells, DU145_cells
113649	T95641	Hs.16400	ESTs; Weakly similar to Hrs [H.sapiens]	2.26	Lu_AD_H23, Lu_SC_H69, PRSC_log
105255	AA227498	Hs.3623	ESTs	2.26	HS578T_cells, 293T_cells, Lu_SC_H345
130094	H43286	Hs.167017	gamma-aminobutyric acid (GABA) B recepto	2.26	Fibroblasts 2, MB231_cells, 293T_cells
111874	R37959	Hs.13358	ESTs	2.26	CALU6_cells, Lu_SC_H520, 293T_cells
107890	AA026030	Hs.61311	ESTs; Weakly similar to CALPAIN 2; LARGE	2.26	HT29_cells, MB-MDA-453, PC3_cells
124628	N74702	Hs.102834	ESTs	2.26	293T_cells, CALU6_cells, CALU6_cells
119707	W67569	Hs.44143	ESTs; Weakly similar to SNF2alpha protei	2.26	293T_cells, OVCAR_cells, Lu_SC_H345
106737	AA470080	Hs.36237	ESTs; Moderately similar to CGI-34 prote	2.26	LNCaP_cells, DU145_cells, MB-MDA-435s
117305	N22798	Hs.43248	EST	2.26	HT29_cells, BT474_cells, Fibroblasts 2
134470	X54942	Hs.83758	CDC28 protein kinase 2	2.26	DU145_cells, CALU6_cells, LNCaP_cells
130734	T99337	Hs.18624	KIAA1052 protein	2.26	Lu_AD_H23, Lu_SC_H345, Lu_SC_H69
128561	R69227	Hs.101489	ESTs	2.26	Lu_SC_H345, DU145_cells, OVCAR_cells
100670	HG2992-H		Beta-Hexosaminidase, Alpha Polypeptide,	2.26	HT29_cells, BT474_cells, Lu_SC_H345
115953	AA443958	Hs.90960	ESTs	2.26	Caco2, 293T_cells, DU145_cells
129612	H17476	Hs.11615	ESTs; Highly similar to map kinase phosph	2.25	CALU6_cells, LNCaP_cells, PC3_cells
111362	N91973	Hs.23595	deoxyribonuclease III; dnaQ/mutD (E. col	2.25	Lu_SC_H520, Lu_AD_H23, RPWE_2
116275	AA485453	Hs.250911	interleukin 13 receptor; alpha 1	2.25	OVCAR_cells, 293T_cells, DU145_cells
114461	AA024848	Hs.126705	ESTs	2.25	EB_cells, Lu_AD_H23, Lu_AD_H23
134083	AA278393	Hs.79013	ESTs	2.25	293T_cells, EB_cells, OVCAR_cells
132470	Z24724	Hs.4934	H.sapiens polyA site DNA	2.25	EB_cells, HS578T_cells, Caco2
114718	AA131328		zo8d1.s1 Stratagene neuroepithelium NT2R		
			SW:COX2_MOUSE P45 CYTOCHROME C OXIDASE P		
129499	R40395	Hs.242908	lecithin-cholesterol acyltransferase	2.25	2.25 MB-MDA-435s, HT29_cells, Lu_SC_H69
124758	R38422	Hs.169168	ESTs	2.25	HMEC (total RNA), Fibroblasts 2, HMEC
130301	X83127	Hs.172471	potassium voltage-gated channel; shaker-	2.25	293T_cells, RPWE_2, Lu_SC_H460
131263	R38334	Hs.24950	regulator of G-protein signalling 5	2.25	EB_cells, OVCAR_cells, A549_cells
107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.c	2.25	Lu_AD_H23, EB_cells, Lu_SC_H69
133262	N72009	Hs.206710	ESTs	2.24	LNCaP_cells, HMEC, EB_cells
132985	AA093619	Hs.62113	KIAA0717 protein	2.24	Lu_SC_H345, DU145_cells, LNCaP_cells
114172	Z39043	Hs.21421	ESTs; Weakly similar to cysteine desulfu	2.24	EB_cells, Lu_AD_H23, Lu_AD_358
127847	AA913387	Hs.126717	ESTs	2.24	293T_cells, CALU6_cells, Lu_SC_H520
106499	AA452244	Hs.16727	ESTs	2.24	LNCaP_cells, DU145_cells, Lu_SC_H69
105095	AA150088	Hs.27023	KIAA0917 protein	2.24	Lu_SC_H345, MB-MDA-453, Lu_SC_H69
108876	AA134361	Hs.191453	ESTs	2.24	DU145_cells, LNCaP_cells, CALU6_cells
121971	AA429667	Hs.120405	ESTs	2.24	EB_cells, Lu_SC_H345, Lu_AD_H23
114334	Z41342	Hs.22941	ESTs	2.24	Lu_AD_H23, 293T_cells, CALU6_cells
114565	AA063001	Hs.103527	SH2 domain protein 2A	2.24	DU145_cells, PC3_cells, EB_cells
115766	AA421761	Hs.77603	ESTs	2.24	Lu_SC_H460, MCF7, HMEC (total RNA)
130989	AA608546	Hs.21906	ESTs	2.24	Fibroblasts 2, MB-MDA-435s, MB231_cells
116304	AA489461	Hs.64742	H sapiens mRNA for KIAA0540 protein; par	2.24	PC3_cells, LNCaP_cells, DU145_cells
111154	N66545	Hs.29169	ESTs	2.24	BT474_cells, EB_cells, LNCaP_cells
105561	AA262881	Hs.16029	ESTs; Weakly similar to alternatively sp	2.23	OVCAR_cells, MB-MDA-435s, HMEC
105939	AA404421	Hs.12258	ESTs	2.23	HS578T_cells, A549_cells, HMEC
126379	AI085342	Hs.166146	Homer; neuronal immediate early gene; 3	2.23	EB_cells, LNCaP_cells, DU145_cells
106610	AA458882	Hs.4832	ESTs; Moderately similar to Lasp-1 prote	2.23	HS578T_cells, PC3_cells, RPWE_2
132786	AA424545	Hs.56851	H sapiens mRNA expressed in placenta	2.23	DU145_cells, MCF7, Lu_SC_H345
107206	D20728	Hs.30767	ESTs	2.23	EB_cells, Lu_AD_H23, Fibroblasts 2
133708	R42172	Hs.75667	synaptophysin	2.23	BT474_cells, Fibroblasts 2, MB-MDA-435s
135123	AA227567	Hs.9482	target of myb1 (chicken) homolog	2.23	Lu_SC_H345, CALU6_cells, Lu_SC_H69
132156	AA157401	Hs.4113	S-adenosylhomocysteine hydrolase-like 1	2.23	BT474_cells, MB231_cells, EB_cells
116934	H75624	Hs.39662	ESTs	2.23	DU145_cells, 293T_cells, LNCaP_cells
133660	R87373		ym88e05.r1 Soares adult brain N2b4HB55Y		CALU6_cells, Lu_SC_H345, Lu_SC_H460
			IMAGE:166016 5', mRNA seq.	2.23	
119468	W23633	Hs.125043	ESTs	2.23	DU145_cells, A549_cells, PC3_cells
101247	L33801	Hs.78802	glycogen synthase kinase 3 beta	2.23	293T_cells, MB-MDA-453, OVCAR_cells
126008	AA253460		zs06f04.s1 NCI_CGAP_GCB1 H sapiens cDNA		LNCaP_cells, EB_cells, MB-MDA-435s
122938	AA477119		zu37c7.s1 Soares ovary tumor NbHOT H sap		2.23 HT29_cells, PRSC_log, Fibroblasts 2
			TR:G288289 G288289 MITOCHONDRIAL D-LOOP		
				2.23	PC3_cells, MCF7, MB-MDA-435s

114148	Z38804	Hs.184777	ESTs; Moderately similar to OPIOID BINDI MOLECULE PRECURSOR [H.sapiens]	2.23	HS578T_cells, Fibroblasts 2, Lu_SC_H345
103433	X98001	Hs.78948	Rab geranylgeranyltransferase; beta subu	2.22	LNCaP_cells, EB_cells, 293T_cells
132954	AA027112	Hs.216194	ESTs	2.22	EB_cells, Lu_AD_H23, Fibroblasts 2
133228	N90029	Hs.6831	H sapiens clone 1400 unknown protein mRN	2.22	293T_cells, PC3_cells, DU145_cells
103891	AA242887	Hs.124186	ring finger protein 2	2.22	EB_cells, Lu_SC_H69, Lu_SC_H345
124883	R75630	Hs.177242	ESTs	2.22	EB_cells, Lu_AD_H23, Lu_SC_H345
109921	H05734	Hs.30559	ESTs	2.22	Lu_SQ_H520, 293T_cells, RPWE_2
127306	A1305162	Hs.193687	ESTs	2.22	MCF7, HT29_cells, MB-MDA-453
102707	U77456	Hs.78103	nucleosome assembly protein 1-like 4	2.22	Caco2, EB_cells, CALU6_cells
106193	AA427625	Hs.23272	ESTs	2.22	293T_cells, EB_cells, A549_cells
118819	N79045	Hs.50800	ESTs; Weakly similar to III ALU SUBFAMI	2.22	Lu_SC_H345, Lu_SC_H69, DU145_cells
134326	U16306	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	2.22	HS578T_cells, PRSC_log, CALU6_cells
112241	R51248	Hs.16027	ESTs	2.22	293T_cells, HMEC (total RNA), HMEC (total RNA)
123693	AA609591	Hs.112728	ESTs	2.22	HT29_cells, HMEC (total RNA), BT474_cells
129052	AA496297	Hs.182740	ribosomal protein S11	2.22	EB_cells, Lu_AD_H23, Lu_AD_358
122481	AA448271	Hs.99126	ESTs	2.21	Lu_AD_H23, HT29_cells, Lu_AD_358
128895	R37753	Hs.106985	ESTs	2.21	EB_cells, Lu_AD_H23, Lu_SC_H345
124691	R05835	Hs.110153	ESTs; Weakly similar to B-CELL GROWTH FA	2.21	EB_cells, Lu_AD_H23, Lu_AD_358
131556	AA442853	Hs.2869	cyclin-dependent kinase 5; regulatory su	2.21	HT29_cells, Lu_LC_H460, Lu_SC_H69
128869	AA424570	Hs.106736	ESTs	2.21	EB_cells, Lu_AD_H23, Lu_SC_H69
107114	AA610089	Hs.11776	U4/U6-associated RNA splicing factor	2.21	MCF7, Lu_SC_H345, DU145_cells
106255	AA431191	Hs.161489	ESTs	2.21	EB_cells, Caco2, DU145_cells
130724	AA370091	Hs.179680	ESTs	2.2	EB_cells, Lu_AD_H23, Lu_SC_H69
105483	AA255874	Hs.23458	ESTs	2.2	LNCaP_cells, DU145_cells, PC3_cells
118970	N93503	Hs.54961	stoned B/TFIIA-alpha/beta-like factor	2.2	293T_cells, HS578T_cells, OVCAR_cells
120805	AA346041	Hs.96844	ESTs	2.2	HT29_cells, HS578T_cells, 293T_cells
106158	AA425382	Hs.6553	ESTs	2.2	CALU6_cells, PC3_cells, EB_cells
102121	U14391	Hs.82251	myosin IC	2.2	A549_cells, EB_cells, Caco2
109446	AA232125	Hs.87062	ESTs	2.2	HT29_cells, Lu_LC_H460, CALU6_cells
129515	AA490882	Hs.112227	ESTs	2.2	Lu_SC_H345, BT474_cells, Caco2
113128	T49325	Hs.8977	ESTs	2.2	Lu_SQ_H520, Lu_AD_H23, Lu_AD_358
127289	A1041014	Hs.220752	ESTs	2.2	EB_cells, Lu_AD_H23, Lu_AD_H23
129912	AA047344	Hs.107213	ESTs; Highly similar to NY-REN-6 antigen	2.2	CALU6_cells, A549_cells, EB_cells
115700	AA411685	Hs.67709	ESTs	2.2	OVCAR_cells, EB_cells, Caco2
106267	AA431873	Hs.4988	H sapiens clone 24711 mRNA seq	2.2	Lu_SQ_H520, EB_cells, PC3_cells
112881	T03593	Hs.182814	ESTs	2.19	A549_cells, OVCAR_cells, 293T_cells
116902	H70739		yu69f11.s1 Weizmann Olfactory Epithelium IMAGE:239085 3' similar to contains LTR	2.19	LNCaP_cells, DU145_cells, PC3_cells
105621	AA280865	Hs.6375	H sapiens mRNA; cDNA DKFZp564K0222 (from	2.19	HMEC, Caco2, HMEC (total RNA)
126991	R31652	Hs.821	biglycan	2.19	Fibroblasts 2, Lu_SC_H69, HS578T_cells
125466	R08234	Hs.180461	ESTs	2.19	Lu_AD_358, Lu_AD_H23, Lu_SQ_H520
108491	AA082973		zn7g1.s1 Stratagene hNT neuron (#937233) to gb:M3672 6S RIBOSOMAL PROTEIN L7A (H	2.19	Lu_AD_358, RPWE_2, Lu_LC_H460
109978	H09356	Hs.22528	ESTs	2.19	PRSC_log, Lu_SC_H345, Lu_SC_H69
106990	AA521354	Hs.24758	ESTs	2.19	EB_cells, LNCaP_cells, OVCAR_cells
122362	AA443919	Hs.96840	ESTs	2.19	EB_cells, Lu_AD_358, PRSC_con
125367	A1016490	Hs.81964	SEC24 (S. cerevisiae) related gene famil	2.19	HT29_cells, Lu_SC_H69, Lu_AD_H23
110716	H97188	Hs.35096	ESTs	2.19	DU145_cells, Fibroblasts 2, PRSC_con
129297	R11267	Hs.180570	H sapiens chromosome 19; cosmid F22329	2.19	293T_cells, MB-MDA-435s, A549_cells
104992	AA102652	Hs.22753	ESTs; Weakly similar to coded for by C.	2.18	MCF7, MB-MDA-453, Lu_SQ_H520
119896	W84738	Hs.137319	ESTs	2.18	293T_cells, 293T_cells, OVCAR_cells
118594	N69022	Hs.49599	ESTs	2.18	Lu_SC_H69, Lu_AD_H23, Lu_SC_H345
129786	H98977	Hs.246109	ESTs	2.18	293T_cells, 293T_cells, 293T_cells
104325	D81608	Hs.150675	polymerase (RNA) II (DNA directed) polyp	2.18	PC3_cells, Lu_SC_H345, LNCaP_cells
123022	AA480909		aa28f10.s1 NCI_CGAP_GCB1 H sapiens cDNA Alu repetitive element; contains element	2.18	OVCAR_cells, DU145_cells, LNCaP_cells
133572	W94333	Hs.7499	translocase of inner mitochondrial membr	2.18	Caco2, LNCaP_cells, Lu_SQ_H520
133363	AA479713	Hs.71962	ESTs	2.18	EB_cells, Lu_AD_H23, Fibroblasts 2
135361	AA053319	Hs.167700	ESTs	2.18	EB_cells, 293T_cells, Caco2
128319	AA808904	Hs.115095	ESTs; Weakly similar to RHO-RELATED GTP-DU145_cells	2.18	Lu_SC_H345, OVCAR_cells,
128660	AA011597	Hs.177398	ESTs	2.18	EB_cells, Lu_AD_H23, Lu_SQ_H520
114877	AA235618	Hs.205125	ESTs	2.18	DU145_cells, 293T_cells, OVCAR_cells
125925	H28737		ESTs; Moderately similar to III ALU SUB	2.18	Lu_SC_H69, Lu_SC_H345, HS578T_cells
113427	T85105	Hs.15471	ESTs	2.18	EB_cells, Lu_AD_H23, Lu_SC_H69
117500	N31909	Hs.44278	ESTs	2.18	PRSC_con, Lu_SC_H345, PRSC_log
131384	F13608	Hs.26226	ESTs	2.18	293T_cells, LNCaP_cells, OVCAR_cells
134499	U70370	Hs.84136	paired-like homeodomain transcription fa	2.18	Caco2, BT474_cells, MB231_cells
128154	AA922969	Hs.127100	ESTs	2.17	MB-MDA-453, MB-MDA-453, Lu_SC_H345
134585	T48154	Hs.168655	H sapiens mRNA for H-2K binding factor-2	2.17	LNCaP_cells, 293T_cells, PRSC_log
104987	AA101723	Hs.16683	ESTs	2.17	EB_cells, MCF7, DU145_cells
132992	AA091017	Hs.6226	ESTs	2.17	Caco2, LNCaP_cells, DU145_cells
135311	M36089	Hs.98493	X-ray repair complementing defective rep	2.17	HMEC (total RNA), Fibroblasts 2, HMEC
113171	T54613	Hs.9761	EST	2.17	HT29_cells, PRSC_con, Lu_SQ_H520
117736	N46999	Hs.46648	ESTs	2.16	PRSC_log, OVCAR_cells, A549_cells

125181	W58461	Hs.12396	ESTs	2.16	LNCaP_cells, DU145_cells, 293T_cells
120187	Z40251	Hs.56974	ESTs	2.16	LNCaP_cells, MB-MDA-453, HMEC (total RNA)
100308	D50532	Hs.54403	macrophage lectin 2 (calcium dependent)	2.16	HT29_cells, Lu_AD_H23, Lu_AD_H23
110960	N50887	Hs.26549	ESTs; Weakly similar to KIAA0449 protein	2.16	Caco2, A549_cells, LNCaP_cells
113608	T93113		ESTs; Moderately similar to IIII ALU SUB	2.16	Lu_SC_H69, CALU6_cells, 293T_cells
107538	Z21089	Hs.50094	ESTs; Weakly similar to KALIRIN [R.norve	2.16	HS578T_cells, 293T_cells, DU145_cells
128703	S76992	Hs.104005	vav 2 oncogene	2.16	RPWE_2, Lu_SC_H69, HT29_cells
126065	A1366484		ESTs	2.16	293T_cells, CALU6_cells, A549_cells
130000	AA465727	Hs.124084	ESTs; Weakly similar to IIII ALU SUBFAMI	2.16	DU145_cells, LNCaP_cells, OVCAR_cells
120407	AA235040	Hs.107283	ESTs	2.16	EB_cells, 293T_cells, A549_cells
121199	AA400371	Hs.97792	ESTs	2.16	Lu_AD_358, Lu_AD_H23, A549_cells
114963	AA243867	Hs.193055	ESTs	2.16	DU145_cells, PRSC_con, LNCaP_cells
100343	D63874	Hs.189509	high-mobility group (nonhistone chromoso	2.15	CALU6_cells, MB-MDA-453, Caco2
125077	T88822		yd32f5.s1 Soares fetal liver spleen 1NFL	2.15	Lu_AD_H23, Lu_SC_H69, Lu_SC_H345
117286	N22181		yw36d12.s1 Morton Fetal Cochlea H sapien	2.15	293T_cells, Lu_SC_H345, Lu_SC_H69
132876	AA130603	Hs.169683	ESTs; Moderately similar to IIII ALU SUB	2.15	EB_cells, LNCaP_cells, HS578T_cells
133834	AA147510	Hs.154737	serine protease; umbilical endothelium	2.15	DU145_cells, EB_cells, Caco2
126908	AA169866		ESTs; Weakly similar to IIII ALU SUBFAMI	2.15	DU145_cells, LNCaP_cells, OVCAR_cells
106900	AA490142	Hs.6193	ESTs	2.15	Fibroblasts 2, Lu_AD_H23, PRSC_con
129398	AA437374	Hs.234573	H sapiens mRNA for TL132	2.15	MCF7, DU145_cells, LNCaP_cells
114512	AA044274	Hs.165215	ESTs	2.15	Lu_AD_358, MB-MDA-453, HS578T_cells
134381	U56637	Hs.184270	capping protein (actin filament) muscle	2.15	LNCaP_cells, EB_cells, PC3_cells
118848	N80671	Hs.220255	ESTs	2.14	EB_cells, DU145_cells, MCF7
115526	AA342049	Hs.69606	ESTs	2.14	293T_cells, Caco2, Lu_SC_H69
123460	AA598981	Hs.251122	EST	2.14	Lu_SC_H345, DU145_cells, MCF7
119812	W73951	Hs.58348	ESTs; Weakly similar to CORNIFIN A [H.sa	2.14	293T_cells, HS578T_cells, CALU6_cells
105263	AA227926	Hs.6682	ESTs	2.14	A549_cells, HMEC (total RNA), EB_cells
129242	W81679	Hs.5174	ribosomal protein S17	2.14	293T_cells, CALU6_cells, HMEC (total RNA)
132348	AA037285	Hs.170311	heterogeneous nuclear ribonucleoprotein	2.14	A549_cells, HT29_cells, Lu_SC_H520
114425	AA015763	Hs.132812	ESTs	2.14	293T_cells, HS578T_cells, PRSC_con
127759	A1369384		arylsulfatase D	2.14	DU145_cells, LNCaP_cells, EB_cells
134069	U29607	Hs.78935	methionine aminopeptidase; eIF-2-associa	2.14	Lu_SC_H345, DU145_cells, MCF7
116158	AA461187	Hs.61762	ESTs	2.14	Lu_SC_H69, MCF7, MB-MDA-453
125627	R35166	Hs.14881	ESTs	2.14	HT29_cells, Fibroblasts 2, BT474_cells
118684	N71364	Hs.109510	ESTs	2.14	OVCAR_cells, PRSC_con, HS578T_cells
119419	T97977	Hs.60260	ESTs	2.14	Lu_AD_H23, Lu_SC_H520, Lu_SC_H520
133097	N67515	Hs.6479	ESTs; Weakly similar to KIAA0872 protein	2.14	EB_cells, Lu_AD_H23, Lu_AD_358
112121	R45445	Hs.252723	H sapiens mRNA; cDNA DKFZp434D115 (from	2.13	Lu_AD_H23, Lu_AD_358, BT474_cells
114894	AA236019	Hs.188803	ESTs	2.13	MB-MDA-453, MCF7, Lu_SC_H520
124087	H08773		yl94d5.s1 Soares infant brain 1NIB H sap	2.13	Lu_SC_H69, Fibroblasts 2, HMEC (total RNA)
111902	R39191	Hs.109445	KIAA1020 protein	2.13	Caco2, 293T_cells, Lu_SC_H69
119943	W86835	Hs.14158	copine III	2.13	LNCaP_cells, PC3_cells, HS578T_cells
109276	AA196306	Hs.86045	ESTs	2.13	Lu_SC_H345, Lu_SC_H69, Lu_SC_H460
117351	N24581	Hs.43230	ESTs	2.13	HS578T_cells, CALU6_cells, PRSC_con
116046	AA453461	Hs.94491	H sapiens clone 23585 mRNA seq	2.13	LNCaP_cells, Caco2, EB_cells
112785	R96478	Hs.16586	ESTs	2.13	EB_cells, Lu_AD_H23, Lu_SC_H69
115835	AA428576	Hs.41371	ESTs	2.13	EB_cells, Lu_SC_H345, OVCAR_cells
127499	T49891	Hs.119252	tumor protein; translationally-controlle	2.13	EB_cells, PRSC_con, LNCaP_cells
129951	AA019475	Hs.74615	platelet-derived growth factor receptor;	2.13	EB_cells, Lu_AD_H23, Lu_SC_H69
124270	H79560	Hs.107840	ESTs	2.13	OVCAR_cells, 293T_cells, 293T_cells
133766	D52420	Hs.184326	cell division cycle 10 (homologous to CD	2.12	CALU6_cells, DU145_cells, PC3_cells
109248	AA194720	Hs.189996	ESTs; Highly similar to sec61 homolog [H	2.12	HT29_cells, MB231_cells, HMEC (total RNA)
106724	AA465226	Hs.28631	ESTs	2.12	EB_cells, 293T_cells, DU145_cells
100571	HG2264-H		Atpase, Ca2+ Transporting, Plasma Membra	2.12	EB_cells, Lu_AD_H23, Lu_SC_H69
133017	AA450187	Hs.178518	ESTs	2.12	OVCAR_cells, PC3_cells, 293T_cells
124313	H94650	Hs.108002	ESTs	2.12	MB-MDA-453, Lu_SC_H345, HT29_cells
113059	T26925	Hs.172684	vesicle-associated membrane protein 8 (e	2.12	MB-MDA-453, PC3_cells, LNCaP_cells
113241	T63313	Hs.226136	ESTs; Moderately similar to IIII ALU SUB	2.12	HMEC (total RNA), BT474_cells, HMEC
111952	R40782	Hs.21296	ESTs	2.12	HT29_cells, PC3_cells, A549_cells
113965	W86519	Hs.19631	ESTs	2.12	PC3_cells, EB_cells, LNCaP_cells
108059	AA043944	Hs.62663	ESTs	2.12	EB_cells, OVCAR_cells, 293T_cells
124235	H63994	Hs.221134	ESTs	2.12	Fibroblasts 2, MB-MDA-453, PRSC_con
106400	AA447621	Hs.31257	ESTs	2.12	DU145_cells, EB_cells, Caco2
119590	W44798	Hs.55876	ESTs	2.12	PRSC_log, Lu_SC_H69, Lu_SC_H345
112434	R63068	Hs.159793	EST	2.11	HS578T_cells, LNCaP_cells, OVCAR_cells
122731	AA457549		aa92b1.s1 Stratagene fetal retina 93722		
			gb:X5275_ma3 LEUKOSIALIN PRECURSOR (HU		
115348	AA281562	Hs.88860	ESTs	2.11	2.11 MB-MDA-453, RPWE_2, MCF7
128873	AA226768	Hs.109463	ESTs; Weakly similar to predicted using	2.11	EB_cells, Lu_AD_H23, Fibroblasts 2
133742	T54301	Hs.75844	ESTs	2.11	MB-MDA-435s, EB_cells, LNCaP_cells
102099	U11870	Hs.194778	interleukin 8 receptor; alpha	2.11	EB_cells, CALU6_cells, DU145_cells
125840	H05787	Hs.12064	ubiquitin specific protease 22	2.11	Lu_AD_358, PC3_cells, PRSC_con
105501	AA256604	Hs.31930	ESTs	2.1	EB_cells, LNCaP_cells, Caco2
111576	R10334	Hs.15489	ESTs	2.1	Fibroblasts 2, HS578T_cells, MB-MDA-435s
104275	C02170	Hs.39387	ESTs; Weakly similar to weak similarity	2.1	Lu_SC_H69, PRSC_log, Lu_SC_H345
117803	N48620	Hs.28483	pregnancy specific beta-1-glycoprotein 9	2.1	HT29_cells, MB231_cells, Lu_SC_H69
					HT29_cells, HMEC, RPWE_2

122725	AA457407	Hs.152204	transmembrane protease; serine 2	2.1	Lu_SC_H69, Lu_LC_H460, Lu_SC_H345
120987	AA398233	Hs.111894	KIAA0108 gene product	2.1	Fibroblasts 2, PRSC_con, MCF7
105932	AA403305	Hs.12185	ESTs; Weakly similar to myosin phosphata	2.1	LNCaP_cells, MCF7, OVCAR_cells
118398	N64706	Hs.137282	ESTs	2.1	Lu_SC_H345, HT29_cells, HMEC
103679	Z86000		Human DNA seq from PAC 151B14 on chromos		
			receptor subtype 3 (SSTR3), tRNA, ESTs,	2.1	CALU6_cells, A549_cells, Lu_SC_H345
130303	L40392	Hs.180789	H sapiens (clone S164) mRNA; 3' end of c	2.1	PC3_cells, DU145_cells, LNCaP_cells
122815	AA461080	Hs.139446	ESTs	2.1	HT29_cells, BT474_cells, MB231_cells
105598	AA279439	Hs.20594	ESTs; Weakly similar to misato [D.melano	2.1	EB_cells, Lu_SC_H345, LNCaP_cells
124869	R69088	Hs.28728	ESTs; Weakly similar to F55A12.9 [C.eleg	2.1	HT29_cells, BT474_cells, MB231_cells
129599	F10720	Hs.180804	ESTs	2.1	HS578T_cells, HT29_cells, HT29_cells
110338	H40359	Hs.177256	ESTs	2.09	MCF7, A549_cells, MB-MDA-435s
134092	H17490	Hs.7905	ESTs; Highly similar to sorting nexin 9	2.09	EB_cells, Fibroblasts 2, HS578T_cells
133002	AF006082	Hs.62461	ARP2 (actin-related protein 2; yeast) ho	2.09	EB_cells, HS578T_cells, A549_cells
115570	AA398343	Hs.94943	ESTs	2.09	Lu_SC_H345, PC3_cells, LNCaP_cells
120055	W93299	Hs.59363	ESTs; Weakly similar to cytokeratin 20 [2.09	HMEC (total RNA), HS578T_cells, HS578T_cells
116332	AA491208	Hs.62620	ESTs	2.09	EB_cells, Lu_AD_H23, Lu_SC_H69
105415	AA243768	Hs.4232	ESTs; Highly similar to match to ESTs Z4	2.09	LNCaP_cells, Lu_AD_H23, MB-MDA-453
116607	D80354	Hs.256321	EST	2.09	LNCaP_cells, DU145_cells, RPWE_2
126731	AA593973	Hs.232217	ESTs; Weakly similar to IIII ALU SUBFAMI	2.09	MB231_cells, HT29_cells, HMEC
102276	U30999	Hs.10247	activated leucocyte cell adhesion molecu	2.09	PC3_cells, HS578T_cells, DU145_cells
113666	T96077	Hs.17738	EST	2.09	Lu_AD_H23, Lu_AD_H23, Lu_SQ_H520
101183	L19779	Hs.795	H2A histone family; member O	2.09	LNCaP_cells, MCF7, OVCAR_cells
112177	R49025	Hs.22996	ESTs	2.09	Lu_AD_H23, Lu_AD_358, Lu_SC_H69
115038	AA252360	Hs.87968	ESTs	2.08	BT474_cells, MB231_cells, HT29_cells
109638	F04432	Hs.17904	ESTs	2.08	EB_cells, DU145_cells, PC3_cells
109592	F02475	Hs.26370	ESTs	2.08	Lu_AD_H23, Lu_SQ_H520, Lu_LC_H460
133740	U68142	Hs.170160	RAB2; member RAS oncogene family-like	2.08	LNCaP_cells, MB-MDA-453, EB_cells
126716	AA031700	Hs.251962	ESTs	2.08	HS578T_cells, Fibroblasts 2, Lu_SC_H69
124055	F10904	Hs.100516	H sapiens clone 23605 mRNA seq	2.08	Lu_SC_H345, OVCAR_cells, DU145_cells
113283	T66813	Hs.12947	EST	2.08	EB_cells, Lu_SC_H69, Lu_AD_H23
120097	W95068	Hs.59621	ESTs	2.08	HS578T_cells, A549_cells, CALU6_cells
102066	U08471	Hs.352	folate receptor 3 (gamma)	2.08	EB_cells, Lu_AD_H23, Lu_AD_358
108712	AA121993		zm24d11.s1 Stratagene pancreas (#93728)		
			similar to gb:Y433 GLUTATHIONE PEROXIDAS		
134453	X70683	Hs.83484	SRY (sex determining region Y)-box 4	2.08	2.08 Lu_SQ_H520, HT29_cells, BT474_cells
103883	AA232836	Hs.87363	ESTs	2.08	EB_cells, Lu_SC_H345, Lu_SC_H69
105313	AA233856	Hs.16930	ESTs	2.08	HT29_cells, 293T_cells, 293T_cells
113669	T96148	Hs.17762	ESTs	2.08	DU145_cells, MB-MDA-435s, HS578T_cells
120380	AA227904	Hs.104223	ESTs	2.08	EB_cells, Lu_SQ_H520, Fibroblasts 2
121045	AA398554	Hs.181012	double-stranded RNA-binding zinc finger	2.08	293T_cells, CALU6_cells, A549_cells
104949	AA070735	Hs.146090	ESTs	2.08	293T_cells, PC3_cells, OVCAR_cells
118751	N74210	Hs.50454	EST	2.08	Lu_SC_H69, Lu_SC_H345, RPWE_2
112399	R60920	Hs.26419	H sapiens clone 24510 mRNA seq	2.08	Lu_AD_H23, Lu_SC_H69, Lu_SC_H345
129994	AA599443	Hs.38194	ESTs; Moderately similar to IIII ALU SUB	2.08	EB_cells, Lu_AD_H23, Lu_SC_H69
116402	AA600054	Hs.65302	ESTs	2.08	DU145_cells, EB_cells, HS578T_cells
125307	Z40583	Hs.101259	ESTs	2.08	HT29_cells, BT474_cells, Lu_AD_H23
105047	AA132453	Hs.15396	ESTs	2.08	HMEC, HMEC (total RNA), EB_cells
128659	T95280	Hs.103315	trinucleotide repeat containing 1	2.08	Caco2, HT29_cells, LNCaP_cells
122301	AA437378	Hs.98791	ESTs	2.08	EB_cells, Lu_AD_H23, Lu_SC_H69
121974	AA429804	Hs.229675	EST	2.08	Lu_SC_H345, Lu_AD_H23, Lu_AD_358
116905	H71420		ys8c12.s1 Soares fetal liver spleen 1NFL		HS578T_cells, 293T_cells, OVCAR_cells
			3' similar to contains Alu repetitive e	2.08	
106703	AA463979	Hs.21264	KIAA0782 protein	2.08	Lu_AD_H23, EB_cells, PRSC_con
121908	AA427858	Hs.98534	EST	2.07	EB_cells, Caco2, PRSC_con
135119	T23992	Hs.94769	ESTs; Moderately similar to RAS-RELATED	2.07	293T_cells, Lu_SC_H345, CALU6_cells
103558	Z19574	Hs.2785	keratin 17	2.07	HS578T_cells, PRSC_con, OVCAR_cells
124209	H57317	Hs.193433	ESTs	2.07	RPWE_2, HMEC (total RNA), HMEC
133936	AA045083	Hs.77719	gamma-glutamyl carboxylase	2.07	Fibroblasts 2, OVCAR_cells, 293T_cells
116246	AA479961	Hs.42913	ESTs; Highly similar to ubiquitin-conjug	2.07	Fibroblasts 2, MB-MDA-453, PRSC_con
123230	AA490134	Hs.105308	EST	2.07	EB_cells, LNCaP_cells, LNCaP_cells
127378	AA452696		zx39b05.r1 Soares_total_fetus_Nb2HF8_9w		Lu_AD_H23, Lu_SC_H69, Lu_SC_H345
			to contains Alu repetitive element;cont	2.07	
110464	H53013	Hs.221901	ESTs	2.07	HS578T_cells, LNCaP_cells, EB_cells
135191	X07619	Hs.169876	cytochrome P450; subfamily IID (debrisoq	2.07	Fibroblasts 2, Lu_SQ_H520, Lu_SQ_H520
			polypeptide 7a (pseudogene)	2.07	
101267	L36818	Hs.75339	inositol polyphosphate phosphatase-like	2.07	Lu_AD_H23, Lu_SC_H69, Lu_AD_358
105185	AA191495	Hs.189937	ESTs	2.07	Lu_SC_H345, OVCAR_cells, Caco2
125366	H60192	Hs.76853	ESTs; Weakly similar to human homolog of	2.07	Lu_SC_H69, Lu_AD_H23, Lu_SC_H345
117472	N30131	Hs.93738	DKFZP434M098 protein	2.07	DU145_cells, Lu_LC_H460, Lu_AD_358
114235	Z39710	Hs.25341	ESTs	2.07	EB_cells, Lu_SC_H69, 293T_cells
109081	AA165268	Hs.72488	ESTs	2.07	DU145_cells, BT474_cells, Lu_SC_H69
112596	R78212	Hs.163705	ESTs	2.07	Lu_SC_H69, Lu_SC_H345, PC3_cells
109254	AA194940	Hs.85956	ESTs; Weakly similar to Iine-1 protein O	2.07	MB-MDA-435s, Lu_SQ_H520, MB-MDA-453
105898	AA401144	Hs.27354	ESTs	2.07	HS578T_cells, 293T_cells, OVCAR_cells
116290	AA488691	Hs.57969	phenylalanine-tRNA synthetase	2.06	EB_cells, 293T_cells, PRSC_con
					Lu_AD_H23, Lu_SC_H345, PRSC_log

122529	AA449828	Hs.99229	ESTs	2.06	DU145_cells, HS578T_cells, 293T_cells
104612	R99199	Hs.173063	transducin-like enhancer of split 2; hom	2.06	MB-MDA-435s, 293T_cells, 293T_cells
116465	AA621650	Hs.41045	ESTs; Weakly similar to KIAA0734 protein	2.06	MB231_cells, HT29_cells, Lu_AD_358
123155	AA488414	Hs.76127	hect (homologous to the E6-AP (UBE3A) ca domain (RLD) 1	2.06	
126752	AI073373	Hs.183275	ESTs	2.06	DU145_cells, CALU6_cells, PC3_cells
126455	N80749	Hs.111515	ESTs; Weakly similar to predicted using	2.06	LNCaP_cells, EB_cells, DU145_cells
129339	R77869	Hs.28506	ESTs	2.06	CALU6_cells, PRSC_log, OVCAR_cells
115021	AA252028	Hs.39168	ESTs	2.06	EB_cells, BT474_cells, Lu_AD_H23
129054	T67231	Hs.168289	succinate dehydrogenase complex; subunit	2.06	Lu_SQ_H520, Fibroblasts 2, EB_cells
101261	L35545	Hs.82353	endothelial cell protein C/activated pro	2.06	Caco2, LNCaP_cells, EB_cells
132697	AA281951	Hs.5518	H sapiens mRNA; cDNA DKFZp566J2146 (from	2.06	EB_cells, RPWE_2, DU145_cells
124380	N26536	Hs.84999	ATPase; Cu++ transporting; beta polypept	2.06	2.06 OVCAR_cells, LNCaP_cells, DU145_cells
103967	AA303711	Hs.144700	ephrin-B1	2.06	Caco2, Caco2, 293T_cells
119403	T92935	Hs.119908	ESTs; Highly similar to nucleolar protei	2.06	HT29_cells, HMEC (total RNA), HMEC
125755	R66080	Hs.191268	H sapiens mRNA; cDNA DKFZp434N174 (from	2.06	HMEC, EB_cells, HMEC (total RNA)
101843	M93405	Hs.170008	methylmalonate-semialdehyde dehydrogenas	2.05	2.06 LNCaP_cells, DU145_cells, OVCAR_cells
113032	T24024	Hs.7387	DKFZP564B116 protein	2.05	LNCaP_cells, MB-MDA-453, EB_cells
112563	R72632	Hs.29282	ESTs	2.05	EB_cells, A549_cells, A549_cells
126432	AA583825	Hs.235860	ESTs	2.05	MCF7, HS578T_cells, PRSC_con
101636	M57763	Hs.89474	ADP-ribosylation factor 6	2.05	MB231_cells, HT29_cells, Fibroblasts 2
125174	W51835	Hs.231082	EST	2.05	DU145_cells, LNCaP_cells, PC3_cells
106168	AA425943	Hs.82208	acyl-Coenzyme A dehydrogenase; very long	2.05	EB_cells, Fibroblasts 2, Lu_AD_H23
135343	AA236796	Hs.9914	folistatin	2.05	OVCAR_cells, PC3_cells, EB_cells
105267	AA227956	Hs.25348	folistatin-like 3 (secreted glycoprotei	2.05	HMEC (total RNA), PC3_cells, HMEC
134331	AA452020	Hs.234156	ESTs; Weakly similar to CGI-128 protein	2.05	HMEC, RPWE_2, HMEC (total RNA)
121634	AA417012	Hs.28921	ESTs	2.05	EB_cells, CALU6_cells, A549_cells
131394	R72637	Hs.26343	ESTs	2.05	HS578T_cells, EB_cells, Lu_SC_H345
111526	R08260	Hs.20131	ESTs	2.05	EB_cells, Lu_SC_H69, Lu_AD_H23
125049	T79840	Hs.111798	ESTs	2.05	Lu_AD_H23, Lu_SC_H69, BT474_cells
120433	AA237077	Hs.180777	H sapiens mRNA; cDNA DKFZp564M0264 (from	2.05	HT29_cells, Lu_AD_H23, Lu_SC_H345
129498	AA449789	Hs.75511	connective tissue growth factor	2.05	2.05 DU145_cells, CALU6_cells, PC3_cells
127805	AA740921	Hs.1197	heat shock 10kD protein 1 (chaperonin 10	2.05	HS578T_cells, PRSC_log, PRSC_con
109275	AA196287	Hs.20303	ESTs; Moderately similar to IIII ALU SUB	2.05	DU145_cells, LNCaP_cells, OVCAR_cells
120683	AA290987	Hs.49657	ESTs; Weakly similar to contains similar	2.04	EB_cells, MB-MDA-453, Fibroblasts 2
135415	X60655	Hs.99967	even-skipped homeo box 1 (homolog of Dro	2.04	Lu_AD_358, Lu_SQ_H520, Lu_LC_H460
132925	AA252759	Hs.238296	DKFZP434A033 protein	2.04	Lu_AD_H23, RPWE_2, Lu_SQ_H520
101875	M97287	Hs.74592	special AT-rich seq binding protein 1 (b	2.04	293T_cells, HS578T_cells, LNCaP_cells
101463	M22490	Hs.68879	bone morphogenetic protein 4	2.04	EB_cells, Lu_SC_H69, 293T_cells
129177	T95005	Hs.209587	ESTs	2.04	PRSC_con, HT29_cells, MB231_cells
130726	W88946	Hs.18508	putative glycine-N-acyltransferase	2.04	293T_cells, MB-MDA-435s, Lu_SC_H69
105549	AA262417	Hs.5415	ESTs	2.04	HT29_cells, Fibroblasts 2, MB-MDA-435s
124543	N63706	Hs.104573	ESTs	2.04	DU145_cells, OVCAR_cells, PC3_cells
123062	AA482069	Hs.100847	ESTs	2.04	Caco2, 293T_cells, DU145_cells
109464	AA232857	Hs.87100	ESTs	2.04	Lu_AD_358, HT29_cells, HT29_cells
129619	AA610116	Hs.11663	tetraspan NET-6 protein	2.04	DU145_cells, Lu_AD_H23, LNCaP_cells
127545	AA935809	Hs.115899	ESTs	2.04	BT474_cells, Caco2, LNCaP_cells
133068	R73427	Hs.235712	ESTs	2.04	BT474_cells, MB-MDA-435s, MB-MDA-453
113609	T93263	Hs.16875	ESTs; Weakly similar to hypothetical pro	2.04	Caco2, OVCAR_cells, MCF7
106645	AA460270	Hs.27695	midline 1 (Opitz/BBB syndrome)	2.04	EB_cells, Lu_SC_H345, PRSC_con
126256	Z21124		HSAAADNVE TEST1, Human adult Testis tiss	2.04	A549_cells, 293T_cells, Caco2
129697	R00841	Hs.172069	DKFZP434C212 protein	2.04	Fibroblasts 2, Fibroblasts 2, MCF7
126730	T19477		A1426R Heart H sapiens cDNA clone A1426,	2.04	HT29_cells, Lu_SQ_H520, BT474_cells
125244	W86466	Hs.132756	ESTs; Weakly similar to KIAA0591 protein	2.04	EB_cells, Lu_AD_H23, Lu_SC_H69
134762	M91036	Hs.242985	hemoglobin; gamma G	2.04	EB_cells, Lu_AD_H23, Lu_LC_H460
119564	W38206		Accession not listed in Genbank	2.04	MB231_cells, Lu_AD_358, HT29_cells
132523	AB002332	Hs.50722	clock (mouse) homolog	2.04	BT474_cells, HT29_cells, Lu_AD_H23
127758	AI337031	Hs.180195	ESTs	2.04	PC3_cells, OVCAR_cells, PRSC_log
126471	AA158755	Hs.175652	ESTs; Weakly similar to IIII ALU SUBFAMI	2.04	293T_cells, MB-MDA-435s, A549_cells
110911	N45120	Hs.22305	ESTs	2.03	EB_cells, Lu_AD_358, Lu_LC_H460
122317	AA442742	Hs.8693	ESTs; Weakly similar to IIII ALU SUBFAMI	2.03	Lu_AD_H23, RPWE_2, Lu_LC_H460
100253	D38024	Hs.247951	Humn facioscapulohumeral muscular dystro	2.03	EB_cells, Fibroblasts 2, Lu_SC_H345
120431	AA236884	Hs.247323	H sapiens mRNA for G4 protein (G4 gene;	2.03	Lu_AD_H23, Lu_AD_358, Lu_SQ_H520
122449	AA447638	Hs.104977	ESTs	2.03	Lu_SC_H69, EB_cells, Lu_SC_H345
100961	J00148		Accession not listed in Genbank	2.03	Lu_SC_H345, Lu_SC_H345, Lu_SQ_H520
130908	W86389	Hs.21122	ESTs; Moderately similar to KIAA0438 [H.	2.03	HT29_cells, BT474_cells, HMEC
102643	U67849		Human beta-galactoside alpha2,6-sialyitr	2.03	293T_cells, Lu_SC_H345, OVCAR_cells
127932	AA398510	Hs.133148	ESTs	2.03	HT29_cells, 293T_cells, Lu_SC_H345
109207	AA190906	Hs.204692	ESTs	2.03	EB_cells, Lu_SC_H345, Lu_SC_H69
102598	U62962	Hs.106673	eukaryotic translation initiation factor	2.03	Lu_SQ_H520, Lu_SC_H345, Lu_SC_H69
124470	N51702	Hs.101392	ESTs	2.03	EB_cells, DU145_cells, MCF7
104961	AA076672	Hs.33905	ESTs	2.03	HT29_cells, Fibroblasts 2, HMEC (total RNA)
124164	H30667	Hs.7535	ESTs; Highly similar to COBW-like placen	2.03	Caco2, LNCaP_cells, EB_cells
126468	AA242853	Hs.237856	ESTs; Moderately similar to cAMP inducib	2.03	CALU6_cells, CALU6_cells, A549_cells
129683	W05348	Hs.158196	DKFZP434B103 protein	2.03	MB231_cells, BT474_cells, Fibroblasts 2
105350	AA235737	Hs.186571	ATPase; Na+/K+ transporting; alpha 3 pol	2.03	HT29_cells, MB-MDA-435s, Lu_AD_H23
					MB-MDA-453, Lu_SQ_H520, Lu_AD_358

129794	AA447772	Hs.14520	eukaryotic translation initiation factor	2.03	EB_cells, Lu_AD_358, Lu_AD_H23
115664	AA405974	Hs.54673	tumor necrosis factor (ligand) superfamily	2.03	Lu_AD_358, HT29_cells, HT29_cells
119096	R41672	Hs.91471	ATPase type IV; phospholipid transportin	2.03	HT29_cells, MB231_cells, BT474_cells
133866	L36151	Hs.171625	phosphatidylinositol 4-kinase; catalytic	2.03	293T_cells, DU145_cells, LNCaP_cells
132055	N69440	Hs.38132	ESTs	2.03	Lu_SC_H345, MB-MDA-453, MB-MDA-435s
125691	AI034361	Hs.135150	lung type-I cell membrane-associated gly	2.03	Lu_SC_H345, LNCaP_cells, DU145_cells
121376	AA405699	Hs.166232	ESTs; Moderately similar to SODIUM- AND TRANSPORTER 2 [H.sapiens]	2.03	LNCaP_cells, HT29_cells, RPWE_2
105289	AA233178	Hs.103000	KIAA0831 protein	2.02	PC3_cells, Lu_AD_H23, MB231_cells
100967	J02621	Hs.251064	high-mobility group (nonhistone chromoso	2.02	MCF7, DU145_cells, OVCAR_cells
124430	N38913	Hs.221575	ESTs	2.02	MB-MDA-435s, Fibroblasts 2, EB_cells
128322	AI306331	Hs.133296	ESTs	2.02	HT29_cells, MB-MDA-435s, Lu_SC_H345
131077	X91809	Hs.22698	G alpha interacting protein	2.02	Lu_AD_H23, RPWE_2, MCF7
108033	AA040923	Hs.92200	KIAA0480 gene product	2.02	MCF7, Fibroblasts 2, DU145_cells
107550	AA001045	Hs.46783	ESTs	2.02	DU145_cells, PC3_cells, OVCAR_cells
109475	AA233159	Hs.87131	ESTs	2.02	HT29_cells, MB-MDA-435s, Lu_SC_H69
111400	R00144	Hs.189771	ESTs	2.02	HT29_cells, Fibroblasts 2, HMEC
117516	N32495	Hs.151560	ESTs	2.02	HT29_cells, HMEC (total RNA), Fibroblasts 2
120506	AA257955	Hs.173705	ESTs; Weakly similar to IIII ALU CLASS C	2.02	MCF7, Fibroblasts 2, LNCaP_cells
130850	N39306	Hs.20237	DKFZP566C134 protein	2.02	EB_cells, Lu_AD_H23, Lu_LC_H460
123118	AA486571	Hs.105696	ESTs; Moderately similar to IIII ALU SUB	2.02	CALU6_cells, 293T_cells, PRSC_log
111285	N71704	Hs.4310	eukaryotic translation initiation factor	2.02	293T_cells, PC3_cells, EB_cells
119106	R42362	Hs.91785	ESTs	2.02	CALU6_cells, MB-MDA-453, PC3_cells
111370	N92915	Hs.94631	brefeldin A-inhibited guanine nucleotide	2.02	EB_cells, OVCAR_cells, LNCaP_cells
125013	T67261	Hs.154431	ESTs; Weakly similar to neuronal thread	2.02	Lu_SC_H345, Lu_SC_H69, PRSC_con
129762	AA460273	Hs.12372	KIAA0517 protein	2.02	EB_cells, MB-MDA-435s, OVCAR_cells
120704	AA291970	Hs.107054	KIAA0821 protein	2.01	Lu_SC_H69, EB_cells, MB-MDA-453
105355	AA235985	Hs.26938	Human DNA seq from clone 126A5 on chromo		
			genes (one with DnaJ domains); the gene		
			family member HKR3. Contains ESTs; STSs;	2.01	Lu_AD_H23, Lu_LC_H460, Lu_SQ_H520
125952	AA017723		small inducible cytokine A5 (RANTES)	2.01	LNCaP_cells, DU145_cells, MB231_cells
103478	Y07755	Hs.38991	S100 calcium-binding protein A2	2.01	HMEC (total RNA), HMEC, RPWE_2
133544	T33873	Hs.74624	protein tyrosine phosphatase; receptor t	2.01	Lu_SC_H345, BT474_cells, HT29_cells
112746	R93237		yq11e10.s1 Soares fetal liver spleen 1NF		
			IMAGE:196650 3', mRNA seq.	2.01	PC3_cells, LNCaP_cells, OVCAR_cells
118513	N67504	Hs.40061	ESTs	2.01	Lu_SC_H345, Lu_SC_H69, PRSC_con
123423	AA598484	Hs.238476	EST	2.01	EB_cells, Lu_AD_H23, Lu_SC_H345
127854	AA769520		ESTs; Weakly similar to REGULATOR OF MIT	2.01	HS578T_cells, CALU6_cells,
			Lu_SQ_H520		
111843	R36969	Hs.18888	ESTs	2.01	Lu_AD_H23, Lu_AD_358, Lu_SQ_H520
100221	D28383		Human mRNA for ATP synthase B chain, 5'U	2.01	EB_cells, Lu_AD_H23, LNCaP_cells
129966	AA452237	Hs.194443	ESTs; Weakly similar to BC37295_2 [H.sap	2.01	Lu_SC_H345, Lu_SC_H69, DU145_cells
106798	AA478968	Hs.20558	ESTs	2.01	EB_cells, Lu_AD_H23, Lu_LC_H460
114636	AA085374		zn13d5.s1 Stratagene hNT neuron (#937233		
			gb:L8441 CYTOCHROME C OXIDASE POLYPEPTI		
125348	H21585	Hs.191277	ESTs; Moderately similar to ATP binding	2.01	2.01 EB_cells, CALU6_cells, OVCAR_cells
130620	AA233245	Hs.16773	ESTs	2.01	EB_cells, HS578T_cells, PC3_cells
106471	AA450118	Hs.25722	ESTs; Weakly similar to ZINC FINGER PROT	2.01	EB_cells, DU145_cells, 293T_cells
134175	T33128	Hs.7966	ESTs	2	OVCAR_cells, LNCaP_cells, EB_cells
117291	N22289		yw36g08.s1 Morton Fetal Cochlea H sapien	2	Lu_SC_H345, Fibroblasts 2, Lu_AD_H23
134199	U47635	Hs.79877	myotubularin related protein 6	2	MB-MDA-453, OVCAR_cells, CALU6_cells
128758	AA129545	Hs.181165	eukaryotic translation elongation factor	2	EB_cells, PC3_cells, LNCaP_cells
112005	R42569	Hs.22444	ESTs	2	Lu_SC_H69, EB_cells, Lu_SC_H345
122521	AA449433	Hs.149227	ESTs; Weakly similar to PROLINE-RICH PRO2	2	Lu_AD_H23, PRSC_log, Lu_AD_358
130356	X84373	Hs.155017	nuclear receptor interacting protein 1	2	HT29_cells, RPWE_2, MB231_cells
114067	Z38153	Hs.26921	ESTs	2	DU145_cells, PC3_cells, MCF7
107136	AA620795	Hs.8207	ESTs	2	293T_cells, MB-MDA-435s, HT29_cells
					LNCaP_cells, PC3_cells, EB_cells

Table 3

Pkey:	Unique Eos probeset identifier number				
ExAccn:	Exemplar Accession number, Genbank accession number				
UnigeneID:	Unigene number				
Unigene Title:	Unigene gene title				
Pkey	Ex Accn	UG_ID	Complete_Title	Ratio BS/Met	Top 3 expressing cell lines
302347	AF039400	Hs.194659	chloride channel; calcium activated; fam	19.71	EB, NCI-H520, NCI-H23
316304	AI936587	Hs.221599	ESTs	14.49	PRSC_con, RPWE-2, OVCA-R
339196			CH22_FF113D11.GENSCAN.3-1	10.37	NCI-H69, PRSC_con, NCI-H345
336171			CH22_FGENES.708_3	9.45	NCI-H69, NCI-H460, NCI-H23
338895			CH22_DJ32110.GENSCAN.9-2	9.31	PC3, BT474, OVCA-R
333625			CH22_FGENES.223_2	8.96	NCI-H69, PRSC_con, NCI-H345
333730			CH22_FGENES.258_1	8.82	NCI-H69, BT474, MB-MDA-231
320244	AA296922	Hs.129778	gastrointestinal peptide	8.22	BT474, CALU6, DU145
333643			CH22_FGENES.232_2	7.66	MCF7, NCI-H69, LnCap
333423			CH22_FGENES.147_3	7.57	HT29, MB-MDA-231, EB
302332	AI833168	Hs.184507	H sapiens Chromosome 16 BAC clone CIT987	7.55	MB-MDA-231, HT29, MB-MDA-453
333588			CH22_FGENES.206_2	7.46	HT29, OVCA-R, BT474
322033	AL137507		EST cluster (not in UniGene)	7.35	PRSC_con, PRSC_log, NCI-H345
308601	AI719930		EST singleton (not in UniGene) with exon	6.83	PC3, DU145, DU145
339044			CH22_DA59H18.GENSCAN.27-5	6.46	NCI-H69, NCI-H345, PRSC_log
314516	AA371513	Hs.231748	ESTs	6.41	EB, OVCA-R, Caco2
327805			CH.05_hs gjl5867968	6.28	NCI-H69, NCI-H345, PRSC_con
334239			CH22_FGENES.364_2	6.09	NCI-H520, MB-MDA-435s, MB-MDA-453
332958			CH22_FGENES.48_15	6.04	NCI-H69, PRSC_con, PRSC_log
313386	W85772	Hs.173924	ESTs	5.88	MB-MDA-231, OVCA-R, BT474
314350	AL037927	Hs.190675	ESTs; Moderately similar to IIII ALU SUB	5.84	OVCA-R, CALU6, EB
337170			CH22_FGENES.564-1	5.67	LnCap, CALU6, NCI-H69
337503			CH22_FGENES.803-1	5.66	NCI-H345, PRSC_con, RPWE-2
337562			CH22_C65E1.GENSCAN.1-2	5.53	HT29, MB-MDA-453, BT474
337219			CH22_FGENES.614-3	5.45	NCI-H69, NCI-H345, PRSC_log
311331	AI679622	Hs.32225	immunoglobulin alpha 1	5.43	NCI-H69, NCI-H23, NCI-H345
314251	AA713589		EST cluster (not in UniGene)	5.41	PC3, EB, LnCap
336246			CH22_FGENES.746_5	5.34	NCI-H69, NCI-H345, PRSC_log
335009			CH22_FGENES.472_13	5.31	EB, EB, NCI-H69
339365			CH22_BA354I12.GENSCAN.34-1	5.25	PRSC_con, NCI-H69, PRSC_log
336088			CH22_FGENES.688_17	5.21	PRSC_con, Caco2, PRSC_log
334966			CH22_FGENES.465_36	5.16	DU145, BT474, MB-MDA-231
334666			CH22_FGENES.418_18	5.15	NCI-H69, NCI-H345, PRSC_log
316830	AW182106	Hs.127821	ESTs	5.12	NCI-H345, PRSC_con, PRSC_log
339413			CH22_DJ579N16.GENSCAN.5-8	5.06	NCI-H69, NCI-H345, PRSC_log
337951			CH22_EM:AC005500.GENSCAN.94-1	5.01	NCI-H345, NCI-H69, PRSC_con
330153			CH.21_p2 gjl4325335	5	PRSC_con, PRSC_log, NCI-H69
333987			CH22_FGENES.310_11	4.96	MB-MDA-231, MB-MDA-453, MB-MDA-453
334304			CH22_FGENES.373_7	4.96	OVCA-R, CALU6, NCI-H23
338990			CH22_DA59H18.GENSCAN.6-6	4.95	PRSC_log, PRSC_con, NCI-H69
333152			CH22_FGENES.89_1	4.89	MB-MDA-435s, OVCA-R, A549
327049			CH.21_hs gjl6531965	4.87	PRSC_con, NCI-H345, PRSC_log
337225			CH22_FGENES.626-3	4.83	DU145, CALU6, EB
333496			CH22_FGENES.168_6	4.81	NCI-H69, NCI-H345, PRSC_con
334451			CH22_FGENES.387_11	4.79	RPWE-2, PRSC_con, NCI-H69
333594			CH22_FGENES.210_3	4.78	OVCA-R, PC3, HT29
333635			CH22_FGENES.228_2	4.78	NCI-H69, PRSC_log, PRSC_con
336796			CH22_FGENES.176-6	4.73	NCI-H69, NCI-H345, PRSC_log
333313			CH22_FGENES.138_5	4.72	NCI-H69, NCI-H345, PRSC_log
336833			CH22_FGENES.242-2	4.7	NCI-H345, NCI-H69, PRSC_con
336090			CH22_FGENES.689_2	4.7	NCI-H69, PRSC_con, PRSC_log
336645			CH22_FGENES.26-1	4.63	HT29, OVCA-R, DU145
334565			CH22_FGENES.405_5	4.62	NCI-H345, PRSC_log, RPWE-2
333242			CH22_FGENES.111_6	4.56	NCI-H345, PRSC_log, PRSC_con
326304			CH.17_hs gjl5867277	4.48	OVCA-R, EB, DU145
337445			CH22_FGENES.769-4	4.47	RPWE-2, NCI-H69, PRSC_log
327413			CH.02_hs gjl5867750	4.46	NCI-H69, PRSC_log, NCI-H345
327990			CH.06_hs gjl5868218	4.44	PRSC_con, PRSC_log, RPWE-2
325038	H38304	Hs.21782	ESTs	4.43	PRSC_con, MB-MDA-231, HT29
314923	AI732489	Hs.136370	ESTs	4.4	HT29, MB-MDA-231, NCI-358
328859			CH.07_hs gjl6381928	4.4	OVCA-R, BT474, A549
334476			CH22_FGENES.394_7	4.38	OVCA-R, PC3, EB
336092			CH22_FGENES.689_6	4.35	PRSC_con, Caco2, PRSC_log
333965			CH22_FGENES.305_3	4.35	NCI-H69, NCI-H345, PRSC_log

336402			CH22_FGENES.823_17	4.34	RPWE-2, HT29, OVCA-R
337947			CH22_EM:AC005500.GENSCAN.90-5	4.33	OVCA-R, DU145, PC3
337504			CH22_FGENES.803-2	4.33	NCI-H345, PRSC_con, PRSC_log
336813			CH22_FGENES.213-6	4.33	DU145, HT29, OVCA-R
338069			CH22_EM:AC005500.GENSCAN.166-14	4.33	NCI-H69, PRSC_con, NCI-H345
318538	N28625	Hs.74034	caveolin 1; caveolae protein; 22kD	4.31	PC3, A549, BT474
333631			CH22_FGENES.227_2	4.3	OVCA-R, PRSC_con, LnCap
302646	M14268		EST	4.27	PRSC_con, PRSC_log, RPWE-2
336049			CH22_FGENES.681_2	4.26	HT29, DU145, DU145
335667			CH22_FGENES.590_18	4.25	NCI-H520, Caco2, MB-MDA-453
320352	Y13323	Hs.145296	disintegrin protease	4.25	MB-MDA-231, DU145, BT474
304480	AA430373		EST singleton (not in UniGene) with exon	4.22	NCI-358, NCI-H460, NCI-H23
327273			CH.01_hs gi 5867466	4.22	NCI-H69, NCI-H345, PRSC_con
334540			CH22_FGENES.403_5	4.17	NCI-H69, NCI-H345, PRSC_log
334719			CH22_FGENES.421_30	4.17	NCI-H69, NCI-H345, RPWE-2
327827			CH.05_hs gi 5867968	4.17	OVCA-R, NCI-H69, CALU6
333599			CH22_FGENES.212_2	4.17	PRSC_log, NCI-H69, PRSC_con
329638			CH.12_p2 gi 3779004	4.16	DU145, MB-MDA-231, HT29
307556	AI281651		EST singleton (not in UniGene) with exon	4.16	BT474, HT29, CALU6
336836			CH22_FGENES.247-11	4.15	PRSC_con, NCI-H345, NCI-H69
323187	AL121180	Hs.240038	ESTs	4.14	NCI-H345, MB-MDA-435s, RPWE-2
336397			CH22_FGENES.823_12	4.13	NCI-H345, PRSC_con, RPWE-2
325007	AA736429		EST cluster (not in UniGene)	4.13	NCI-H69, PRSC_con, NCI-H345
300199	AI304386	Hs.150836	ESTs	4.11	NCI-H345, PRSC_con, PRSC_log
335832			CH22_FGENES.620_6	4.08	NCI-H69, NCI-H345, PRSC_log
312778	AI631655	Hs.197919	ESTs	4.07	NCI-358, NCI-H23, PRSC_con
323164	AA765301	Hs.151858	ESTs	4.06	NCI-H23, A549, HT29
315871	AW135312	Hs.117237	ESTs	4.05	MB-MDA-231, EB, MCF7
337452			CH22_FGENES.775-1	4.02	PRSC_con, PRSC_log, NCI-H345
335265			CH22_FGENES.521_1	4.01	NCI-H69, MCF7, RPWE-2
335200			CH22_FGENES.508_9	4.01	NCI-H69, PRSC_log, PRSC_con
336917			CH22_FGENES.346-4	3.99	PRSC_con, NCI-H345, PRSC_log
336584			CH22_FGENES.847_1	3.98	PRSC_log, PRSC_con, RPWE-2
333382			CH22_FGENES.143_21	3.97	EB, A549, HT29
329436			CH.Y_hs gi 5868883	3.97	BT474, PC3, HT29
336929			CH22_FGENES.349-3	3.94	NCI-H69, NCI-H345, PRSC_log
337238			CH22_FGENES.641-3	3.92	NCI-H69, NCI-H345, PRSC_log
333875			CH22_FGENES.291_11	3.92	PRSC_con, RPWE-2, PRSC_log
337069			CH22_FGENES.448-2	3.9	NCI-H69, LnCap, RPWE-2
332491	M24470	Hs.1435	guanosine monophosphate reductase	3.86	OVCA-R, MB-MDA-435s, CALU6
304623	AA521331		EST singleton (not in UniGene) with exon	3.86	OVCA-R, DU145, PC3
335348			CH22_FGENES.537_4	3.85	HT29, MB-MDA-231, PC3
334568			CH22_FGENES.405_9	3.85	NCI-H69, NCI-H345, PRSC_log
336924			CH22_FGENES.347-9	3.84	NCI-H345, PRSC_log, RPWE-2
301654	H81795		EST	3.84	NCI-H520, LnCap, NCI-358
334677			CH22_FGENES.418_30	3.83	PRSC_con, NCI-H345, NCI-H69
326688			CH.20_hs gi 5867582	3.83	NCI-H345, PRSC_con, PRSC_log
327790			CH.05_hs gi 5867977	3.8	PRSC_con, PRSC_log, NCI-H345
334591			CH22_FGENES.408_1	3.8	NCI-H69, PRSC_log, NCI-H345
337974			CH22_EM:AC005500.GENSCAN.106-3	3.78	PRSC_log, PRSC_con, NCI-H345
311274	AW293128	Hs.197101	ESTs	3.78	NCI-H345, PRSC_con, RPWE-2
326668			CH.20_hs gi 6552455	3.78	NCI-H345, NCI-H69, PRSC_log
304195	N35382		EST singleton (not in UniGene) with exon	3.77	NCI-H69, RPWE-2, PRSC_con
336294			CH22_FGENES.786_4	3.77	PRSC_con, PRSC_log, NCI-H69
311613	AL046311	Hs.252443	ESTs; Weakly similar to III ALU SUBFAM1	3.76	HT29, BT474, MB-MDA-231
338123			CH22_EM:AC005500.GENSCAN.195-5	3.75	MB-MDA-231, HT29, BT474
318230	AA558125		EST cluster (not in UniGene)	3.74	RPWE-2, PRSC_con, NCI-H345
303985	AW514501	Hs.156110	Immunoglobulin kappa variable 1D-8	3.73	MB-MDA-231, BT474, PRSC_con
336502			CH22_FGENES.833_8	3.72	NCI-H345, RPWE-2, PRSC_con
334063			CH22_FGENES.327_17	3.71	NCI-H69, NCI-H345, PRSC_con
333600			CH22_FGENES.213_2	3.7	NCI-H69, OVCA-R, PC3
339424			CH22_DJ579N16.GENSCAN.14-3	3.69	NCI-H69, NCI-H345, PRSC_con
336862			CH22_FGENES.297-2	3.67	NCI-H345, PRSC_con, PRSC_log
334823			CH22_FGENES.437_5	3.67	RPWE-2, PRSC_log, PRSC_con
329940			CH.16_p2 gi 6165199	3.66	CALU6, EB, MCF7
300275	AI632123	Hs.231521	ESTs	3.66	PRSC_con, NCI-H69, RPWE-2
328820			CH.07_hs gi 5868330	3.66	NCI-H69, NCI-H345, PRSC_con
332398	AA446446	Hs.104788	H sapiens clone 24554 unknown mRNA	3.66	PRSC_con, PRSC_log, NCI-H345
325791			CH.14_hs gi 6682476	3.65	NCI-H345, BT474, LnCap
300672	R14469	Hs.256573	ESTs	3.65	MCF7, MB-MDA-453, MB-MDA-435s
338344			CH22_EM:AC005500.GENSCAN.312-8	3.65	NCI-H345, PRSC_log, PRSC_con
333257			CH22_FGENES.118_5	3.65	DU145, EB, OVCA-R
332140	AA620724	Hs.112890	ESTs	3.65	MB-MDA-453, DU145, MCF7
337489			CH22_FGENES.799-2	3.63	NCI-H345, NCI-H69, PRSC_log
305167	AA663080		EST singleton (not in UniGene) with exon	3.63	OVCA-R, MB-MDA-231, MB-MDA-435s
336200			CH22_FGENES.719_4	3.61	NCI-H69, PRSC_log, NCI-H345

339208			CH22_FF113D11.GENSCAN.6-3	3.59	PRSC_con, NCI-H69, PRSC_log
320090	AB002058	Hs.113275	purinergic receptor P2X-like 1; orphan r	3.58	OVCA-R, LnCap, NCI-H69
335999			CH22_FGENES.657_1	3.57	NCI-H345, NCI-H69, PRSC_con
332909			CH22_FGENES.36_13	3.57	NCI-H345, PRSC_con, PRSC_log
306531	AA991423		EST singleton (not in UniGene) with exon	3.56	BT474, MB-MDA-453, MB-MDA-435s
333261			CH22_FGENES.119_1	3.55	HT29, CALU6, MB-MDA-231
303883	AA176396	Hs.169624	ESTs	3.54	NCI-H69, NCI-H345, RPWE-2
335831			CH22_FGENES.620_5	3.53	MCF7, BT474, OVCA-R
333983			CH22_FGENES.310_7	3.52	NCI-H345, PRSC_con, PRSC_log
333623			CH22_FGENES.222_2	3.51	NCI-H69, PRSC_con, PRSC_log
333997			CH22_FGENES.310_22	3.5	NCI-H345, PRSC_con, PRSC_log
325623			CH.14_hs gij5867000	3.5	CALU6, HT29, BT474
309151	AI935829	Hs.140	immunoglobulin gamma 3 (Gm marker)	3.49	EB, MCF7, MB-MDA-453
305080	AA641485		EST singleton (not in UniGene) with exon	3.49	NCI-H23, NCI-H460, NCI-358
339268			CH22_BA354112.GENSCAN.10-6	3.47	NCI-H69, NCI-H345, PRSC_con
310048	AI198352	Hs.105077	ESTs	3.47	Caco2, PRSC_con, NCI-H69
314758	AA521458	Hs.192738	ESTs	3.46	NCI-H23, NCI-H23, NCI-H520
334664			CH22_FGENES.418_15	3.45	NCI-H69, PRSC_log, PRSC_con
334661			CH22_FGENES.418_9	3.45	NCI-H69, PRSC_con, PRSC_log
330984	H38678	Hs.32766	H sapiens clone 24803 mRNA seq	3.44	OVCA-R, MCF7, PC3
333464			CH22_FGENES.160_1	3.44	NCI-H69, MB-MDA-231, MCF7
333580			CH22_FGENES.199_2	3.42	PRSC_con, NCI-H69, PRSC_log
313356	AI266254	Hs.132929	ESTs	3.42	RPWE-2, PRSC_con, NCI-H345
334518			CH22_FGENES.400_1	3.41	PRSC_log, PRSC_con, RPWE-2
333627			CH22_FGENES.225_2	3.4	HT29, BT474, BT474
309641	AW194230	Hs.253100	EST	3.4	HT29, MB-MDA-453, MCF7
338221			CH22_EM:AC005500.GENSCAN.246-10	3.4	NCI-H69, PRSC_log, NCI-H345
312993	AI392673	Hs.125230	ESTs	3.4	PRSC_log, NCI-H345, NCI-H345
318336	AI971806	Hs.164158	ESTs	3.38	OVCA-R, EB, CALU6
326218			CH.17_hs gij5867226	3.38	NCI-H460, NCI-H69, NCI-H345
336231			CH22_FGENES.736_3	3.38	NCI-H69, NCI-H345, PRSC_log
307912	AI382224		EST singleton (not in UniGene) with exon	3.37	NCI-H345, PRSC_con, RPWE-2
336161			CH22_FGENES.707_6	3.37	NCI-H69, NCI-H345, RPWE-2
300875	AW134756	Hs.192477	ESTs	3.37	RPWE-2, PRSC_log, PRSC_con
336593			CH22_FGENES.135_1	3.37	PRSC_con, NCI-H69, RPWE-2
310696	AI431620	Hs.160875	ESTs	3.36	HT29, OVCA-R, BT474
304745	AA577771		EST singleton (not in UniGene) with exon	3.36	NCI-H345, RPWE-2, PRSC_con
308911	AI860287	Hs.156110	immunoglobulin kappa variable 1D-8	3.36	EB, DU145, CALU6
336347			CH22_FGENES.815_3	3.36	NCI-H69, PRSC_log, PRSC_con
334906			CH22_FGENES.452_21	3.33	Caco2, CALU6, MB-MDA-453
334548			CH22_FGENES.403_13	3.33	NCI-H345, PRSC_con, NCI-H69
336695			CH22_FGENES.48_4	3.32	NCI-H69, PRSC_log, PRSC_con
316684	AA807187	Hs.220783	ESTs; Weakly similar to WNT-1 PROTO-ONCO	3.31	DU145, EB, MB-MDA-231
315901	AI521558	Hs.179718	v-myb avian myeloblastosis viral oncogen	3.3	Caco2, LnCap, NCI-H69
320115	T93574		EST cluster (not in UniGene)	3.3	DU145, HT29, CALU6
307847	AI363993	Hs.157273	EST	3.3	NCI-H345, PRSC_con, PRSC_log
327899			CH.06_hs gij5868156	3.28	BT474, MB-MDA-231, A549
304612	AA514207		EST singleton (not in UniGene) with exon	3.28	DU145, CALU6, LnCap
330021			CH.16_p2 gij6671889	3.27	A549, HT29, EB
338132			CH22_EM:AC005500.GENSCAN.200-2	3.27	MB-MDA-231, CALU6, EB
323690	AA317497	Hs.188897	ESTs	3.27	RPWE-2, NCI-H345, MCF7
327362			CH.01_hs gij6552412	3.26	NCI-H69, RPWE-2, PRSC_log
333488			CH22_FGENES.167_3	3.26	NCI-H69, NCI-H345, PRSC_log
334106			CH22_FGENES.330_5	3.26	NCI-H69, PRSC_con, PRSC_log
306990	AI129298	Hs.146491	EST; Weakly similar to FERRITIN HEAVY CH	3.26	NCI-H345, PRSC_log, PRSC_con
328420			CH.07_hs gij5868411	3.26	NCI-H69, NCI-H345, PRSC_log
336214			CH22_FGENES.722_8	3.26	MCF7, EB, OVCA-R
330565	U51095	Hs.1545	caudal type homeo box transcription fact	3.25	EB, DU145, HT29
333879			CH22_FGENES.291_15	3.25	PRSC_con, PRSC_log, NCI-H69
300145	AI240850	Hs.232016	ESTs	3.25	NCI-H345, PRSC_con, PRSC_log
327581			CH.03_hs gij5867825	3.25	EB, DU145, MB-MDA-453
308153	AI500429	Hs.1103	transforming growth factor; beta 1	3.24	MCF7, EB, EB
308337	AI608947		EST singleton (not in UniGene) with exon	3.24	PRSC_log, PRSC_con, NCI-H345
329406			CH.X_hs gij6682547	3.23	DU145, HT29, MB-MDA-231
325482			CH.12_hs gij5866957	3.23	NCI-H69, NCI-H345, PRSC_con
337544			CH22_FGENES.833-7	3.22	NCI-H69, NCI-H345, PRSC_con
337204			CH22_FGENES.595-1	3.22	NCI-H69, PRSC_con, PRSC_log
309451	AW105128	Hs.246687	EST	3.22	PRSC_con, RPWE-2, NCI-H345
337259			CH22_FGENES.649-3	3.2	PRSC_con, NCI-H345, NCI-H69
336489			CH22_FGENES.831_10	3.2	CALU6, MB-MDA-435s, Caco2
334804			CH22_FGENES.435_4	3.18	PRSC_log, PRSC_con, RPWE-2
335739			CH22_FGENES.601_10	3.18	NCI-H69, RPWE-2, PRSC_con
306264	AA935305	Hs.179779	ribosomal protein L37	3.17	LnCap, NCI-H69, EB
329386			CH.X_hs gij6004484	3.17	RPWE-2, NCI-H345, PRSC_log
323479	AA278246		EST cluster (not in UniGene)	3.16	PRSC_con, NCI-H345, RPWE-2
304731	AA576085		EST singleton (not in UniGene) with exon	3.16	NCI-H69, LnCap, DU145

339419			CH22_DJ579N16.GENSCAN.11-11	3.15	NCI-H69, PRSC_log, RPWE-2
301202	AI536797	Hs.173155	ESTs	3.15	LnCap, NCI-H69, Caco2
333608			CH22_FGENES.216_3	3.15	NCI-H345, PRSC_con, PRSC_log
339193			CH22_FF113D11.GENSCAN.1-5	3.14	NCI-H69, NCI-H345, PRSC_con
310527	AW293404	Hs.211986	ESTs	3.14	PRSC_log, PRSC_con, RPWE-2
321146	AA707443	Hs.183983	ESTs	3.14	PRSC_con, NCI-H69, PRSC_log
333271			CH22_FGENES.121_2	3.13	NCI-H345, NCI-H69, RPWE-2
330280			CH.05_p2 gij6671910	3.13	NCI-H69, NCI-H345, PRSC_log
309977	AW451663		EST singleton (not in UniGene) with exon	3.13	PRSC_con, PRSC_log, RPWE-2
307588	AI285535		EST singleton (not in UniGene) with exon	3.13	MB-MDA-231, BT474, BT474
330551	U39840	Hs.105440	hepatocyte nuclear factor 3; alpha	3.13	MB-MDA-453, LnCap, Caco2
314404	AW104203	Hs.157505	ESTs	3.13	DU145, EB, OVCA-R
334030			CH22_FGENES.320_2	3.13	NCI-H69, NCI-H345, PRSC_con
309108	AI925949		EST singleton (not in UniGene) with exon	3.13	BT474, MCF7, EB
317516	AI733250	Hs.192262	ESTs	3.12	OVCA-R, EB, MB-MDA-453
304161	H71886		EST singleton (not in UniGene) with exon	3.12	PRSC_con, NCI-H69, RPWE-2
334590			CH22_FGENES.407_13	3.12	NCI-H69, NCI-H345, PRSC_con
333408			CH22_FGENES.145_6	3.11	PRSC_log, RPWE-2, PRSC_con
330387	H14624	Hs.31386	ESTs; Highly similar to secreted apoptos	3.11	DU145, OVCA-R, PC3
332567	N23730	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	3.11	EB, MB-MDA-453, MCF7
333682			CH22_FGENES.247_10	3.1	PRSC_con, PRSC_log, RPWE-2
323152	AI680562	Hs.246192	ESTs; Weakly similar to REGULATOR OF MIT	3.1	3.1 PC3, MB-MDA-453, DU145
311142	AI638441	Hs.195649	ESTs	3.1	PRSC_con, RPWE-2, PRSC_log
333441			CH22_FGENES.151_5	3.1	RPWE-2, NCI-H345, PRSC_log
326459			CH.19_hs gij5867400	3.09	EB, CALU6, PC3
313493	AA910339	Hs.126868	ESTs	3.09	NCI-H345, PRSC_con, RPWE-2
339356			CH22_BA354I12.GENSCAN.31-1	3.08	NCI-H69, NCI-H345, PRSC_log
333629			CH22_FGENES.226_5	3.08	NCI-H69, NCI-H345, PRSC_log
304127	H42981		EST singleton (not in UniGene) with exon	3.07	LnCap, PRSC_con, DU145
325691			CH.14_hs gij5867021	3.07	NCI-H345, PRSC_con, NCI-H69
333014			CH22_FGENES.61_6	3.07	PRSC_con, PRSC_log, NCI-H345
327379			CH.02_hs gij5867795	3.07	PRSC_con, PRSC_log, NCI-H69
337816			CH22_EM:AC005500.GENSCAN.13-1	3.06	NCI-H69, PRSC_con, PRSC_log
337954			CH22_EM:AC005500.GENSCAN.96-3	3.06	PRSC_log, NCI-H69, NCI-H345
328109			CH.06_hs gij5868020	3.05	HT29, BT474, MB-MDA-231
338527			CH22_EM:AC005500.GENSCAN.396-15	3.05	NCI-H69, NCI-H345, PRSC_con
320083	T87761		EST cluster (not in UniGene)	3.05	BT474, MB-MDA-435s, MCF7
333466			CH22_FGENES.161_2	3.05	NCI-H345, RPWE-2, PRSC_log
334788			CH22_FGENES.432_13	3.04	EB, A549, CALU6
302681	X97550		EST	3.04	OVCA-R, EB, MB-MDA-453
336238			CH22_FGENES.743_3	3.03	NCI-H69, PRSC_log, PRSC_con
337606			CH22_C20H12.GENSCAN.17-2	3.02	HT29, BT474, MB-MDA-231
333545			CH22_FGENES.180_1	3.02	NCI-H69, NCI-H345, RPWE-2
309782	AW275156	Hs.156110	Immunoglobulin kappa variable 1D-8	3.02	PRSC_log, PRSC_con, RPWE-2
324277	AA429440	Hs.207285	ESTs	3.02	BT474, MB-MDA-231, HT29
321074	H38098	Hs.32756	ESTs	3.02	PC3, BT474, MB-MDA-231
337094			CH22_FGENES.465-19	3.01	PRSC_con, PRSC_log, RPWE-2
313913	AW391342		EST cluster (not in UniGene)	3	NCI-H345, RPWE-2, PRSC_log
329140			CH.X_hs gij6017060	3	EB, DU145, PC3
335331			CH22_FGENES.535_4	3	MB-MDA-435s, HT29, BT474
334827			CH22_FGENES.437_9	2.99	CALU6, EB, DU145
326029			CH.17_hs gij5867176	2.99	NCI-H345, RPWE-2, PRSC_con
303100	T09353		EST	2.99	MB-MDA-453, NCI-H345, RPWE-2
328768			CH.07_hs gij6017031	2.99	NCI-H345, PRSC_con, NCI-H69
329392			CH.X_hs gij6478815	2.98	NCI-H69, NCI-H345, PRSC_con
305168	AA663105		EST singleton (not in UniGene) with exon	2.98	LnCap, NCI-H345, MCF7
300992	AA601213	Hs.191798	ESTs	2.98	Caco2, HT29, NCI-358
334474			CH22_FGENES.394_5	2.98	NCI-H69, PRSC_con, RPWE-2
322647	AA007534	Hs.125062	ESTs	2.98	HT29, OVCA-R, A549
310620	AI341328	Hs.178953	ESTs	2.97	PRSC_con, RPWE-2, PRSC_log
328276			CH.07_hs gij6004471	2.97	NCI-H345, NCI-H69, RPWE-2
331018	N26904	Hs.24048	ESTs; Weakly similar to FK506/rapamycin-	2.96	Caco2, NCI-H460, A549
321523	H78472	Hs.191325	ESTs; Weakly similar to cDNA EST yk414c9	2.96	PRSC_con, PRSC_log, NCI-H345
339280			CH22_BA354I12.GENSCAN.14-12	2.96	NCI-H69, PRSC_log, NCI-H345
305967	AA886428		EST singleton (not in UniGene) with exon	2.96	NCI-H520, NCI-358, MB-MDA-453
335755			CH22_FGENES.604_4	2.95	EB, A549, MB-MDA-453
323907	AL043098	Hs.165387	ESTs	2.95	PRSC_con, NCI-H345, PRSC_log
330370			CH.X_p2 gij6580495	2.95	EB, DU145, MB-MDA-435s
334529			CH22_FGENES.402_9	2.94	EB, MCF7, DU145
339256			CH22_BA354I12.GENSCAN.7-11	2.94	NCI-H69, NCI-H345, PRSC_con
334783			CH22_FGENES.432_8	2.94	A549, Caco2, PC3
335266			CH22_FGENES.521_2	2.94	NCI-H69, PRSC_con, PRSC_con
323707	AA845957	Hs.128385	ESTs	2.94	NCI-H345, PRSC_con, PRSC_log
336199			CH22_FGENES.719_3	2.93	NCI-H69, NCI-H345, PRSC_log
338326			CH22_EM:AC005500.GENSCAN.308-2	2.93	NCI-H69, NCI-H345, NCI-358
333652			CH22_FGENES.239_1	2.93	PC3, OVCA-R, BT474

336479		CH22_FGENES.829_39	2.92	NCI-H69, PRSC_con, PRSC_log
336086		CH22_FGENES.688_15	2.92	PRSC_con, Caco2, CALU6
338516		CH22_EM:AC005500.GENSCAN.392-6	2.92	NCI-H69, NCI-H345, PRSC_con
320121	T93657	EST cluster (not in UniGene)	2.92	EB, BT474, HT29
305782	AA844730	EST singleton (not in UniGene) with exon	2.92	MB-MDA-453, MCF7, DU145
339304		CH22_BA354112.GENSCAN.20-16	2.91	PRSC_con, PRSC_log, NCI-H69
327472		CH.02_hs gjj5867775	2.91	PRSC_log, PRSC_con, RPWE-2
311458	AW139426 Hs.244718	ESTs	2.91	PRSC_con, PRSC_log, RPWE-2
338431		CH22_EM:AC005500.GENSCAN.351-4	2.9	BT474, MCF7, MB-MDA-453
339230		CH22_BA354112.GENSCAN.1-6	2.89	NCI-H69, NCI-H345, PRSC_log
320586	NM_00365	EST cluster (not in UniGene)	2.89	OVCA-R, HT29, MB-MDA-231
304777	AA581692 Hs.2186	eukaryotic translation elongation factor	2.89	OVCA-R, EB, MCF7
337768		CH22_EM:AC000097.GENSCAN.119-6	2.88	NCI-H69, LnCap, DU145
319465	AA319115 Hs.191558	ESTs	2.88	NCI-H460, NCI-H520, NCI-358
319068	W93011 Hs.110155	ESTs	2.87	BT474, MB-MDA-453, MB-MDA-435s
330958	H08815 Hs.159824	EST	2.87	OVCA-R, PC3, A549
334215		CH22_FGENES.357_7	2.87	NCI-H69, PRSC_con, PRSC_log
333568		CH22_FGENES.185_1	2.87	PRSC_con, PRSC_log, NCI-H69
333142		CH22_FGENES.85_5	2.87	NCI-H69, HT29, HT29
330239		CH.05_p2 gjj6671857	2.87	MB-MDA-453, MB-MDA-453, EB
302120	R55140 Hs.31075	ESTs; Weakly similar to Weak similarity	2.87	CALU6, MB-MDA-435s, BT474
338679		CH22_EM:AC005500.GENSCAN.470-1	2.86	NCI-H345, PRSC_log, PRSC_con
329041		CH.X_hs gjj5868564	2.86	LnCap, PRSC_con, RPWE-2
333541		CH22_FGENES.178_3	2.86	NCI-H69, NCI-H345, PRSC_con
337011		CH22_FGENES.427-6	2.86	NCI-H69, PRSC_log, PRSC_con
324031	AA375646	EST cluster (not in UniGene)	2.86	NCI-H345, PRSC_log, LnCap
331842	AA416586 Hs.98232	ESTs	2.86	DU145, OVCA-R, HT29
336599		CH22_FGENES.350_3	2.85	LnCap, NCI-H69, NCI-H345
337586		CH22_C20H12.GENSCAN.5-4	2.85	NCI-H345, NCI-H69, PRSC_con
336177		CH22_FGENES.712_2	2.85	NCI-H69, PRSC_log, RPWE-2
337522		CH22_FGENES.819-1	2.85	CALU6, OVCA-R, HT29
338596		CH22_EM:AC005500.GENSCAN.437-2	2.85	NCI-H69, PRSC_con, NCI-H345
309522	AW150044 Hs.252259	ribosomal protein S3	2.85	MB-MDA-453, MB-MDA-435s, MB-MDA-435s
336981		CH22_FGENES.397-7	2.85	NCI-H69, PRSC_con, PRSC_log
330286		CH.05_p2 gjj6671913	2.84	NCI-H345, PRSC_log, NCI-H69
333713		CH22_FGENES.251_2	2.84	RPWE-2, PRSC_con, NCI-H69
335068		CH22_FGENES.483_5	2.83	MB-MDA-231, NCI-H345, RPWE-2
305075	AA641288 Hs.181165	eukaryotic translation elongation factor	2.83	EB, LnCap, DU145
326380		CH.19_hs gjj5867327	2.82	NCI-H69, PRSC_con, PRSC_log
334970		CH22_FGENES.466_3	2.82	PRSC_con, NCI-H69, RPWE-2
337097		CH22_FGENES.471-1	2.82	NCI-H345, NCI-H69, PRSC_log
323676	AI702835	EST cluster (not in UniGene)	2.82	LnCap, A549, CALU6
333785		CH22_FGENES.274_4	2.82	OVCA-R, Caco2, MB-MDA-453
334175		CH22_FGENES.349_10	2.81	RPWE-2, BT474, MCF7
337865		CH22_EM:AC005500.GENSCAN.46-5	2.81	Caco2, NCI-H23, BT474
302585	AA083564 Hs.249220	H sapiens mRNA for hTbr2; complete cds	2.81	EB, DU145, MB-MDA-453
336623		CH22_FGENES.4-5	2.81	NCI-H345, PRSC_con, NCI-H69
332854		CH22_FGENES.22_1	2.8	RPWE-2, PRSC_log, PRSC_con
336978		CH22_FGENES.384-10	2.8	PRSC_con, NCI-H345, RPWE-2
326874		CH.20_hs gjj6682507	2.8	RPWE-2, NCI-H345, PRSC_log
315121	AA565011 Hs.105902	ESTs	2.8	NCI-H345, PRSC_log, RPWE-2
311185	AI638294 Hs.224665	ESTs	2.8	NCI-H69, NCI-H345, PRSC_log
334682		CH22_FGENES.419_4	2.8	NCI-H69, PRSC_log, RPWE-2
316845	AW418715 Hs.250388	ESTs	2.79	RPWE-2, NCI-H345, PRSC_log
331599	N74626 Hs.50535	ESTs	2.79	A549, MB-MDA-453, MB-MDA-435s
315681	AW022054 Hs.136591	ESTs	2.78	NCI-H460, MB-MDA-453, MCF7
313012	AI207390 Hs.143929	ESTs	2.78	DU145, MB-MDA-453, MCF7
313476	AA010267	EST cluster (not in UniGene)	2.78	NCI-H520, NCI-H460, HT29
327277		CH.01_hs gjj5867473	2.78	DU145, CALU6, EB
310981	AI494514 Hs.171380	ESTs	2.78	LnCap, RPWE-2, NCI-H460
335090		CH22_FGENES.490_1	2.77	NCI-H69, PRSC_log, PRSC_con
328581		CH.07_hs gjj6006033	2.77	HT29, MB-MDA-453, MCF7
333219		CH22_FGENES.104_11	2.77	NCI-H69, PRSC_log, NCI-H345
308311	AI581855	EST singleton (not in UniGene) with exon	2.77	MB-MDA-231, HT29, CALU6
329760		CH.14_p2 gjj6048280	2.77	CALU6, DU145, EB
303925	AW469999 Hs.258523	ESTs	2.77	NCI-H69, LnCap, MB-MDA-231
337628		CH22_C20H12.GENSCAN.28-31	2.77	NCI-H69, LnCap, MB-MDA-453
333520		CH22_FGENES.174_3	2.77	NCI-H69, NCI-H345, PRSC_con
303168	AA872479 Hs.197770	ESTs; Weakly similar to estrogen-respons	2.76	DU145, OVCA-R, MB-MDA-453
313451	AW138189 Hs.122672	ESTs	2.76	OVCA-R, EB, DU145
328474		CH.07_hs gjj5868446	2.76	NCI-H69, NCI-H345, RPWE-2
331988	AA477414 Hs.9242	purine-rich element binding protein B	2.76	MB-MDA-435s, A549, OVCA-R
306180	AA922503	EST singleton (not in UniGene) with exon	2.76	NCI-H69, DU145, LnCap
321071	AA013011 Hs.241502	Cdc42 effector protein 4	2.76	PRSC_log, PRSC_con, NCI-H345
302972	W73400	EST	2.76	NCI-H345, RPWE-2, NCI-H69
305185	AA663985 Hs.248038	major histocompatibility complex; class	2.75	DU145, A549, BT474

335998			CH22_FGENES.656_16	2.75	NCI-H69, PRSC_con, RPWE-2
319138	R11699	Hs.73818	ubiquinol-cytochrome c reductase hinge p	2.75	NCI-H345, NCI-H69, PRSC_con
336387			CH22_FGENES.822_7	2.75	PRSC_con, RPWE-2, PRSC_log
338054			CH22_EM:AC005500.GENSCAN.158-2	2.75	OVCA-R, EB, DU145
316041	AA719183		EST cluster (not in UniGene)	2.74	DU145, MCF7, MB-MDA-453
336863			CH22_FGENES.297_4	2.74	MB-MDA-453, MCF7, OVCA-R
335975			CH22_FGENES.652_9	2.74	CALU6, EB, A549
302952	AF103179		EST	2.74	CALU6, MB-MDA-435s, BT474
326122			CH.17_hs gjl5867194	2.74	HT29, Caco2, PC3
337427			CH22_FGENES.761-4	2.74	RPWE-2, NCI-H69, PRSC_log
308063	AI469244	Hs.119252	tumor protein; translationally-controlle	2.74	NCI-358, NCI-H23, Caco2
325433			CH.12_hs gjl5866936	2.74	NCI-H345, PRSC_con, RPWE-2
316252	AI572633	Hs.190406	ESTs	2.74	OVCA-R, MCF7, A549
310837	AI418688	Hs.170301	ESTs	2.74	NCI-H345, PRSC_con, RPWE-2
313562	AW467335	Hs.257676	ESTs	2.74	HT29, MCF7, MB-MDA-231
335455			CH22_FGENES.562_15	2.74	NCI-H69, LnCap, PRSC_con
304792	AA583101	Hs.29797	ribosomal protein L10	2.73	EB, OVCA-R, MB-MDA-453
331979	AA469937	Hs.105322	EST	2.73	MCF7, BT474, NCI-H460
336198			CH22_FGENES.719_2	2.73	NCI-H69, PRSC_con, PRSC_log
314698	AI660452	Hs.187127	ESTs	2.73	MB-MDA-231, LnCap, BT474
307954	AI419692		EST singleton (not in UniGene) with exon	2.73	HT29, HT29, EB
318288	AI088590	Hs.134702	ESTs	2.73	PRSC_log, NCI-H345, PRSC_con
327833			CH.05_hs gjl5867968	2.73	BT474, PC3, MB-MDA-231
300221	AW449602	Hs.217953	ESTs; Highly similar to NK-TUMOR RECOGNI	2.73	NCI-H520, NCI-358, MB-MDA-453
326039			CH.17_hs gjl5867179	2.73	MB-MDA-453, EB, EB
318457	AI149678	Hs.143952	ESTs	2.72	PRSC_con, PRSC_log, NCI-H345
336753			CH22_FGENES.128-9	2.72	MB-MDA-435s, NCI-H520, MCF7
330086			CH.19_p2 gjl6015293	2.72	HT29, MB-MDA-453, MCF7
333566			CH22_FGENES.183_2	2.72	HT29, BT474, OVCA-R
339384			CH22_BA232E17.GENSCAN.3-22	2.71	NCI-H69, NCI-H345, PRSC_log
338668			CH22_EM:AC005500.GENSCAN.465-1	2.71	NCI-H69, RPWE-2, PRSC_con
300798	AI382618	Hs.194613	ESTs	2.71	PRSC_con, NCI-H345, PRSC_log
303745	AI142379		EST	2.71	PRSC_log, PRSC_con, RPWE-2
305197	AA666301		EST singleton (not in UniGene) with exon	2.71	EB, NCI-H520, OVCA-R
338725			CH22_EM:AC005500.GENSCAN.499-1	2.7	CALU6, MB-MDA-453, PC3
307799	AI351112		EST singleton (not in UniGene) with exon	2.7	HT29, BT474, MCF7
309598	AW173642	Hs.250106	EST	2.69	NCI-358, NCI-H69, NCI-H23
302727	L10141		EST	2.69	OVCA-R, BT474, PC3
308544	AI695133		EST singleton (not in UniGene) with exon	2.69	HT29, CALU6, MB-MDA-435s
322877	AA079727		EST cluster (not in UniGene)	2.69	NCI-H345, NCI-H69, PRSC_con
325695			CH.14_hs gjl6552446	2.69	NCI-H69, NCI-H460, NCI-H460
307728	AI335557		EST singleton (not in UniGene) with exon	2.68	NCI-H69, PRSC_log, NCI-358
302399	N79624		EST	2.68	NCI-H69, PRSC_con, NCI-H345
309343	AW028652		EST singleton (not in UniGene) with exon	2.68	HT29, MB-MDA-231, MB-MDA-231
339360			CH22_BA354112.GENSCAN.32-2	2.68	NCI-H69, PRSC_log, PRSC_con
337821			CH22_EM:AC005500.GENSCAN.13-11	2.68	PRSC_con, PRSC_log, PRSC_log
337338			CH22_FGENES.717-7	2.68	NCI-H69, PRSC_con, PRSC_log
334510			CH22_FGENES.398_8	2.68	NCI-H460, NCI-H23, NCI-358
300918	AA491286	Hs.128792	ESTs	2.68	MB-MDA-435s, CALU6, DU145
335536			CH22_FGENES.574_2	2.67	NCI-H69, NCI-H345, PRSC_log
335311			CH22_FGENES.532_4	2.67	MB-MDA-435s, Caco2, A549
338959			CH22_DJ32110.GENSCAN.23-31	2.67	NCI-H345, PRSC_con, NCI-H69
339081			CH22_DA59H18.GENSCAN.37-10	2.67	NCI-H345, RPWE-2, NCI-H69
334068			CH22_FGENES.327_23	2.67	PRSC_con, RPWE-2, PRSC_log
338976			CH22_DA59H18.GENSCAN.1-3	2.66	PRSC_con, PRSC_log, RPWE-2
325524			CH.12_hs gjl5866981	2.66	NCI-H345, RPWE-2, PRSC_con
333069			CH22_FGENES.76_5	2.66	NCI-H69, NCI-H345, PRSC_con
336203			CH22_FGENES.719_7	2.66	OVCA-R, PC3, A549
333133			CH22_FGENES.83_9	2.66	HT29, OVCA-R, A549
304074	T77842	Hs.142528	ESTs	2.65	DU145, CALU6, EB
330919	AA224594	Hs.86941	ESTs	2.65	PRSC_con, RPWE-2, LnCap
333248			CH22_FGENES.115_5	2.65	NCI-H345, PRSC_con, MB-MDA-231
336665			CH22_FGENES.42-2	2.65	NCI-H69, PRSC_log, PRSC_con
315322	AA770599		EST cluster (not in UniGene)	2.65	A549, MB-MDA-453, MB-MDA-435s
307474	AI264023		EST singleton (not in UniGene) with exon	2.65	NCI-H69, NCI-H345, RPWE-2
320221	AL050020	Hs.127384	DKFZP564C196 protein	2.65	MB-MDA-453, MCF7, HT29
301767	AW361892		EST	2.65	NCI-H345, PRSC_con, PRSC_log
327246			CH.01_hs gjl5867547	2.65	EB, OVCA-R, DU145
337403			CH22_FGENES.752-2	2.65	PRSC_con, PRSC_log, RPWE-2
328221			CH.06_hs gjl5868099	2.64	MCF7, MB-MDA-231, BT474
336759			CH22_FGENES.133-2	2.64	NCI-H69, PRSC_log, PRSC_con
327532			CH.02_hs gjl6469818	2.64	PC3, CALU6, A549
305621	AA789095		EST singleton (not in UniGene) with exon	2.64	HT29, MB-MDA-231, MB-MDA-453
322931	AA099329	Hs.151764	ESTs	2.64	PRSC_con, RPWE-2, NCI-H345
327278			CH.01_hs gjl5867473	2.64	EB, NCI-H460, NCI-H69
332235	N51413	Hs.109284	ESTs	2.64	DU145, EB, OVCA-R

332792			CH22_FGENES.3_2	2.63	HT29, Caco2, A549
312340	AI862668	Hs.176333	ESTs	2.63	NCI-358, NCI-358, HT29
337484			CH22_FGENES.795-8	2.63	NCI-H69, NCI-H345, PRSC_con
325783			CH.14_hs gij6456780	2.63	EB, OVCA-R, PC3
303672	AW502380	Hs.210527	ESTs	2.63	PRSC_log, NCI-H345, NCI-H69
306009	AA894560		EST singleton (not in UniGene) with exon	2.63	HT29, MB-MDA-231, CALU6
308548	AI695484		EST singleton (not in UniGene) with exon	2.63	PC3, A549, NCI-358
337930			CH22_EM:AC005500.GENSCAN.81-3	2.62	PC3, OVCA-R, MCF7
327791			CH.05_hs gij5867977	2.62	PRSC_log, PRSC_con, NCI-H345
330925	AA232678	Hs.87073	ESTs	2.62	OVCA-R, MCF7, LnCap
327259			CH.01_hs gij5867454	2.62	NCI-H345, PRSC_con, RPWE-2
302150	AF061756	Hs.152531	heart and neural crest derivatives expe	2.61	OVCA-R, PC3, A549
304881	AA598501	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	2.61	MB-MDA-435s, NCI-H23, MCF7
335956			CH22_FGENES.647_3	2.61	DU145, PRSC_con, PC3
326506			CH.19_hs gij5867435	2.61	RPWE-2, NCI-H460, NCI-358
335863			CH22_FGENES.629_8	2.61	PC3, HT29, NCI-358
334752			CH22_FGENES.428_1	2.61	PRSC_con, NCI-H69, PRSC_log
333288			CH22_FGENES.128_19	2.61	HT29, NCI-358, Caco2
306709	AI024215	Hs.131477	EST	2.61	MB-MDA-435s, MCF7, BT474
305816	AA854776		EST singleton (not in UniGene) with exon	2.6	MB-MDA-453, MCF7, MB-MDA-435s
327264			CH.01_hs gij5867461	2.6	MB-MDA-435s, MB-MDA-435s, MB-MDA-453
310905	AW075527	Hs.252259	ribosomal protein S3	2.6	OVCA-R, EB, DU145
324492	AA479507	Hs.135179	ESTs	2.6	DU145, EB, OVCA-R
322649	AA526549		EST cluster (not in UniGene)	2.6	PRSC_con, RPWE-2, PRSC_log
329384			CH.X_hs gij5868869	2.6	NCI-H69, NCI-H345, PRSC_con
321240	M62378		EST cluster (not in UniGene)	2.6	BT474, CALU6, MB-MDA-231
302751	AA299576	Hs.156110	Immunoglobulin kappa variable 1D-8	2.59	MCF7, MB-MDA-453, OVCA-R
305841	AA860348		EST singleton (not in UniGene) with exon	2.59	NCI-H345, PRSC_log, PRSC_con
324180	AA402242	Hs.122799	ESTs	2.58	EB, PC3, HT29
334196			CH22_FGENES.353_4	2.58	NCI-H345, NCI-H69, PRSC_con
338451			CH22_EM:AC005500.GENSCAN.359-39	2.58	MB-MDA-435s, NCI-H23, MCF7
300333	AW297396	Hs.227052	ESTs	2.58	PRSC_con, PRSC_log, NCI-H69
305046	AA632201		EST singleton (not in UniGene) with exon	2.58	NCI-H460, MB-MDA-453, MB-MDA-435s
305648	AA807652	Hs.156110	Immunoglobulin kappa variable 1D-8	2.57	PRSC_con, RPWE-2, NCI-H345
301744	W22230		EST	2.57	PRSC_con, PRSC_log, NCI-H345
329182			CH.X_hs gij6056331	2.57	PRSC_con, RPWE-2, NCI-H345
318178	AW137425	Hs.158401	ESTs	2.57	MB-MDA-231, PRSC_con, BT474
330057			CH.17_p2 gij6478962	2.57	NCI-H345, RPWE-2, PRSC_con
326552			CH.19_hs gij5867308	2.57	NCI-H345, PRSC_con, RPWE-2
311956	T67085	Hs.188464	ESTs	2.57	HT29, MB-MDA-453, NCI-H460
327185			CH.01_hs gij6117805	2.57	CALU6, HT29, EB
302183	NM_00224		EST	2.57	MCF7, PC3, OVCA-R
327263			CH.01_hs gij6525274	2.56	PRSC_con, NCI-H69, PRSC_log
339164			CH22_DA59H18.GENSCAN.69-4	2.56	NCI-H69, PRSC_con, NCI-H345
332763	AA063554	Hs.90959	ESTs	2.56	RPWE-2, NCI-H345, PRSC_con
330579	U67733	Hs.154437	phosphodiesterase 2A; cGMP-stimulated	2.55	HT29, CALU6, PC3
329948			CH.16_p2 gij5540101	2.55	NCI-H460, MCF7, MB-MDA-453
300282	AW044305	Hs.236131	ESTs; Highly similar to homeodomain-inte	2.55	NCI-H460, NCI-H23, NCI-H23
335448			CH22_FGENES.562_5	2.55	MB-MDA-453, BT474, MCF7
330959	H09174	Hs.26484	HIRA-interacting protein 3	2.55	MB-MDA-453, HT29, MCF7
307262	AI202100		EST singleton (not in UniGene) with exon	2.55	MCF7, DU145, MB-MDA-435s
335806			CH22_FGENES.616_8	2.55	NCI-H345, NCI-H69, PRSC_con
335782			CH22_FGENES.609_4	2.55	Caco2, MB-MDA-453, MB-MDA-435s
301703	AW301478		EST	2.55	PC3, MCF7, MB-MDA-453
329018			CH.X_hs gij6249620	2.54	NCI-H69, PRSC_log, PRSC_con
329870			CH.14_p2 gij6706435	2.54	NCI-H23, NCI-H460, NCI-358
334504			CH22_FGENES.398_2	2.54	HT29, BT474, MB-MDA-231
304707	AA564846		EST singleton (not in UniGene) with exon	2.53	NCI-H520, EB, NCI-H460
329326			CH.X_hs gij5868806	2.53	MB-MDA-231, NCI-H345, NCI-H69
334418			CH22_FGENES.384_5	2.53	NCI-H23, NCI-358, NCI-H460
338124			CH22_EM:AC005500.GENSCAN.196-2	2.53	NCI-H69, PRSC_con, PRSC_log
318423	AI362671	Hs.214491	ESTs	2.53	OVCA-R, EB, DU145
333006			CH22_FGENES.60_3	2.53	NCI-H69, PRSC_con, PRSC_log
333668			CH22_FGENES.245_2	2.53	NCI-H69, PRSC_log, PRSC_con
333567			CH22_FGENES.184_2	2.53	NCI-H69, NCI-H345, PRSC_con
309592	AW172384		EST singleton (not in UniGene) with exon	2.52	LnCap, NCI-H69, DU145
328989			CH.09_hs gij5868535	2.52	MB-MDA-435s, OVCA-R, EB
326725			CH.20_hs gij6552456	2.52	PRSC_con, NCI-H345, NCI-H69
302996	AF054663		EST	2.52	HT29, BT474, CALU6
335733			CH22_FGENES.601_3	2.52	NCI-H69, PRSC_log, NCI-H345
336000			CH22_FGENES.658_1	2.52	LnCap, OVCA-R, DU145
327774			CH.05_hs gij5867964	2.52	DU145, CALU6, HT29
328557			CH.07_hs gij5868489	2.52	MB-MDA-453, MB-MDA-435s, MCF7
328228			CH.06_hs gij5868105	2.52	NCI-H69, NCI-H345, PRSC_con
328305			CH.07_hs gij6004478	2.52	NCI-H69, NCI-H460, PRSC_log
334010			CH22_FGENES.313_1	2.51	NCI-H69, PRSC_log, PRSC_con

339033		CH22_DA59H18.GENSCAN.26-1	2.51	NCI-H69, NCI-H345, PRSC_con
335340		CH22_FGENES.535_17	2.51	NCI-H69, PRSC_con, PRSC_log
300156	AI245582	Hs.233395 ESTs	2.51	PRSC_con, PRSC_log, NCI-H345
305880	AA866065	Hs.156110 Immunoglobulin kappa variable 1D-8	2.5	EB, OVCA-R, DU145
310841	AI968009	Hs.232024 ESTs	2.5	LnCap, NCI-358, CALU6
336908		CH22_FGENES.343-2	2.5	NCI-H345, RPWE-2, PRSC_log
304674	AA541735	EST singleton (not in UniGene) with exon	2.5	RPWE-2, NCI-H69, MCF7
314521	AW503939	Hs.107149 ESTs; Weakly similar to PTB-ASSOCIATED S2.5	2.5	NCI-H460, EB, Caco2
307592	AI285739	EST singleton (not in UniGene) with exon	2.5	PRSC_con, NCI-H345, PRSC_log
331476	N26190	Hs.43768 ESTs	2.5	NCI-H345, NCI-H69, PRSC_con
325803		CH.14_hs gjl6552451	2.5	NCI-H345, RPWE-2, PRSC_con
306549	AA993796	EST singleton (not in UniGene) with exon	2.49	A549, OVCA-R, CALU6
304833	AA586504	EST singleton (not in UniGene) with exon	2.49	MCF7, DU145, LnCap
336333		CH22_FGENES.813_1	2.49	NCI-H345, PRSC_con, PRSC_log
332320	T71134	Hs.100551 EST	2.49	NCI-H345, LnCap, RPWE-2
328236		CH.06_hs gjl5868117	2.49	PRSC_con, NCI-H345, PRSC_log
317335	AI656979	Hs.130210 ESTs	2.49	MCF7, MB-MDA-453, PC3
339188		CH22_DA59H18.GENSCAN.72-16	2.48	NCI-H69, PRSC_con, PRSC_log
334235		CH22_FGENES.361_19	2.48	NCI-H520, MB-MDA-453, A549
301214	AW450950	Hs.157034 ESTs; Weakly similar to Unknown [H.sapie	2.48	HT29, A549, A549
332843		CH22_FGENES.19_1	2.48	DU145, CALU6, EB
337431		CH22_FGENES.763-7	2.48	PRSC_con, RPWE-2, NCI-H69
336757		CH22_FGENES.131-1	2.48	NCI-H69, PRSC_log, PRSC_con
305403	AA723748	EST singleton (not in UniGene) with exon	2.48	NCI-H23, DU145, OVCA-R
330065		CH.19_p2 gjl6165044	2.48	PRSC_con, PRSC_log, NCI-H69
309245	AI972447	EST singleton (not in UniGene) with exon	2.48	MB-MDA-231, NCI-H69, HT29
328876		CH.07_hs gjl6525286	2.47	MB-MDA-231, CALU6, PC3
333944		CH22_FGENES.302_2	2.47	NCI-H69, RPWE-2, PRSC_log
328504		CH.07_hs gjl5868471	2.47	LnCap, MB-MDA-453, MB-MDA-435s
338120		CH22_EM:AC005500.GENSCAN.195-1	2.47	MB-MDA-231, NCI-H69, PRSC_con
306710	AI024221	EST singleton (not in UniGene) with exon	2.47	OVCA-R, EB, LnCap
305064	AA636012	EST singleton (not in UniGene) with exon	2.47	NCI-H69, RPWE-2, PRSC_con
329995		CH.16_p2 gjl4567166	2.47	OVCA-R, DU145, MB-MDA-453
315694	AI821743	Hs.168418 ESTs; Moderately similar to III ALU SUB	2.46	EB, A549, LnCap
331004	H64622	Hs.32748 ESTs	2.46	EB, MCF7, MB-MDA-435s
305259	AA679225	EST singleton (not in UniGene) with exon	2.46	PRSC_con, NCI-H345, RPWE-2
304576	AA496563	EST singleton (not in UniGene) with exon	2.46	PRSC_con, RPWE-2, PRSC_log
318887	R60487	Hs.21065 ESTs	2.46	NCI-H345, Caco2, Caco2
308954	AI868958	EST singleton (not in UniGene) with exon	2.46	PRSC_con, PRSC_log, RPWE-2
301140	AI807692	Hs.207128 ESTs	2.46	OVCA-R, MB-MDA-231, HT29
322085	AA088500	Hs.170298 ESTs	2.46	PRSC_log, PRSC_con, NCI-H345
339130		CH22_DA59H18.GENSCAN.56-3	2.46	NCI-H345, PRSC_con, RPWE-2
337612		CH22_C20H12.GENSCAN.22-5	2.46	EB, A549, Caco2
313765	AW206181	Hs.185981 ESTs; Weakly similar to gag [H.sapiens]	2.45	RPWE-2, PRSC_log, PRSC_con
311665	AW294254	Hs.223742 ESTs	2.45	PRSC_log, RPWE-2, PRSC_con
328620		CH.07_hs gjl5868241	2.45	MB-MDA-453, MCF7, MB-MDA-435s
305361	AA708902	EST singleton (not in UniGene) with exon	2.45	HT29, MB-MDA-435s, A549
336243		CH22_FGENES.746_1	2.44	OVCA-R, MB-MDA-453, MB-MDA-435s
320299	H08323	Hs.177181 ESTs	2.44	PRSC_con, RPWE-2, NCI-H345
302535	H48676	EST	2.44	MB-MDA-453, EB, DU145
333465		CH22_FGENES.160_2	2.44	NCI-H69, PRSC_con, PRSC_log
334109		CH22_FGENES.330_8	2.44	NCI-H69, NCI-H345, PRSC_log
301749	F12998	Hs.90790 ESTs	2.44	NCI-H345, RPWE-2, PRSC_log
324575	AW502257	EST cluster (not in UniGene)	2.44	NCI-H345, PRSC_con, RPWE-2
337114		CH22_FGENES.494-17	2.44	NCI-H69, PRSC_log, PRSC_con
336087		CH22_FGENES.688_16	2.44	PRSC_con, Caco2, PRSC_log
315678	AI657119	Hs.120036 ESTs	2.44	NCI-358, PC3, NCI-H23
333258		CH22_FGENES.118_6	2.44	MB-MDA-231, HT29, CALU6
303798	V00505	Hs.36977 hemoglobin; delta	2.44	MB-MDA-435s, MCF7, MB-MDA-453
309759	AW268822	EST singleton (not in UniGene) with exon	2.44	MB-MDA-453, EB, MCF7
318946	AI122843	EST cluster (not in UniGene)	2.44	PC3, OVCA-R, DU145
321986	AL133656	EST cluster (not in UniGene)	2.44	DU145, CALU6, CALU6
338151		CH22_EM:AC005500.GENSCAN.207-5	2.44	PRSC_con, PRSC_log, RPWE-2
327056		CH.21_hs gjl6531965	2.44	PRSC_con, NCI-H345, RPWE-2
309605	AW182800	EST singleton (not in UniGene) with exon	2.43	NCI-358, NCI-H23, NCI-H520
335783		CH22_FGENES.610_3	2.43	PRSC_con, PRSC_log, NCI-H345
325790		CH.14_hs gjl6381957	2.43	MB-MDA-435s, MB-MDA-453, MB-MDA-453
339342		CH22_BA354112.GENSCAN.27-10	2.43	BT474, MB-MDA-231, MB-MDA-453
335777		CH22_FGENES.607_13	2.43	DU145, EB, BT474
309972	AW450350	Hs.257283 ESTs	2.43	MCF7, MB-MDA-453, OVCA-R
308718	AI798009	EST singleton (not in UniGene) with exon	2.43	NCI-H345, PRSC_con, PRSC_log
338087		CH22_EM:AC005500.GENSCAN.174-16	2.43	DU145, PC3, CALU6
306930	AI124518	EST singleton (not in UniGene) with exon	2.43	NCI-H69, MCF7, BT474
319032	AW409728	Hs.80449 ESTs; Weakly similar to cytoplasmic dyne	2.43	RPWE-2, A549, NCI-H69
304330	AA157834	EST singleton (not in UniGene) with exon	2.43	MB-MDA-453, PC3, OVCA-R
320638	R54766	Hs.101120 ESTs	2.43	MCF7, MB-MDA-435s, MB-MDA-453

335281			CH22_FGENES.524_4	2.43	PC3, LnCap, A549
317431	AI675790	Hs.132453	ESTs	2.43	NCI-H345, RPWE-2, PRSC_log
306511	AA988891		EST singleton (not in UniGene) with exon	2.43	OVCA-R, EB, DU145
333298			CH22_FGENES.133_4	2.43	EB, DU145, PC3
328436			CH.07_hs gjl5868417	2.43	EB, LnCap, A549
333420			CH22_FGENES.146_11	2.43	NCI-H345, NCI-H69, PRSC_log
338113			CH22_EM:AC005500.GENSCAN.188-13	2.42	DU145, EB, CALU6
335188			CH22_FGENES.507_3	2.42	EB, A549, BT474
329164			CH.X_hs gjl5868691	2.42	RPWE-2, PRSC_con, PRSC_log
336316			CH22_FGENES.799_11	2.42	MB-MDA-435s, MCF7, NCI-H69
310831	AI927594	Hs.161142	ESTs	2.42	NCI-H345, PRSC_con, PRSC_log
327334			CH.01_hs gjl5902477	2.42	MB-MDA-453, MB-MDA-435s, MCF7
334017			CH22_FGENES.315_2	2.42	PRSC_con, PRSC_log, RPWE-2
308138	AI494446		EST singleton (not in UniGene) with exon	2.42	DU145, LnCap, EB
333074			CH22_FGENES.76_10	2.42	NCI-H69, RPWE-2, PRSC_log
306546	AA993109		EST singleton (not in UniGene) with exon	2.42	HT29, CALU6, LnCap
336516			CH22_FGENES.836_1	2.42	NCI-H69, PRSC_con, PRSC_log
306791	AI042387		EST singleton (not in UniGene) with exon	2.42	CALU6, DU145, EB
329411			CH.X_hs gjl6682549	2.42	OVCA-R, EB, LnCap
308659	AI750091		EST singleton (not in UniGene) with exon	2.41	EB, DU145, CALU6
313504	AI190405	Hs.143127	ESTs	2.41	DU145, EB, CALU6
326073			CH.17_hs gjl6682495	2.41	DU145, A549, MB-MDA-435s
334047			CH22_FGENES.326_5	2.41	PRSC_con, PRSC_log, NCI-H345
325464			CH.12_hs gjl5866947	2.41	NCI-358, NCI-H23, NCI-H460
334764			CH22_FGENES.428_13	2.41	NCI-H69, NCI-H345, RPWE-2
312737	AI033500	Hs.132895	ESTs	2.41	OVCA-R, DU145, CALU6
306591	AI000248		EST singleton (not in UniGene) with exon	2.41	MB-MDA-231, MCF7, DU145
333582			CH22_FGENES.201_2	2.41	NCI-H69, PRSC_con, PRSC_log
337843			CH22_EM:AC005500.GENSCAN.30-8	2.4	EB, LnCap, A549
335284			CH22_FGENES.526_6	2.4	NCI-H69, NCI-H345, PRSC_log
305134	AA653159		EST singleton (not in UniGene) with exon	2.4	DU145, HT29, MB-MDA-453
335527			CH22_FGENES.572_7	2.4	DU145, OVCA-R, EB
336795			CH22_FGENES.176-5	2.4	NCI-H69, NCI-H345, PRSC_log
303144	AF202889		EST	2.4	PRSC_con, PRSC_log, NCI-H69
334948			CH22_FGENES.465_15	2.4	PRSC_con, PRSC_log, RPWE-2
328860			CH.07_hs gjl6381928	2.4	PRSC_con, PRSC_log, NCI-H345
322929	AI365585	Hs.146246	ESTs	2.4	NCI-H460, A549, HT29
333561			CH22_FGENES.180_18	2.4	OVCA-R, EB, DU145
338239			CH22_EM:AC005500.GENSCAN.264-5	2.4	NCI-H69, NCI-H345, PRSC_con
323670	AL040411	Hs.161763	ESTs; Weakly similar to KIAA0738 protein	2.4	DU145, MB-MDA-453, EB
305903	AA873085		EST singleton (not in UniGene) with exon	2.4	MCF7, A549, NCI-H520
312573	AW297673	Hs.190526	ESTs	2.4	LnCap, NCI-H460, NCI-H23
334470			CH22_FGENES.394_1	2.4	NCI-H520, HT29, NCI-H23
333272			CH22_FGENES.122_1	2.39	NCI-H345, PRSC_con, RPWE-2
304010	AW518383	Hs.177592	ribosomal protein; large; P1	2.39	DU145, CALU6, EB
337316			CH22_FGENES.692-1	2.39	MCF7, BT474, OVCA-R
316769	AI914939	Hs.212184	ESTs	2.39	PRSC_con, NCI-H345, RPWE-2
336280			CH22_FGENES.763_4	2.39	NCI-H345, PRSC_log, PRSC_con
331223	T98872	Hs.194181	ESTs	2.39	DU145, HT29, PC3
337172			CH22_FGENES.565-2	2.39	EB, OVCA-R, DU145
300625	AI671992	Hs.143631	ESTs; Weakly similar to WASP-family prot	2.39	EB, NCI-H520, LnCap
337092			CH22_FGENES.465-12	2.39	PRSC_con, PRSC_log, NCI-H69
334528			CH22_FGENES.402_8	2.39	NCI-H345, PRSC_con, NCI-H69
338411			CH22_EM:AC005500.GENSCAN.341-7	2.39	NCI-H345, NCI-H69, PRSC_con
331344	AA357927	Hs.70208	ESTs	2.39	PC3, EB, A549
334044			CH22_FGENES.323_2	2.38	MB-MDA-231, MCF7, LnCap
333918			CH22_FGENES.296_7	2.38	RPWE-2, NCI-H345, EB
317168	AI042614	Hs.125910	ESTs	2.38	NCI-H345, PRSC_con, RPWE-2
333424			CH22_FGENES.147_4	2.38	DU145, MCF7, OVCA-R
317779	AW450515	Hs.128381	ESTs	2.38	EB, DU145, OVCA-R
315142	AI380577	Hs.190219	ESTs	2.38	OVCA-R, EB, CALU6
310471	AW270515	Hs.149596	ESTs	2.38	NCI-H460, NCI-H23, NCI-H23
325049	AW410339	Hs.256310	ESTs; Weakly similar to centaurin beta2	2.38	PRSC_con, RPWE-2, NCI-H345
305234	AA670431		EST singleton (not in UniGene) with exon	2.38	MB-MDA-453, MB-MDA-231, A549
337760			CH22_EM:AC000097.GENSCAN.116-8	2.38	PRSC_con, PRSC_log, RPWE-2
311502	AW204380	Hs.208662	ESTs	2.38	NCI-H345, NCI-H69, LnCap
337548			CH22_FGENES.844-5	2.38	MB-MDA-453, MCF7, CALU6
326981			CH.21_hs gjl6588016	2.38	NCI-H345, NCI-H69, PRSC_con
309600	AW182066		EST singleton (not in UniGene) with exon	2.37	RPWE-2, NCI-358, NCI-H69
328936			CH.08_hs gjl5868500	2.37	OVCA-R, MB-MDA-453, CALU6
327937			CH.06_hs gjl5868192	2.37	BT474, EB, OVCA-R
328282			CH.07_hs gjl5868353	2.37	DU145, CALU6, CALU6
303607	AL046388	Hs.208206	ESTs; Weakly similar to Naf1 alpha prote	2.37	LnCap, PRSC_log, NCI-H345
304227	N94974	Hs.75344	ribosomal protein S4; X-linked	2.37	EB, PC3, OVCA-R
314101	AW452279	Hs.257542	ESTs	2.37	OVCA-R, CALU6, CALU6
325026	AI671168	Hs.12285	ESTs	2.37	NCI-H345, PRSC_con, PRSC_log

315015	AI659989	Hs.132625	ESTs	2.37	MB-MDA-453, MB-MDA-231, LnCap
328662			CH.07_hs gij6004473	2.37	NCI-H345, RPWE-2, PRSC_con
305867	AA864572		EST singleton (not in UniGene) with exon	2.37	MCF7, MB-MDA-453, MB-MDA-231
333296			CH22_FGENES.132_3	2.37	EB, PC3, CALU6
331070	R01116	Hs.182059	ESTs	2.36	OVCA-R, MB-MDA-453, A549
333698			CH22_FGENES.250_12	2.36	HT29, OVCA-R, Caco2
316423	AA758756	Hs.121380	ESTs	2.36	HT29, MCF7, MB-MDA-435s
323189	AL121194	Hs.120589	ESTs	2.36	PC3, NCI-H460, DU145
318889	Z43296	Hs.18720	programmed cell death 8 (apoptosis-induc	2.36	OVCA-R, A549, MB-MDA-453
334237			CH22_FGENES.362_1	2.36	NCI-H345, NCI-H69, LnCap
315931	AI700148	Hs.117328	ESTs	2.36	MCF7, NCI-H345, DU145
326884			CH.20_hs gij6682511	2.36	A549, EB, PC3
333132			CH22_FGENES.83_8	2.36	NCI-H69, HT29, EB
306574	AA995719	Hs.76067	heat shock 27kD protein 1	2.36	RPWE-2, PRSC_log, PRSC_con
324416	AI669524	Hs.194115	ESTs	2.36	NCI-H345, RPWE-2, PRSC_con
329496			CH.10_p2 gij3983518	2.35	HT29, MCF7, MB-MDA-231
320994	H22381		EST cluster (not in UniGene)	2.35	NCI-H23, A549, CALU6
320481	AA461139	Hs.24372	ESTs; Weakly similar to dJ207H1.1 [H.sap	2.35	PRSC_con, RPWE-2, PRSC_log
309958	AW444488		EST singleton (not in UniGene) with exon	2.35	NCI-H345, PRSC_con, PRSC_log
327009			CH.21_hs gij5867664	2.35	HT29, BT474, MCF7
309594	AW172821	Hs.181165	eukaryotic translation elongation factor	2.35	HT29, DU145, EB
335468			CH22_FGENES.567_4	2.35	NCI-H69, PRSC_con, NCI-H345
304269	AA069029		EST singleton (not in UniGene) with exon	2.35	PRSC_con, PRSC_log, RPWE-2
305877	AA865649		EST singleton (not in UniGene) with exon	2.35	A549, MCF7, OVCA-R
305700	AA815428		EST singleton (not in UniGene) with exon	2.35	PRSC_con, NCI-H345, PRSC_log
326423			CH.19_hs gij5867369	2.34	PC3, MCF7, LnCap
334560			CH22_FGENES.404_3	2.34	HT29, NCI-H460, MB-MDA-435s
337100			CH22_FGENES.472_3	2.34	PRSC_log, PRSC_con, RPWE-2
301505	AW014374	Hs.144849	ESTs	2.34	CALU6, MB-MDA-231, DU145
312142	AW298359	Hs.221069	ESTs	2.34	PRSC_con, RPWE-2, PRSC_log
305787	AA845035		EST singleton (not in UniGene) with exon	2.34	NCI-H23, NCI-H520, NCI-H460
338686			CH22_EM:AC005500.GENSCAN.472-5	2.33	BT474, MB-MDA-231, MB-MDA-453
331977	AA465207	Hs.125887	ESTs	2.33	OVCA-R, A549, MB-MDA-435s
314687	M79114	Hs.135177	ESTs	2.33	NCI-H69, PRSC_con, NCI-H345
336089			CH22_FGENES.688_18	2.33	PRSC_con, Caco2, PRSC_log
338952			CH22_DJ32110.GENSCAN.23-22	2.33	PC3, OVCA-R, HT29
334612			CH22_FGENES.411_11	2.33	OVCA-R, MB-MDA-453, EB
338223			CH22_EM:AC005500.GENSCAN.250-10	2.33	DU145, MB-MDA-453, MCF7
327845			CH.05_hs gij6531962	2.32	OVCA-R, MB-MDA-453, PC3
308187	AI538108	Hs.156110	Immunoglobulin kappa variable 1D-8	2.32	NCI-H69, NCI-358, PRSC_con
317767	AW294164	Hs.128340	ESTs; Weakly similar to Cdc42 GTPase-act	2.32	BT474, CALU6, MB-MDA-231
330468	L10343	Hs.112341	protease inhibitor 3; skin-derived (SKAL	2.32	PC3, Caco2, HT29
319003	R17712		EST cluster (not in UniGene)	2.32	MCF7, PC3, MB-MDA-453
323022	AI066733	Hs.133865	ESTs	2.32	CALU6, MB-MDA-231, DU145
303148	R73167	Hs.127317	ESTs; Weakly similar to CYTOCHROME P450	2.32	NCI-H345, PRSC_con, RPWE-2
303215	AW250314		EST	2.32	NCI-H345, PRSC_con, PRSC_log
318891	H10477	Hs.196208	ESTs; Weakly similar to IIII ALU SUBFAM1	2.32	NCI-H69, LnCap, NCI-H345
336653			CH22_FGENES.33-4	2.32	DU145, EB, LnCap
333329			CH22_FGENES.138_22	2.32	DU145, BT474, MB-MDA-231
301980	U69962	Hs.121498	potassium voltage-gated channel; Shab-re	2.31	NCI-H345, MB-MDA-231, LnCap
336968			CH22_FGENES.375-28	2.31	HT29, BT474, EB
308539	AI694191		EST singleton (not in UniGene) with exon	2.31	NCI-H345, NCI-H69, PRSC_log
326417			CH.19_hs gij5867362	2.31	HT29, MCF7, BT474
328851			CH.07_hs gij6381923	2.31	NCI-H520, NCI-H460, NCI-H23
329254			CH.X_hs gij5868733	2.31	RPWE-2, NCI-H345, PRSC_con
303075	W88779	Hs.59125	ESTs	2.3	DU145, OVCA-R, EB
335131			CH22_FGENES.497_15	2.3	NCI-H69, NCI-H345, PRSC_log
303129	AA308334	Hs.172210	MUF1 protein	2.3	LnCap, DU145, HT29
327067			CH.21_hs gij6531965	2.3	NCI-H345, NCI-H69, MB-MDA-435s
324064	AW137650		EST cluster (not in UniGene)	2.3	DU145, HT29, EB
325965			CH.16_hs gij5867147	2.3	NCI-H69, NCI-H345, RPWE-2
334525			CH22_FGENES.402_4	2.3	NCI-H345, PRSC_con, NCI-H69
336654			CH22_FGENES.34-2	2.3	BT474, PC3, MB-MDA-453
302348	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	2.3	LnCap, CALU6, DU145
309275	AI989570		EST singleton (not in UniGene) with exon	2.3	NCI-H460, NCI-H23, NCI-H520
329246			CH.X_hs gij5868732	2.3	NCI-H69, NCI-H345, PRSC_log
305557	AA774834		EST singleton (not in UniGene) with exon	2.3	CALU6, CALU6, MCF7
322907	AA084941		EST cluster (not in UniGene)	2.3	MB-MDA-231, CALU6, EB
318683	AI703241	Hs.202653	ESTs; Weakly similar to Xin [M.musculus]	2.29	NCI-H345, PRSC_con, RPWE-2
309233	AI971416		EST singleton (not in UniGene) with exon	2.29	CALU6, OVCA-R, EB
308913	AI860692	Hs.119122	ribosomal protein L13a	2.29	MB-MDA-435s, MCF7, HT29
335827			CH22_FGENES.620_1	2.29	PRSC_con, PRSC_log, RPWE-2
334066			CH22_FGENES.327_21	2.29	PRSC_con, PRSC_log, NCI-H345
302656	AW293005	Hs.220905	ESTs	2.29	NCI-H23, Caco2, CALU6
308974	AI872290	Hs.140	Immunoglobulin gamma 3 (Gm marker)	2.29	CALU6, A549, NCI-H69
333607			CH22_FGENES.216_2	2.29	OVCA-R, MCF7, A549

335174			CH22_FGENES.504_4	2.29	HT29, A549, MB-MDA-453
332028	AA489680	Hs.134406	ESTs; Weakly similar to Dim1p homolog [H	2.29	EB, A549, DU145
336417			CH22_FGENES.823_39	2.29	NCI-H69, NCI-H345, PRSC_log
323426	AA251401		EST cluster (not in UniGene)	2.29	HT29, MB-MDA-231, BT474
336618			CH22_FGENES.2-1	2.29	NCI-358, NCI-H460, NCI-H69
310017	AI188739	Hs.148488	ESTs	2.29	NCI-H345, PRSC_log, PRSC_con
334055			CH22_FGENES.327_6	2.28	DU145, OVCA-R, MB-MDA-453
337168			CH22_FGENES.562-28	2.28	NCI-H69, PRSC_log, NCI-H345
329824			CH.14_p2 g 6630758	2.28	NCI-H23, CALU6, RPWE-2
333891			CH22_FGENES.292_13	2.28	NCI-H69, MB-MDA-231, RPWE-2
339127			CH22_DA59H18.GENSCAN.55-1	2.28	PRSC_con, NCI-H345, RPWE-2
305686	AA812726		EST singleton (not in UniGene) with exon	2.28	NCI-H520, NCI-H23, NCI-H460
329782			CH.14_p2 g 5912597	2.28	NCI-H69, NCI-H345, PRSC_log
311059	AI810001	Hs.175346	ESTs	2.28	MCF7, BT474, MB-MDA-435s
336934			CH22_FGENES.351-1	2.28	BT474, HT29, MB-MDA-435s
314893	AA761093		EST cluster (not in UniGene)	2.28	OVCA-R, HT29, DU145
331596	N72574	Hs.50220	ESTs	2.28	A549, MCF7, NCI-358
330729	AA258559	Hs.3736	ESTs; Weakly similar to DELTA-LIKE PROTE	2.28	MB-MDA-231, CALU6, MCF7
338285			CH22_EM:AC005500.GENSCAN.293-3	2.27	NCI-H69, PRSC_log, PRSC_con
300154	AI245127	Hs.179331	ESTs	2.27	NCI-H23, NCI-H520, NCI-358
306383	AA969078	Hs.183698	ribosomal protein L29	2.27	RPWE-2, NCI-H345, PRSC_log
309005	AI884454		EST singleton (not in UniGene) with exon	2.27	A549, MCF7, BT474
332995			CH22_FGENES.58_2	2.27	RPWE-2, NCI-H345, PRSC_log
337426			CH22_FGENES.761-3	2.27	DU145, EB, CALU6
337778			CH22_EM:AC000097.GENSCAN.119-20	2.27	NCI-H69, PRSC_con, PRSC_log
329705			CH.14_p2 g 6065790	2.27	PRSC_con, PRSC_log, RPWE-2
335971			CH22_FGENES.652_4	2.27	PRSC_log, MB-MDA-231, NCI-H23
315862	AI075846	Hs.133996	ESTs	2.27	HT29, MB-MDA-435s, OVCA-R
316466	AI911204	Hs.126365	ESTs	2.27	NCI-H460, NCI-358, BT474
334430			CH22_FGENES.385_3	2.27	NCI-H345, NCI-H69, PRSC_con
331941	AA452257	Hs.99272	ESTs	2.26	PRSC_con, LnCap, PRSC_log
301230	AW269804	Hs.153019	ESTs	2.26	NCI-H345, PRSC_log, NCI-H520
317394	AI935024	Hs.190518	ESTs	2.26	NCI-H345, PRSC_con, PRSC_log
306220	AA928363		EST singleton (not in UniGene) with exon	2.26	NCI-H345, PRSC_con, PRSC_log
304134	H54627		EST singleton (not in UniGene) with exon	2.26	DU145, CALU6, PC3
335421			CH22_FGENES.551_1	2.26	NCI-H69, PRSC_con, PRSC_log
305260	AA679280	Hs.156110	Immunoglobulin kappa variable 1D-8	2.26	NCI-H345, NCI-H69, PRSC_con
303592	AA421129		EST	2.26	CALU6, OVCA-R, DU145
317982	AI004985	Hs.130607	ESTs	2.26	PC3, MB-MDA-435s, A549
325304			CH.11_hs g 5866910	2.26	MCF7, CALU6, A549
334118			CH22_FGENES.330_19	2.26	PRSC_con, NCI-H69, PRSC_log
335687			CH22_FGENES.596_2	2.26	A549, CALU6, LnCap
334035			CH22_FGENES.322_3	2.26	NCI-H345, PRSC_con, RPWE-2
305454	AA738413		EST singleton (not in UniGene) with exon	2.25	EB, HT29, CALU6
335902			CH22_FGENES.635_10	2.25	EB, DU145, HT29
339215			CH22_FF113D11.GENSCAN.6-10	2.25	PRSC_con, PRSC_log, RPWE-2
328810			CH.07_hs g 5868327	2.25	PC3, OVCA-R, MB-MDA-453
337396			CH22_FGENES.749-1	2.25	EB, A549, DU145
336808			CH22_FGENES.205-3	2.25	NCI-H345, NCI-H69, PRSC_con
305808	AA853958		EST singleton (not in UniGene) with exon	2.24	MB-MDA-453, DU145, EB
333571			CH22_FGENES.188_2	2.24	MCF7, MB-MDA-453, PC3
323023	AA225188	Hs.258539	ESTs	2.24	EB, DU145, CALU6
334626			CH22_FGENES.416_2	2.24	NCI-H69, NCI-H345, PRSC_log
333593			CH22_FGENES.210_2	2.24	NCI-H69, NCI-H345, PRSC_con
326708			CH.20_hs g 5867593	2.24	NCI-H460, NCI-H23, NCI-H520
314502	AI041717	Hs.132141	ESTs	2.23	NCI-H345, RPWE-2, PRSC_con
309181	AI951727		EST singleton (not in UniGene) with exon	2.23	PRSC_con, PC3, MB-MDA-231
324926	H56196	Hs.117798	ESTs	2.23	EB, EB, DU145
333632			CH22_FGENES.227_3	2.23	CALU6, CALU6, MB-MDA-453
328243			CH.06_hs g 6056292	2.23	PC3, LnCap, LnCap
327037			CH.21_hs g 6531965	2.23	LnCap, DU145, EB
307380	AI222985		EST singleton (not in UniGene) with exon	2.23	NCI-H345, PRSC_con, PRSC_log
334766			CH22_FGENES.428_15	2.23	PRSC_log, NCI-H345, RPWE-2
335236			CH22_FGENES.515_8	2.23	OVCA-R, MCF7, BT474
336615			CH22_FGENES.613_5	2.23	NCI-H69, PRSC_log, PRSC_con
307558	AI281998		EST singleton (not in UniGene) with exon	2.23	DU145, OVCA-R, CALU6
308029	AI457115	Hs.62954	ferritin; heavy polypeptide 1	2.23	EB, OVCA-R, MB-MDA-453
331508	N47559	Hs.46732	EST	2.23	MB-MDA-453, MCF7, BT474
320980	AJ237672	Hs.214142	5,10-methylenetetrahydrofolate reductase	2.23	OVCA-R, EB, EB
304241	AA010976		EST singleton (not in UniGene) with exon	2.23	BT474, MB-MDA-435s, MB-MDA-231
314682	AI190864	Hs.178226	ESTs; Weakly similar to IIII ALU SUBFAMI	2.23	MB-MDA-231, MCF7, OVCA-R
308382	AI624301		EST singleton (not in UniGene) with exon	2.22	OVCA-R, BT474, CALU6
314476	AW207857	Hs.169604	ESTs	2.22	DU145, EB, A549
327864			CH.06_hs g 5868130	2.22	NCI-H69, PRSC_log, PRSC_con
337279			CH22_FGENES.665-2	2.22	NCI-H345, NCI-H69, PRSC_con
302263	AA325517		EST	2.22	BT474, NCI-H520, DU145

322840	AA083710	EST cluster (not in UniGene)	2.22	HT29, MB-MDA-453, CALU6
307574	AI283549	EST singleton (not in UniGene) with exon	2.22	OVCA-R, CALU6, BT474
319027	AA716612	EST cluster (not in UniGene)	2.22	LnCap, NCI-H69, NCI-H69
305925	AA877883	EST singleton (not in UniGene) with exon	2.22	NCI-H345, NCI-H69, NCI-H69
329725		CH.14_p2 gij6065785	2.22	NCI-H69, PRSC_con, NCI-H345
316194	AW298529 Hs.255774	ESTs	2.22	CALU6, EB, NCI-H520
301119	AF142579	EST	2.22	A549, OVCA-R, EB
333815		CH22_FGENES.282_4	2.22	MB-MDA-435s, EB, MB-MDA-453
334358		CH22_FGENES.378_1	2.22	NCI-H345, RPWE-2, PRSC_con
303763	AF043250 Hs.30928	DNA segment on chromosome 19 (unique) 11	2.21	Caco2, NCI-H23, NCI-H520
335593		CH22_FGENES.581_32	2.21	NCI-H345, PRSC_log, RPWE-2
334026		CH22_FGENES.318_3	2.21	NCI-H69, PRSC_con, NCI-H345
322224	AF086064	EST cluster (not in UniGene)	2.21	PRSC_con, PRSC_log, RPWE-2
309836	AW295497 Hs.157397	ESTs	2.21	NCI-H345, PRSC_con, RPWE-2
332669	M33374 Hs.661	NADH dehydrogenase (ubiquinone) 1 beta s	2.21	NCI-H520, CALU6, OVCA-R
307629	AI300246	EST singleton (not in UniGene) with exon	2.21	MB-MDA-231, MB-MDA-453, HT29
300470	T87841	EST	2.21	PC3, EB, CALU6
330064		CH.19_p2 gij6165044	2.21	NCI-H69, PRSC_con, BT474
338819		CH22_DJ246D7.GENSCAN.1-24	2.21	NCI-H69, RPWE-2, PRSC_log
337797		CH22_EM:AC005500.GENSCAN.3-4	2.21	LnCap, NCI-H69, NCI-H520
328025		CH.06_hs gij5902482	2.2	RPWE-2, PRSC_con, PRSC_log
326240		CH.17_hs gij5867260	2.2	EB, LnCap, MB-MDA-453
312865	AW005376 Hs.173280	ESTs	2.2	DU145, DU145, OVCA-R
338450		CH22_EM:AC005500.GENSCAN.359-36	2.2	MCF7, MB-MDA-453, MB-MDA-435s
302532	U60181 Hs.248115	growth hormone secretagogue receptor	2.2	PRSC_con, PRSC_log, PRSC_log
321132	AA081495	EST cluster (not in UniGene)	2.2	NCI-H23, NCI-H520, NCI-358
337787		CH22_EM:AC000097.GENSCAN.123-3	2.2	EB, PC3, LnCap
337032		CH22_FGENES.438-3	2.2	NCI-H69, NCI-H345, RPWE-2
300026	M11507	AFFX control: transferrin receptor	2.2	HT29, EB, MB-MDA-231
333139		CH22_FGENES.83_16	2.2	HT29, MB-MDA-453, Caco2
334298		CH22_FGENES.372_4	2.2	PRSC_con, PRSC_log, RPWE-2
335002		CH22_FGENES.470_7	2.2	PRSC_con, NCI-H345, NCI-H345
335000		CH22_FGENES.470_5	2.2	EB, PC3, A549
337298		CH22_FGENES.678-3	2.2	NCI-H69, A549, HT29
302461	AF104253 Hs.241381	cofactor required for Sp1 transcriptiona	2.2	EB, CALU6, LnCap
334819		CH22_FGENES.436_15	2.19	CALU6, BT474, Caco2
300426	AW452660 Hs.253296	ESTs	2.19	DU145, CALU6, HT29
302569	AC004472	multiple UniGene matches	2.19	RPWE-2, PRSC_log, PRSC_con
339401		CH22_BA232E17.GENSCAN.7-7	2.19	NCI-H345, NCI-H69, PRSC_log
328791		CH.07_hs gij5868309	2.19	DU145, PC3, HT29
337333		CH22_FGENES.711-3	2.19	NCI-H69, NCI-H345, PRSC_log
339363		CH22_BA354I12.GENSCAN.33-6	2.19	NCI-H69, PRSC_log, PRSC_con
329429		CH.Y_hs gij5868882	2.19	CALU6, HT29, OVCA-R
336927		CH22_FGENES.348-3	2.19	NCI-H69, PRSC_log, NCI-358
336351		CH22_FGENES.816_3	2.19	DU145, EB, MB-MDA-231
313466	AA004731 Hs.148876	ESTs	2.19	CALU6, DU145, OVCA-R
307433	AI244895	EST singleton (not in UniGene) with exon	2.19	NCI-H23, NCI-H23, NCI-358
336590		CH22_FGENES.51_2	2.19	PRSC_con, NCI-H69, PRSC_log
310758	AI770001 Hs.209445	ESTs	2.18	EB, MB-MDA-231, BT474
327823		CH.05_hs gij5867968	2.18	PRSC_con, NCI-H69, NCI-H345
313257	N92638	EST cluster (not in UniGene)	2.18	PRSC_log, RPWE-2, PRSC_con
335377		CH22_FGENES.543_17	2.18	PC3, MB-MDA-435s, CALU6
303958	AL042931	EST singleton (not in UniGene) with exon	2.18	NCI-H345, RPWE-2, PRSC_con
320153	AF064594 Hs.120360	phospholipase A2; group VI	2.18	LnCap, PC3, MB-MDA-435s
335201		CH22_FGENES.508_10	2.18	OVCA-R, DU145, HT29
338591		CH22_EM:AC005500.GENSCAN.434-4	2.18	NCI-H69, NCI-H345, RPWE-2
331958	AA455960 Hs.99405	ESTs	2.18	MCF7, NCI-H23, NCI-H460
337218		CH22_FGENES.614-2	2.18	CALU6, A549, MCF7
309470	AW118833	EST singleton (not in UniGene) with exon	2.18	PC3, EB, MB-MDA-435s
331896	AA435495 Hs.97174	H sapiens mRNA; cDNA DKFZp566E164 (from	2.18	RPWE-2, NCI-H69, PRSC_log
330275		CH.05_p2 gij6671904	2.18	NCI-H345, PRSC_log, PRSC_con
335817		CH22_FGENES.618_5	2.18	A549, Caco2, PC3
332896		CH22_FGENES.35_10	2.18	NCI-H345, RPWE-2, PRSC_log
303294	AA205300	EST	2.17	MB-MDA-435s, A549, MCF7
338703		CH22_EM:AC005500.GENSCAN.480-2	2.17	HT29, BT474, NCI-H69
300115	AI215044 Hs.208130	ESTs	2.17	PC3, OVCA-R, HT29
330979	H22466 Hs.31795	ESTs	2.17	MCF7, EB, MB-MDA-435s
317246	AW105092 Hs.155690	ESTs	2.17	MB-MDA-453, DU145, EB
329078		CH.X_hs gij5868597	2.17	MB-MDA-453, MB-MDA-231, BT474
312554	AI222630 Hs.109390	ESTs	2.17	NCI-H520, OVCA-R, MCF7
323207	AI052795 Hs.192201	ESTs	2.17	NCI-H69, NCI-H345, PRSC_log
301894	AA484435 Hs.41997	alpha-1-B glycoprotein	2.17	PRSC_con, LnCap, PRSC_log
329097		CH.X_hs gij5868624	2.16	MB-MDA-231, MCF7, NCI-358
328328		CH.07_hs gij5868375	2.16	NCI-H345, PRSC_con, NCI-H69
302671	AA522440 Hs.135917	ESTs	2.16	BT474, DU145, A549
329201		CH.X_hs gij5868718	2.16	OVCA-R, PC3, MB-MDA-435s

329902			CH.15_p2 gi 5634760	2.16	PRSC_con, NCI-H69, NCI-H345
334435			CH22_FGENES.385_10	2.16	PRSC_con, NCI-H345, RPWE-2
330742	AA400979	Hs.25691	calcitonin receptor-like receptor activi	2.16	MCF7, MB-MDA-453, PC3
328484			CH.07_hs gi 5868454	2.16	NCI-H69, PRSC_log, NCI-H345
334784			CH22_FGENES.432_9	2.16	PRSC_log, RPWE-2, PRSC_con
337771			CH22_EM:AC000097.GENSCAN.119-10	2.16	NCI-H69, PRSC_con, RPWE-2
300181	AI284955	Hs.157568	ESTs; Weakly similar to ataxin-2 [M.musc	2.16	DU145, EB, CALU6
300268	AI539446	Hs.245450	ESTs	2.16	PRSC_con, RPWE-2, PRSC_log
309575	AW168096	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	2.16	A549, NCI-H23, MB-MDA-453
336548			CH22_FGENES.841_5	2.16	NCI-H345, NCI-H69, MB-MDA-231
328506			CH.07_hs gi 5868471	2.16	EB, A549, CALU6
330189			CH.05_p2 gi 6165182	2.16	NCI-H460, MCF7, MB-MDA-453
305480	AA746500	Hs.25911	HLA-B associated transcript-2	2.16	EB, DU145, NCI-358
302270	R56151		EST	2.16	OVCA-R, MB-MDA-435s, PRSC_con
306669	AI004899		EST singleton (not in UniGene) with exon	2.16	PRSC_log, PRSC_con, NCI-H345
325887			CH.16_hs gi 5867087	2.16	EB, CALU6, NCI-358
327015			CH.21_hs gi 5867664	2.15	EB, PC3, HT29
338576			CH22_EM:AC005500.GENSCAN.429-1	2.15	NCI-H69, NCI-H345, PRSC_con
333592			CH22_FGENES.209_2	2.15	NCI-H69, OVCA-R, PRSC_con
317253	AW071241	Hs.199685	ESTs	2.15	MB-MDA-435s, NCI-H23, MB-MDA-453
302301	R67493	Hs.127150	ESTs; Weakly similar to ZINC FINGER PROT	2.15	PC3, MCF7, MB-MDA-435s
336858			CH22_FGENES.293-8	2.15	RPWE-2, PRSC_con, NCI-H69
308417	AI640693	Hs.2186	eukaryotic translation elongation factor	2.15	EB, OVCA-R, CALU6
338177			CH22_EM:AC005500.GENSCAN.219-5	2.15	NCI-H345, NCI-H23, NCI-H520
337592			CH22_C20H12.GENSCAN.6-7	2.15	PC3, A549, HT29
325945			CH.16_hs gi 5867138	2.15	MB-MDA-453, MB-MDA-435s, DU145
335262			CH22_FGENES.520_3	2.15	EB, PC3, A549
333665			CH22_FGENES.244_1	2.15	PRSC_con, RPWE-2, PRSC_log
333710			CH22_FGENES.250_25	2.14	PRSC_log, NCI-H69, PRSC_con
304927	AA604728	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	2.14	LnCap, PC3, MCF7
336999			CH22_FGENES.417-20	2.14	NCI-H69, NCI-H345, PRSC_con
313283	W32480	Hs.157099	ESTs	2.14	EB, MB-MDA-231, A549
306221	AA928686		EST singleton (not in UniGene) with exon	2.14	NCI-H460, PRSC_con, NCI-H23
333205			CH22_FGENES.102_5	2.14	NCI-H69, PRSC_con, PRSC_log
312932	AI804218	Hs.209614	ESTs	2.14	PRSC_con, NCI-H345, RPWE-2
328938			CH.08_hs gi 5868500	2.14	HT29, PC3, MB-MDA-453
326746			CH.20_hs gi 5867611	2.14	NCI-H345, NCI-H69, PRSC_con
337964			CH22_EM:AC005500.GENSCAN.100-9	2.14	RPWE-2, PRSC_con, PRSC_log
337984			CH22_EM:AC005500.GENSCAN.110-2	2.14	EB, DU145, NCI-H345
337704			CH22_EM:AC000097.GENSCAN.87-6	2.14	NCI-H69, NCI-H460, NCI-358
302162	AF119046		EST	2.14	MB-MDA-435s, PC3, EB
303192	AA081755	Hs.8059	ESTs; Highly similar to SYNAPTOTAGMIN IV	2.14	MB-MDA-435s, MB-MDA-435s, MB-MDA-453
306200	AA926816		EST singleton (not in UniGene) with exon	2.14	MB-MDA-453, CALU6, DU145
303996	AW515979	Hs.84298	CD74 antigen (invariant polypptd of majo	2.14	LnCap, MB-MDA-231, BT474
325409			CH.12_hs gi 5866921	2.14	PRSC_log, PRSC_con, RPWE-2
308558	AI700145	Hs.172182	poly(A)-binding protein; cytoplasmic 1	2.14	MCF7, EB, MB-MDA-435s
302185	AA243837	Hs.156915	ESTs	2.14	MB-MDA-453, MCF7, EB
303021	W39612		EST	2.14	PRSC_con, NCI-H69, RPWE-2
301005	AW451916	Hs.210848	ESTs	2.14	DU145, EB, HT29
336029			CH22_FGENES.672_4	2.14	NCI-H69, PRSC_con, RPWE-2
305443	AA736653		EST singleton (not in UniGene) with exon	2.14	NCI-358, NCI-H520, NCI-H23
335485			CH22_FGENES.570_17	2.13	NCI-H460, MB-MDA-435s, MCF7
304817	AA584712		EST singleton (not in UniGene) with exon	2.13	MCF7, MCF7, NCI-H520
309859	AW298760		EST singleton (not in UniGene) with exon	2.13	NCI-H69, PRSC_con, LnCap
326206			CH.17_hs gi 5867219	2.13	EB, MB-MDA-231, LnCap
303656	AA437189	Hs.122574	ESTs	2.13	LnCap, MB-MDA-435s, EB
334745			CH22_FGENES.426_3	2.13	OVCA-R, DU145, MB-MDA-453
318504	T26453		EST cluster (not in UniGene)	2.13	RPWE-2, LnCap, CALU6
306839	AI077385		EST singleton (not in UniGene) with exon	2.13	MCF7, MB-MDA-453, MB-MDA-435s
303843	W94322	Hs.58094	melanoma inhibitory activity	2.13	MB-MDA-435s, NCI-H345, RPWE-2
308444	AI659398	Hs.197097	EST	2.13	MB-MDA-453, MCF7, BT474
301322	AW448965	Hs.256305	ESTs	2.13	NCI-H345, LnCap, PC3
326997			CH.21_hs gi 5867660	2.13	HT29, A549, CALU6
326793			CH.20_hs gi 5867631	2.13	PRSC_log, PRSC_con, MB-MDA-453
320360	H12405		EST cluster (not in UniGene)	2.12	MB-MDA-231, BT474, HT29
316301	AW206279	Hs.192009	ESTs	2.12	DU145, DU145, EB
335371			CH22_FGENES.543_9	2.12	PC3, MB-MDA-435s, DU145
301178	AA828385		EST	2.12	EB, OVCA-R, LnCap
326136			CH.17_hs gi 5867202	2.12	RPWE-2, PRSC_log, PRSC_con
339213			CH22_FF113D11.GENSCAN.6-8	2.12	OVCA-R, PC3, MB-MDA-231
335980			CH22_FGENES.653_2	2.12	BT474, BT474, OVCA-R
314380	AA758797	Hs.192807	ESTs	2.11	PRSC_con, PRSC_log, RPWE-2
306779	AI041302		EST singleton (not in UniGene) with exon	2.11	NCI-H345, PRSC_con, PRSC_log
335774			CH22_FGENES.607_10	2.11	PC3, A549, MB-MDA-453
334914			CH22_FGENES.457_3	2.11	PRSC_con, NCI-H345, NCI-H69
304619	AA515554	Hs.119598	ribosomal protein L3	2.11	EB, MB-MDA-453, MB-MDA-435s

303358	AI199714	Hs.158149	ESTs	2.11	CALU6, OVCA-R, DU145
306558	AA994743		EST singleton (not in UniGene) with exon	2.11	HT29, MB-MDA-453, CALU6
337781			CH22_EM:AC000097.GENSCAN.121-3	2.11	PRSC_log, PRSC_con, RPWE-2
333140			CH22_FGENES.84_1	2.11	HT29, NCI-H69, OVCA-R
315081	AI247134	Hs.155281	ESTs	2.11	MB-MDA-453, MCF7, HT29
302965	AA446441	Hs.138842	ESTs	2.11	NCI-358, NCI-H23, CALU6
302138	N83965		EST	2.11	PRSC_log, PRSC_con, NCI-H345
320802	D83824	Hs.185055	BENE protein	2.11	A549, PC3, HT29
322152	AA565332		EST cluster (not in UniGene)	2.11	A549, CALU6, EB
326418			CH.19_hs gij5867365	2.1	EB, OVCA-R, DU145
308709	AI783498	Hs.181165	eukaryotic translation elongation factor	2.1	MB-MDA-435s, MB-MDA-453, DU145
332737	C01852	Hs.84359	hypothetical protein	2.1	NCI-H23, A549, DU145
333283			CH22_FGENES.128_13	2.1	NCI-H345, RPWE-2, PRSC_con
328636			CH.07_hs gij6004473	2.1	DU145, EB, MB-MDA-453
329187			CH.X_hs gij5868713	2.1	NCI-358, NCI-H23, NCI-H460
305999	AA889603		EST singleton (not in UniGene) with exon	2.1	HT29, OVCA-R, PC3
333220			CH22_FGENES.104_12	2.1	PRSC_con, PRSC_log, RPWE-2
335092			CH22_FGENES.492_2	2.1	NCI-H69, PRSC_con, NCI-H345
304887	AA599355		EST singleton (not in UniGene) with exon	2.1	DU145, EB, MCF7
325359			CH.12_hs gij5866920	2.1	MB-MDA-453, EB, MB-MDA-435s
330956	H08730	Hs.6933	ESTs	2.1	NCI-H520, PRSC_con, NCI-H345
323786	AW449315	Hs.165795	ESTs	2.1	OVCA-R, A549, LnCap
333619			CH22_FGENES.219_3	2.1	BT474, OVCA-R, HT29
324538	AW502979		EST cluster (not in UniGene)	2.09	CALU6, A549, DU145
303405	AA308601		EST	2.09	DU145, CALU6, NCI-H69
328570			CH.07_hs gij5868231	2.09	LnCap, MB-MDA-231, DU145
308971	AI871218	Hs.224731	EST	2.09	NCI-H23, NCI-H460, NCI-358
330467	K02268	Hs.22584	prodynorphin	2.09	PC3, BT474, MB-MDA-453
334793			CH22_FGENES.433_5	2.09	EB, DU145, LnCap
300908	AA618335	Hs.146137	ESTs; Weakly similar to putative [C.eleg	2.09	NCI-H345, PRSC_log, PRSC_con
309656	AW197060	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	2.09	A549, NCI-H23, NCI-H460
320963	AB029041	Hs.209646	KIAA1118 protein	2.09	PRSC_con, PRSC_log, NCI-H345
310833	AW295351	Hs.169136	ESTs	2.09	PC3, LnCap, MB-MDA-453
335693			CH22_FGENES.596_8	2.09	NCI-H69, LnCap, PRSC_log
325966			CH.16_hs gij5867147	2.09	MCF7, CALU6, MB-MDA-453
329319			CH.X_hs gij6381976	2.09	NCI-H460, EB, DU145
338526			CH22_EM:AC005500.GENSCAN.396-14	2.09	NCI-H69, NCI-H345, PRSC_log
336751			CH22_FGENES.128-5	2.09	NCI-H69, NCI-H345, PRSC_log
325510			CH.12_hs gij5866974	2.09	HT29, OVCA-R, CALU6
323553	AA292626	Hs.122854	ESTs	2.08	NCI-H345, RPWE-2, NCI-358
326343			CH.17_hs gij6525295	2.08	EB, LnCap, DU145
335470			CH22_FGENES.568_3	2.08	NCI-H69, PRSC_con, PRSC_log
320122	T93681	Hs.187515	ESTs	2.08	MCF7, MB-MDA-453, BT474
335320			CH22_FGENES.534_7	2.08	BT474, MB-MDA-231, HT29
307120	AI184343		EST singleton (not in UniGene) with exon	2.08	HT29, MCF7, PC3
338080			CH22_EM:AC005500.GENSCAN.172-11	2.08	LnCap, PC3, HT29
313113	AI056258	Hs.122523	ESTs	2.08	MCF7, DU145, MB-MDA-453
337685			CH22_EM:AC000097.GENSCAN.77-1	2.08	NCI-H69, NCI-H345, PRSC_log
327461			CH.02_hs gij6004455	2.08	NCI-H23, BT474, NCI-358
335895			CH22_FGENES.635_3	2.08	HT29, MB-MDA-231, NCI-H520
303933	AW471472		EST singleton (not in UniGene) with exon	2.08	MB-MDA-231, BT474, NCI-H345
314803	AI935159	Hs.166841	ESTs; Weakly similar to MYOSIN LIGHT CHA NON-MUSCLE ISOZYMES [H.sapiens]	2.08	PC3, A549, BT474
302722	U53530		EST	2.08	DU145, MB-MDA-435s, OVCA-R
307703	AI318588		EST singleton (not in UniGene) with exon	2.08	HT29, MB-MDA-435s, CALU6
310558	AI334965	Hs.176976	ESTs	2.08	A549, LnCap, PC3
315276	AA860090		EST cluster (not in UniGene)	2.08	PC3, MCF7, OVCA-R
306443	AA976950		EST singleton (not in UniGene) with exon	2.07	OVCA-R, PC3, EB
307961	AI421059		EST singleton (not in UniGene) with exon	2.07	HT29, OVCA-R, CALU6
329735			CH.14_p2 gij6065780	2.07	EB, HT29, OVCA-R
335193			CH22_FGENES.507_8	2.07	EB, A549, A549
320347	R34423	Hs.221535	ESTs	2.07	CALU6, A549, EB
316153	AA724474	Hs.147208	ESTs	2.07	MB-MDA-453, PC3, HT29
300921	AW293224	Hs.232165	ESTs	2.07	HT29, CALU6, CALU6
319264	T65096		EST cluster (not in UniGene)	2.07	MB-MDA-453, MCF7, CALU6
330204			CH.05_p2 gij6013606	2.07	OVCA-R, DU145, EB
317070	AI142037	Hs.125379	ESTs	2.07	PRSC_con, NCI-H345, OVCA-R
337645			CH22_EM:AC000097.GENSCAN.10-8	2.07	NCI-H345, PRSC_log, NCI-H69
312501	AW450490	Hs.132886	ESTs	2.07	NCI-H520, CALU6, MCF7
335587			CH22_FGENES.581_26	2.07	NCI-H69, NCI-H345, PRSC_log
311482	AI917706	Hs.129997	ESTs	2.07	NCI-H520, MCF7, MB-MDA-435s
302488	AF161441		EST	2.07	EB, DU145, CALU6
304692	AA554202	Hs.76067	heat shock 27kD protein 1	2.07	MCF7, MB-MDA-453, PC3
325369			CH.12_hs gij5866920	2.07	DU145, DU145, MB-MDA-453
306284	AA936835		EST singleton (not in UniGene) with exon	2.07	BT474, MB-MDA-231, HT29
337402			CH22_FGENES.752-1	2.07	A549, BT474, DU145

327418			CH.02_hs gi 5867750	2.07	MCF7, MB-MDA-453, MB-MDA-435s
317977	AI004775	Hs.205091	ESTs; Weakly similar to WW domain bindin	2.07	BT474, MB-MDA-453, PC3
331870	AA428560	Hs.161845	EST	2.07	MB-MDA-231, MB-MDA-435s, BT474
300750	AA514805	Hs.105464	ESTs	2.07	HT29, BT474, BT474
336657			CH22_FGENES.35-14	2.07	MB-MDA-453, MCF7, NCI-H460
336035			CH22_FGENES.678_6	2.07	NCI-H69, PRSC_con, RPWE-2
325320			CH.11_hs gi 5866870	2.06	NCI-H69, PRSC_log, PRSC_con
306053	AA905312		EST singleton (not in UniGene) with exon	2.06	HT29, OVCA-R, MB-MDA-231
333175			CH22_FGENES.95_2	2.06	LnCap, HT29, DU145
304491	AA437096	Hs.115502	EST	2.06	MB-MDA-435s, CALU6, CALU6
310632	AI697536	Hs.176991	ESTs	2.06	NCI-H69, PRSC_log, NCI-H345
338521			CH22_EM:AC005500.GENSCAN.395-35	2.06	NCI-H345, PRSC_log, PRSC_log
334900			CH22_FGENES.452_14	2.06	A549, CALU6, NCI-H69
337451			CH22_FGENES.774-2	2.06	PRSC_con, PRSC_log, RPWE-2
308792	AI815153	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	2.06	DU145, BT474, MB-MDA-453
336854			CH22_FGENES.280-1	2.06	LnCap, EB, MB-MDA-435s
304485	AA434076		EST singleton (not in UniGene) with exon	2.06	MB-MDA-231, BT474, CALU6
326458			CH.19_hs gi 5867400	2.06	EB, DU145, LnCap
303506	AA340605	Hs.105887	ESTs	2.06	LnCap, MCF7, CALU6
333628			CH22_FGENES.226_2	2.06	NCI-H520, NCI-358, NCI-358
300763	AA190753		EST	2.06	NCI-H69, NCI-H345, PRSC_con
334836			CH22_FGENES.439_6	2.06	NCI-H345, PRSC_con, RPWE-2
335217			CH22_FGENES.512_3	2.06	PRSC_log, PRSC_con, NCI-H69
338970			CH22_DJ32110.GENSCAN.26-3	2.06	A549, MB-MDA-453, LnCap
334842			CH22_FGENES.439_21	2.06	DU145, HT29, CALU6
309309	AW006428	Hs.232857	EST	2.06	EB, DU145, OVCA-R
332949			CH22_FGENES.47_12	2.06	EB, DU145, OVCA-R
310530	AW369663	Hs.150150	ESTs	2.06	PRSC_con, PRSC_log, RPWE-2
329401			CH.X_hs gi 6682544	2.06	NCI-H69, PRSC_con, RPWE-2
316893	AA837332		EST cluster (not in UniGene)	2.06	OVCA-R, MCF7, MB-MDA-453
325022	W95840	Hs.59745	NADH dehydrogenase (ubiquinone) flavopro	2.06	Caco2, NCI-358, OVCA-R
329839			CH.14_p2 gi 6672062	2.05	MB-MDA-231, RPWE-2, CALU6
306668	AI004890		EST singleton (not in UniGene) with exon	2.05	DU145, MB-MDA-453, MCF7
315604	AW137442	Hs.136965	ESTs	2.05	LnCap, EB, PC3
318551	AI909951	Hs.239307	tyrosyl-tRNA synthetase	2.05	NCI-H345, PRSC_con, RPWE-2
339344			CH22_BA354112.GENSCAN.28-1	2.05	BT474, MB-MDA-231, A549
310621	AI632098	Hs.198099	ESTs	2.05	NCI-H69, RPWE-2, MCF7
327051			CH.21_hs gi 6531965	2.05	PRSC_con, NCI-H345, PRSC_log
336827			CH22_FGENES.236-2	2.05	NCI-H345, A549, MB-MDA-231
311846	AI078033	Hs.177170	ESTs; Moderately similar to IIII ALU SUB	2.05	OVCA-R, DU145, CALU6
335036			CH22_FGENES.475_14	2.05	NCI-H69, PRSC_con, NCI-H345
313100	N52880	Hs.122817	ESTs	2.05	RPWE-2, NCI-H345, PRSC_log
301927	AF014459	Hs.113250	retinoblastoma (X-linked; juvenile) 1	2.05	MB-MDA-231, NCI-H345, PRSC_con
326070			CH.17_hs gi 5867175	2.05	MB-MDA-435s, MB-MDA-231, BT474
338514			CH22_EM:AC005500.GENSCAN.392-4	2.05	PRSC_con, PRSC_log, RPWE-2
328098			CH.06_hs gi 5868020	2.05	DU145, CALU6, EB
301102	AA679361	Hs.249487	ESTs	2.05	NCI-H460, PRSC_con, NCI-H23
306193	AA923457		EST singleton (not in UniGene) with exon	2.05	NCI-H345, PRSC_con, RPWE-2
317027	AA883808	Hs.174148	ESTs	2.05	EB, DU145, CALU6
336102			CH22_FGENES.693_2	2.04	LnCap, NCI-H69, PRSC_log
301372	AI239895	Hs.130555	ESTs	2.04	PRSC_con, RPWE-2, PRSC_log
333252			CH22_FGENES.116_4	2.04	NCI-358, A549, HT29
322516	AW372340	Hs.159717	ESTs	2.04	HT29, MB-MDA-231, BT474
324148	AA393624		EST cluster (not in UniGene)	2.04	RPWE-2, PRSC_con, MB-MDA-231
338770			CH22_EM:AC005500.GENSCAN.520-1	2.04	PRSC_con, NCI-H69, NCI-H460
314795	AI798611	Hs.157277	ESTs	2.04	EB, PC3, LnCap
333004			CH22_FGENES.60_1	2.04	A549, NCI-358, DU145
302405	AW245825	Hs.211914	NADH dehydrogenase (ubiquinone) Fe-S pro	2.04	NCI-H520, CALU6, Caco2
323587	AI905527	Hs.141901	ESTs; Moderately similar to IIII ALU SUB	2.04	EB, A549, HT29
300898	AI276278	Hs.157176	ESTs	2.04	PC3, MB-MDA-453, BT474
301506	AI149878	Hs.143519	ESTs; Weakly similar to testicular tekti	2.04	NCI-H69, RPWE-2, NCI-H345
325851			CH.16_hs gi 5867067	2.04	MB-MDA-231, HT29, EB
323945	AI125604	Hs.155117	ESTs	2.04	MCF7, DU145, DU145
303265	AW160951		EST	2.04	LnCap, OVCA-R, DU145
334135			CH22_FGENES.336_2	2.04	PC3, A549, MB-MDA-435s
329793			CH.14_p2 gi 6522661	2.04	DU145, CALU6, HT29
332595	AA256431	Hs.3244	G protein pathway suppressor 2	2.04	A549, CALU6, NCI-H23
316059	AW166388	Hs.250181	ESTs	2.04	MCF7, HT29, A549
324104	AW246071	Hs.133122	ESTs	2.04	Caco2, A549, MCF7
306801	AI052653		EST singleton (not in UniGene) with exon	2.03	EB, LnCap, PC3
338096			CH22_EM:AC005500.GENSCAN.181-14	2.03	DU145, HT29, CALU6
327544			CH.03_hs gi 5867797	2.03	PRSC_con, NCI-H69, NCI-H345
318813	F13195		EST cluster (not in UniGene)	2.03	PRSC_con, RPWE-2, PRSC_log
325289			CH.11_hs gi 5866903	2.03	EB, OVCA-R, A549
311099	T56361	Hs.182167	hemoglobin; gamma A	2.03	HT29, BT474, EB
316079	AA922213	Hs.121735	ESTs	2.03	LnCap, OVCA-R, EB

309533	AW151131	EST singleton (not in UniGene) with exon	2.03	MB-MDA-231, BT474, LnCap
338579		CH22_EM:AC005500.GENSCAN.431-3	2.03	NCI-H69, NCI-H345, RPWE-2
326549		CH.19_hs gi 5867307	2.03	NCI-H69, Caco2, NCI-H345
320012	AI628384 Hs.193745	ESTs	2.03	BT474, MB-MDA-453, MCF7
334111		CH22_FGENES.330_10	2.03	NCI-H69, MB-MDA-231, BT474
327123		CH.21_hs gi 6531971	2.03	NCI-H345, NCI-H69, RPWE-2
324568	AW502311	EST cluster (not in UniGene)	2.03	NCI-H345, NCI-H520, NCI-H460
306012	AA896989	EST singleton (not in UniGene) with exon	2.03	NCI-H69, PRSC_log, PRSC_con
303106	AA012877	EST	2.03	RPWE-2, OVCA-R, EB
302194	U52219 Hs.158329	G protein-coupled receptor 50	2.03	NCI-H520, NCI-H23, PC3
326646		CH.20_hs gi 5867562	2.03	NCI-H460, OVCA-R, HT29
304060	T61464	EST singleton (not in UniGene) with exon	2.03	NCI-H345, PRSC_con, PRSC_log
304667	AA535602	EST singleton (not in UniGene) with exon	2.03	A549, DU145, EB
330514	M83652 Hs.53155	properdin P factor; complement	2.02	NCI-H23, NCI-H460, NCI-358
310324	AI473273 Hs.159674	ESTs; Weakly similar to GLUTAMATE [H.sap	2.02	NCI-H345, MB-MDA-231, BT474
330327		CH.08_p2 gi 5919194	2.02	NCI-H345, NCI-H69, PRSC_log
308447	AI659985	EST singleton (not in UniGene) with exon	2.02	NCI-H345, RPWE-2, PRSC_log
307778	AI344972 Hs.231496	EST	2.02	NCI-H69, CALU6, OVCA-R
319459	T87351 Hs.194121	ESTs	2.02	NCI-H460, NCI-358, NCI-H520
300935	AA513644 Hs.222815	ESTs; Weakly similar to Wiskott-Aldrich	2.02	DU145, EB, OVCA-R
314318	AL037405 Hs.176141	ESTs	2.02	PRSC_con, LnCap, PRSC_log
334779		CH22_FGENES.432_1	2.02	EB, HT29, DU145
336994		CH22_FGENES.410-2	2.02	NCI-H345, PRSC_con, NCI-H69
334076		CH22_FGENES.327_31	2.02	OVCA-R, CALU6, EB
318116	AW452865 Hs.132339	ESTs	2.02	MB-MDA-231, NCI-H69, NCI-H345
326783		CH.20_hs gi 6525298	2.02	NCI-H69, PRSC_con, RPWE-2
336142		CH22_FGENES.705_4	2.02	NCI-H69, PRSC_log, PRSC_con
320913	AA663733	EST cluster (not in UniGene)	2.02	DU145, EB, CALU6
301644	AW239364	EST	2.02	PRSC_con, RPWE-2, PRSC_log
300944	AW081072 Hs.164624	ESTs; Weakly similar to Slit-3 protein [2.01	RPWE-2, NCI-H69, NCI-H23
310080	AW137088 Hs.144857	ESTs	2.01	PRSC_con, NCI-H345, PRSC_log
311248	AI863918 Hs.195078	ESTs	2.01	NCI-H345, NCI-H69, RPWE-2
319207	R87679	EST cluster (not in UniGene)	2.01	HT29, A549, NCI-H460
334760		CH22_FGENES.428_9	2.01	NCI-358, NCI-H69, PRSC_log
338368		CH22_EM:AC005500.GENSCAN.325-2	2.01	NCI-H23, NCI-H520, NCI-H460
317300	AI417007 Hs.166338	ESTs	2.01	NCI-H460, DU145, NCI-H23
323699	AW178750	EST cluster (not in UniGene)	2.01	MCF7, MB-MDA-453, OVCA-R
301366	AA907713 Hs.221667	ESTs	2.01	PRSC_con, NCI-H345, RPWE-2
333306		CH22_FGENES.137_3	2.01	NCI-H69, NCI-H345, PRSC_con
328031		CH.06_hs gi 5902482	2.01	MB-MDA-231, NCI-H345, PRSC_con
301806	AA326007 Hs.12056	asialoglycoprotein receptor 1	2.01	MB-MDA-453, DU145, EB
300993	AA584930 Hs.191777	ESTs; Weakly similar to XAP-5-like prote	2.01	HT29, NCI-H23, NCI-358
320042	T84520	EST cluster (not in UniGene)	2.01	PRSC_con, NCI-H345, NCI-H69
331082	R17059 Hs.22100	ESTs	2.01	EB, DU145, MB-MDA-435s
308851	AI829820	EST singleton (not in UniGene) with exon	2.01	DU145, EB, PC3
301163	AA732066	EST	2.01	OVCA-R, PC3, MB-MDA-435s
304734	AA576428	EST singleton (not in UniGene) with exon	2.01	LnCap, MB-MDA-453, DU145
334855		CH22_FGENES.442_6	2.01	NCI-H345, RPWE-2, PRSC_log
337121		CH22_FGENES.519-1	2.01	NCI-H69, NCI-H345, PRSC_con
331838	AA412498 Hs.104778	ESTs	2.01	BT474, BT474, MCF7
339181		CH22_DA59H18.GENSCAN.72-6	2.01	NCI-H345, PRSC_con, NCI-H69
327564		CH.03_hs gi 5867811	2.01	BT474, HT29, DU145
304108	R63932 Hs.28467	EST	2	BT474, OVCA-R, MCF7
315036	AA534953 Hs.163297	ESTs	2	MB-MDA-435s, MB-MDA-453, LnCap
312777	W92809 Hs.138557	ESTs	2	PRSC_con, NCI-H345, MB-MDA-231
305888	AA868536 Hs.126145	EST	2	HT29, HT29, BT474
323185	R52177	EST cluster (not in UniGene)	2	EB, A549, BT474
308681	AI761307	EST singleton (not in UniGene) with exon	2	RPWE-2, PRSC_con, NCI-H345
325755		CH.14_hs gi 6682474	2	NCI-H345, PRSC_con, PRSC_log
324376	AW499705	EST cluster (not in UniGene)	2	DU145, BT474, PC3
331890	AA432166 Hs.3577	succinate dehydrogenase complex; subunit	2	CALU6, MB-MDA-453, A549

Table 4

		Pkey: Unique Eos probeset identifier number			
		ExAccn: Exemplar Accession number, Genbank accession number			
		UnigeneID: Unigene number			
		Unigene Title: Unigene gene title			
Pkey	Exr_Accn	UniG_ID	Complete_Title	Ratio Met/BS	Top 3 expressing cell lines
313166	AI801098	Hs.151500	ESTs	12.23	Caco2, EB, OVCA-R
334593			CH22_FGENES.408_3	8.06	NCI-H69, OVCA-R, OVCA-R
331084	R20655	Hs.81281	Human clone 23732 mRNA; partial cds	7.89	LnCap, OVCA-R, EB
324598	AA502659	Hs.163986	ESTs	7.77	OVCA-R, EB, CALU6
314071	AA192455	Hs.188690	ESTs	7.76	CALU6, EB, DU145
315178	AW362945	Hs.162459	ESTs	6.81	OVCA-R, EB, CALU6
325519			CH.12_hs gjl6017036	6.34	NCI-H69, NCI-H345, PRSC_con
331433	H68097	Hs.161023	EST	6.16	OVCA-R, A549, EB
315021	AA533447		EST cluster (not in UniGene)	6.15	PC3, EB, CALU6
337695			CH22_EM:AC000097.GENSCAN.84-1	5.84	NCI-H69, NCI-H345, DU145
324048	AA378739		EST cluster (not in UniGene)	5.77	OVCA-R, DU145, EB
300781	AA731209		EST cluster (not in UniGene) with exon h	5.72	MB-MDA-453, MCF7, MB-MDA-435s
320701	AI093177	Hs.134923	ESTs	5.68	A549, NCI-H345, NCI-H69
332471	AA416967	Hs.120980	nuclear receptor co-repressor 2	5.68	LnCap, A549, OVCA-R
331858	AA421163	Hs.163848	ESTs	5.66	OVCA-R, DU145, Caco2
330987	H40988	Hs.131965	ESTs5.35		NCI-H345, OVCA-R, LnCap
322309	AF086372		EST cluster (not in UniGene)	5.31	OVCA-R, DU145, PC3
324733	AA582082	Hs.199410	ESTs	5.17	PRSC_con, PRSC_log, NCI-H345
313577	AA565051	Hs.155029	ESTs	5.16	OVCA-R, PC3, EB
310966	AW271974	Hs.210295	ESTs	5.15	NCI-H69, PRSC_log, PRSC_con
311332	AW292247	Hs.255052	ESTs	5.05	Caco2, OVCA-R, EB
314522	AI732331	Hs.187750	ESTs; Moderately similar to !!!!! ALU CLA	5.04	EB, DU145, HT29
330886	AA135606	Hs.189384	ESTs; Weakly similar to !!!!! ALU SUBFAM1	4.93	OVCA-R, DU145, Caco2
313597	AW162263	Hs.249990	ESTs	4.84	NCI-H460, NCI-H345, NCI-H23
314439	AI539443	Hs.137447	ESTs	4.84	DU145, Caco2, MB-MDA-231
320807	AA086110	Hs.188536	H sapiens clone 24838 mRNA seq	4.83	PC3, OVCA-R, DU145
311804	AA135159	Hs.203349	ESTs	4.82	OVCA-R, PC3, Caco2
321354	AA078493		EST cluster (not in UniGene)	4.81	DU145, EB, OVCA-R
325169	H01560	Hs.163818	ESTs; Weakly similar to !!!!! ALU SUBFAM1	4.8	NCI-H345, DU145, LnCap
312828	AI865455	Hs.211818	ESTs; Moderately similar to !!!!! ALU SUB	4.78	DU145, DU145, DU145
321226	AA311443	Hs.251416	H sapiens mRNA; cDNA DKFZp586E2317 (from	4.75	DU145, OVCA-R, MB-MDA-453
327772			CH.05_hs gjl5867964	4.74	HT29, MB-MDA-231, NCI-H345
315642	AA742222	Hs.120634	ESTs	4.7	DU145, EB, MB-MDA-453
311905	AA555215	Hs.151913	ESTs	4.7	DU145, Caco2, PRSC_con
312754	R99834	Hs.250383	ESTs	4.59	OVCA-R, PC3, EB
336637			CH22_FGENES.13-7	4.58	NCI-H69, PRSC_log, NCI-H345
331644	T99544	Hs.173734	ESTs; Weakly similar to !!!!! ALU CLASS B	4.55	OVCA-R, NCI-H345, Caco2
336984			CH22_FGENES.401-2	4.55	Caco2, Caco2, EB
316261	AW134485	Hs.144967	ESTs	4.53	NCI-H460, NCI-H345, Caco2
300417	AW139492	Hs.245887	ESTs	4.52	DU145, CALU6, EB
300610	N72596	Hs.99120	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.52	OVCA-R, PC3, EB
324718	AI557019	Hs.116467	ESTs	4.5	LnCap, PC3, PRSC_con
332170	F04112	Hs.177178	ESTs	4.47	Caco2, DU145, DU145
324042	AA377589		EST cluster (not in UniGene)	4.45	NCI-H345, PRSC_con, PRSC_log
331148	R73816	Hs.17385	ESTs	4.44	CALU6, OVCA-R, EB
328981			CH.09_hs gjl5868527	4.43	HT29, BT474, NCI-H69
321920	N63915		EST cluster (not in UniGene)	4.34	Caco2, A549, A549
320832	AA214584		EST cluster (not in UniGene)	4.34	NCI-H23, CALU6, OVCA-R
321971	AI680459	Hs.201441	ESTs	4.33	DU145, HT29, CALU6
308572	AI707882		EST singleton (not in UniGene) with exon	4.33	MCF7, NCI-H345, OVCA-R
302459	AF169255		EST cluster (not in UniGene) with exon h	4.28	MB-MDA-231, OVCA-R, LnCap
321847	T08401		EST cluster (not in UniGene)	4.25	MB-MDA-453, MB-MDA-435s, MB-MDA-231
337884			CH22_EM:AC005500.GENSCAN.54-2	4.23	HT29, NCI-H23, MB-MDA-435s
307494	AI269188	Hs.175656	EST	4.23	NCI-H23, NCI-H520, NCI-358
314915	AA573072	Hs.187748	ESTs; Weakly similar to !!!!! ALU SUBFAM1	4.21	PC3, OVCA-R, Caco2
336638			CH22_FGENES.14-2	4.21	NCI-H69, NCI-H345, PRSC_log
319379	T91443	Hs.193963	ESTs	4.2	PC3, OVCA-R, LnCap
312332	R33041	Hs.106200	ESTs	4.19	NCI-H69, OVCA-R, NCI-H460
331445	H89093	Hs.41215	ESTs	4.19	EB, HT29, DU145
315841	AW136397	Hs.247572	ESTs	4.19	Caco2, MB-MDA-453, LnCap
315712	AI950133	Hs.120882	ESTs; Moderately similar to !!!!! ALU SUB	4.18	LnCap, NCI-H345, OVCA-R
319559	AA773876	Hs.251597	ESTs	4.15	NCI-H345, Caco2, DU145
300791	AL138455	Hs.256135	ESTs; Moderately similar to !!!!! ALU SUB	4.13	NCI-358, RPWE-2, NCI-H460

312129	AW300867		EST cluster (not in UniGene)	4.12	OVCA-R, MCF7, A549
321166	AA411263	Hs.128783	ESTs	4.11	OVCA-R, Caco2, PRSC_con
313220	AI971981	Hs.118241	ESTs	4.1	OVCA-R, DU145, Caco2
314022	AW452420	Hs.248678	ESTs	4.1	OVCA-R, EB, PC3
321359	AW474412		EST cluster (not in UniGene)	4.1	DU145, OVCA-R, PC3
328841			CH.07_hs gij6381920	4.09	NCI-H69, PRSC_log, NCI-H345
337898			CH22_EM:AC005500.GENSCAN.56-5	4.09	NCI-H345, NCI-H69, OVCA-R
333245			CH22_FGENES.115_2	4.09	PRSC_log, PRSC_con, NCI-H345
311958	AI247472	Hs.132965	ESTs	4.06	EB, DU145, CALU6
314775	AI149880	Hs.188809	ESTs	4.06	OVCA-R, PC3, EB
317901	AW150944	Hs.250541	ESTs	4.06	BT474, MB-MDA-453, MB-MDA-435s
309985	AW452919		EST singleton (not in UniGene) with exon	4.05	MB-MDA-453, NCI-H23, NCI-H520
311004	AA632846		EST cluster (not in UniGene)	4.05	MB-MDA-453, OVCA-R, EB
323497	AI523613	Hs.221544	ESTs	4.04	LnCap, OVCA-R, EB
332347	W60326	Hs.221716	ESTs	4.04	EB, CALU6, PC3
331388	AA456852	Hs.43543	suppressor of white apricot homolog 2	4.01	A549, EB, Caco2
313197	AI738851	Hs.222487	ESTs	3.96	OVCA-R, EB, PC3
315710	AA931550	Hs.192785	ESTs	3.95	EB, MB-MDA-231, OVCA-R
316897	AA838114		EST cluster (not in UniGene)	3.94	OVCA-R, A549, MB-MDA-453
322564	W86440	Hs.118344	ESTs	3.94	NCI-H460, Caco2, EB
304605	AA513225		EST singleton (not in UniGene) with exon	3.9	NCI-H345, RPWE-2, BT474
325726			CH.14_hs gij6552447	3.9	OVCA-R, LnCap, LnCap
320190	R32047	Hs.141012	ESTs; Weakly similar to IIII ALU SUBFAM1	3.89	DU145, NCI-H23, PRSC_log
331566	N63062	Hs.48703	EST	3.87	NCI-H23, NCI-H460, NCI-358
319403	T98413		EST cluster (not in UniGene)	3.86	NCI-H345, PRSC_log, LnCap
324643	AI436356	Hs.130729	ESTs	3.84	OVCA-R, DU145, NCI-H345
315298	AI969314	Hs.211377	ESTs	3.82	NCI-H345, PRSC_con, PRSC_log
321632	AA419617		EST cluster (not in UniGene)	3.81	EB, OVCA-R, A549
313219	N74924	Hs.182099	ESTs	3.8	EB, Caco2, OVCA-R
330833	AA046804		ESTs; Weakly similar to IIII ALU SUBFAM1	3.8	LnCap, DU145, PC3
327289			CH.01_hs gij5867481	3.79	EB, HT29, DU145
314429	AW300749		EST cluster (not in UniGene)	3.79	OVCA-R, PC3, PRSC_con
314475	AI911160	Hs.127505	ESTs	3.79	DU145, CALU6, NCI-H69
317130	AW293995	Hs.192277	ESTs	3.78	EB, PC3, Caco2
336635			CH22_FGENES.13-5	3.77	NCI-H69, NCI-H345, PRSC_log
333323			CH22_FGENES.138_16	3.76	NCI-H460, NCI-H23, PRSC_con
332135	AA620331	Hs.245351	EST	3.75	NCI-H345, A549, Caco2
316979	AA861087		EST cluster (not in UniGene)	3.75	NCI-H345, NCI-H69, RPWE-2
316435	AI671871	Hs.192618	ESTs; Weakly similar to IIII ALU CLASS C	3.74	MB-MDA-435s, MCF7, MB-MDA-453
315422	AW135357	Hs.192374	ESTs	3.73	OVCA-R, A549, EB
336616			CH22_FGENES.613_5	3.72	NCI-H69, NCI-H345, RPWE-2
320258	W93241		EST cluster (not in UniGene)	3.71	MB-MDA-231, NCI-H69, EB
300463	N52510	Hs.186470	ESTs	3.69	OVCA-R, A549, DU145
306881	AI088695		EST singleton (not in UniGene) with exon	3.68	CALU6, HT29, EB
337304			CH22_FGENES.681-6	3.67	MCF7, MB-MDA-453, LnCap
323693	AW297758	Hs.249721	ESTs	3.67	OVCA-R, MB-MDA-453, DU145
331073	R07998	Hs.18628	ESTs; Weakly similar to IIII ALU SUBFAM1	3.67	RPWE-2, NCI-H345, OVCA-R
318162	AW296277	Hs.132171	ESTs	3.67	MB-MDA-231, DU145, CALU6
318042	AW294522	Hs.149991	ESTs	3.66	EB, HT29, CALU6
308069	AI470895		EST singleton (not in UniGene) with exon	3.64	Caco2, Caco2, NCI-H23
327614			CH.04_hs gij6525283	3.62	NCI-H460, NCI-H345, NCI-H69
337514			CH22_FGENES.809-7	3.62	NCI-358, NCI-H23, NCI-H460
332093	AA608794	Hs.112592	ESTs	3.6	EB, OVCA-R, DU145
327793			CH.05_hs gij5867979	3.59	LnCap, OVCA-R, EB
331053	N70242	Hs.183146	ESTs	3.59	OVCA-R, EB, Caco2
303769	AA134888	Hs.173415	ESTs	3.58	HT29, CALU6, CALU6
319872	R97130	Hs.189699	ESTs	3.58	PRSC_con, LnCap, RPWE-2
317902	AI828602	Hs.211265	ESTs	3.57	CALU6, NCI-H345, OVCA-R
324090	AI656531	Hs.116070	ESTs	3.57	PRSC_con, NCI-H345, PRSC_log
300120	AW204314	Hs.170784	ESTs	3.57	NCI-H69, NCI-H345, PRSC_con
307752	AI339447		EST singleton (not in UniGene) with exon	3.56	NCI-358, HT29, MB-MDA-231
322438	W44531	Hs.167851	ESTs	3.55	NCI-H345, NCI-H69, Caco2
311275	AI659166	Hs.207144	ESTs	3.55	MB-MDA-231, PRSC_con, LnCap
338830			CH22_DJ246D7.GENSCAN.6-7	3.54	LnCap, PC3, OVCA-R
315647	AA648983	Hs.212911	ESTs	3.53	OVCA-R, MB-MDA-453, CALU6
331469	N22273	Hs.39140	ESTs	3.52	EB, A549, CALU6
313445	AI123657	Hs.127264	ESTs	3.51	EB, OVCA-R, A549
330139			CH.21_p2 gij4210430	3.5	EB, CALU6, DU145
304450	AA404521	Hs.10326	coatamer protein complex; subunit epsilon	3.49	NCI-H345, NCI-H69, NCI-H460
325763			CH.14_hs gij6682475	3.49	PC3, BT474, OVCA-R
312803	AA677934	Hs.117864	ESTs	3.47	OVCA-R, Caco2, MB-MDA-453
303654	AA436942	Hs.168308	ESTs	3.46	DU145, NCI-H460, NCI-H69
317924	AI222324	Hs.166306	ESTs; Weakly similar to zinc finger prot	3.46	PRSC_con, PRSC_log, NCI-H69
312354	AA036955	Hs.167040	ESTs	3.44	Caco2, MB-MDA-435s, NCI-H460
337517			CH22_FGENES.814-6	3.43	NCI-H69, HT29, PC3
324865	AA702138	Hs.114103	ESTs	3.42	NCI-H23, NCI-H460, NCI-H520

323755	AW300094	EST cluster (not in UniGene)	3.42	PRSC_con, RPWE-2, NCI-H345
314452	AL042699	Hs.209222 ESTs	3.42	NCI-H345, PRSC_con, PRSC_log
337911		CH22_EM:AC005500.GENSCAN.59-6	3.42	OVCA-R, PC3, HT29
318086	AI025499	Hs.132238 ESTs	3.41	CALU6, LnCap, OVCA-R
311859	AA704705	Hs.181044 ESTs; Weakly similar to Chain A; Human O Complexed With L-Canaline [H.sapiens]	3.41	LnCap, MB-MDA-435s, A549
314409	H15560	Hs.131833 ESTs	3.41	NCI-H69, LnCap, LnCap
323333	AA228883	EST cluster (not in UniGene)	3.41	Caco2, OVCA-R, NCI-H69
325690		CH.14_hs gij5867021	3.4	HT29, CALU6, DU145
314539	AA398216	Hs.190092 ESTs	3.4	MB-MDA-231, BT474, EB
310567	AI691065	Hs.155780 ESTs	3.4	PRSC_con, NCI-H345, NCI-H69
330527	S77356	transcript ch21=oligomycin sensitivity c 8 stomach cancer cell lines, mRNA, 262 n	3.39	NCI-H23, Caco2, A549
314660	AA436007	Hs.188780 ESTs	3.39	OVCA-R, BT474, Caco2
321321	AB033072	EST cluster (not in UniGene)	3.39	NCI-358, EB, Caco2
323356	AA234009	Hs.188715 ESTs	3.38	DU145, CALU6, CALU6
328592		CH.07_hs gij5868227	3.38	MCF7, NCI-358, MB-MDA-231
311116	AI631195	Hs.232193 ESTs	3.36	NCI-H520, NCI-H23, PRSC_log
323853	AA393460	EST cluster (not in UniGene)	3.36	DU145, EB, Caco2
327740		CH.05_hs gij5867943	3.35	EB, LnCap, OVCA-R
326857		CH.20_hs gij6552460	3.33	NCI-H69, MCF7, NCI-H345
317787	AW339612	Hs.249364 ESTs	3.31	NCI-H345, PRSC_con, PRSC_log
325760		CH.14_hs gij6552449	3.3	EB, CALU6, HT29
337513		CH22_FGENES.809-4	3.29	LnCap, NCI-H23, NCI-H460
336606		CH22_FGENES.429_3	3.29	NCI-H69, A549, NCI-H23
322895	AW470295	Hs.192152 ESTs	3.29	DU145, Caco2, EB
314312	AA814971	Hs.257634 ESTs	3.29	RPWE-2, NCI-H69, NCI-H345
328224		CH.06_hs gij5868101	3.28	DU145, NCI-H345, LnCap
336128		CH22_FGENES.701_16	3.27	BT474, NCI-H520, MB-MDA-231
332442	AA281323	Hs.4947 ESTs	3.27	Caco2, PC3, NCI-H345
302514	M14269	EST cluster (not in UniGene) with exon h	3.27	DU145, CALU6, NCI-H520
313749	AW450376	Hs.130803 ESTs	3.26	OVCA-R, NCI-H69, DU145
302891	AI681578	Hs.114164 ESTs	3.26	LnCap, NCI-H345, PRSC_log
334690		CH22_FGENES.420_3	3.25	NCI-H69, RPWE-2, PRSC_con
308676	AI761036	EST singleton (not in UniGene) with exon	3.25	DU145, MB-MDA-231, HT29
304254	AA046273	Hs.111334 ferritin; light polypeptide	3.24	OVCA-R, DU145, A549
311994	AA648314	Hs.13849 ESTs	3.24	NCI-H460, NCI-H23, MB-MDA-453
321020	AB023170	Hs.227850 KIAA0953 protein	3.24	EB, MCF7, MB-MDA-435s
316724	AA810788	Hs.123337 ESTs	3.23	DU145, OVCA-R, BT474
326942		CH.21_hs gij6004446	3.22	HT29, BT474, NCI-H23
324824	AI826999	Hs.224624 ESTs	3.21	OVCA-R, MB-MDA-453, EB
320789	R78712	EST cluster (not in UniGene)	3.21	DU145, LnCap, EB
315070	AW131368	Hs.186736 ESTs	3.21	Caco2, NCI-358, NCI-H460
303794	AW241987	Hs.197025 ESTs	3.19	OVCA-R, PC3, LnCap
310237	AI884313	Hs.158906 ESTs	3.19	NCI-358, NCI-H345, MCF7
313960	AA130859	EST cluster (not in UniGene)	3.18	MB-MDA-231, HT29, BT474
336634		CH22_FGENES.13-4	3.18	NCI-H69, NCI-H345, BT474
301085	AA779058	Hs.190428 ESTs; Weakly similar to NG26 [H.sapiens]	3.17	NCI-H345, NCI-H345, NCI-358
313774	AW136836	Hs.144583 ESTs	3.17	Caco2, EB, OVCA-R
307177	AI188864	EST singleton (not in UniGene) with exon	3.17	EB, CALU6, CALU6
324025	AI174861	Hs.190623 ESTs	3.17	OVCA-R, DU145, PC3
313099	AI307359	Hs.128064 ESTs	3.17	MB-MDA-231, BT474, EB
305536	AA770682	EST singleton (not in UniGene) with exon	3.17	NCI-358, Caco2, HT29
331916	AA446131	Hs.124918 ESTs	3.17	EB, OVCA-R, Caco2
314912	AI431345	Hs.161784 ESTs	3.17	EB, BT474, MCF7
303388	AL039604	EST cluster (not in UniGene) with exon h	3.17	HT29, NCI-358, Caco2
332273	R05818	Hs.173830 ESTs	3.16	MCF7, DU145, EB
314697	AW088739	Hs.243770 ESTs	3.16	MB-MDA-453, DU145, MCF7
335344		CH22_FGENES.536_3	3.15	PRSC_log, NCI-H345, PRSC_con
326162		CH.17_hs gij5867168	3.15	BT474, HT29, HT29
304467	AA424703	EST singleton (not in UniGene) with exon	3.15	NCI-H23, RPWE-2, NCI-H460
339340		CH22_BA354112.GENSCAN.27-8	3.15	LnCap, OVCA-R, MB-MDA-453
325393		CH.12_hs gij5866921	3.13	Caco2, NCI-H23, NCI-358
315367	AA732484	Hs.169399 ESTs	3.13	OVCA-R, EB, MB-MDA-453
307085	AI160868	EST singleton (not in UniGene) with exon	3.12	RPWE-2, PRSC_con, PRSC_log
313001	N29264	Hs.249591 ESTs; Moderately similar to IIII ALU SUB	3.12	NCI-H345, OVCA-R, Caco2
307606	AI290006	EST singleton (not in UniGene) with exon	3.12	MB-MDA-231, HT29, NCI-H23
325710		CH.14_hs gij6682473	3.09	NCI-H69, MB-MDA-453, BT474
313810	AA400079	Hs.257854 ESTs	3.09	EB, DU145, CALU6
335482		CH22_FGENES.570_11	3.09	NCI-H460, NCI-358, NCI-H23
326310		CH.17_hs gij5867277	3.08	MCF7, MB-MDA-453, PC3
325742		CH.14_hs gij6552448	3.08	NCI-H23, NCI-H460, HT29
312467	AI241809	Hs.75458 ribosomal protein L18	3.08	NCI-358, NCI-H23, NCI-H460
327309		CH.01_hs gij6456757	3.07	NCI-H69, MB-MDA-435s, MB-MDA-435s
310583	AW205632	Hs.211198 ESTs	3.07	OVCA-R, A549, Caco2
322373	W25673	Hs.130829 ESTs	3.07	NCI-H69, PRSC_con, NCI-H345

324497	AW152624	Hs.136340	ESTs	3.06	NCI-H345, RPWE-2, PRSC_con
315095	AA831815	Hs.243788	ESTs	3.06	Caco2, DU145, EB
302445	N79647		EST cluster (not in UniGene) with exon h	3.05	OVCA-R, A549, NCI-H460
302842	AW383226	Hs.163834	ESTs; Highly similar to Chp [R.norvegica]	3.05	A549, DU145, NCI-H23
317346	AA952875	Hs.221274	ESTs	3.04	BT474, HT29, HT29
334650			CH22_FGENES.417_17	3.04	MCF7, BT474, OVCA-R
306644	AI002913		EST singleton (not in UniGene) with exon	3.04	CALU6, MCF7, BT474
322682	AI110679		EST cluster (not in UniGene)	3.03	NCI-H345, RPWE-2, OVCA-R
311065	AW204582	Hs.224906	ESTs	3.03	PRSC_log, PRSC_con, NCI-H460
318623	AA355439	Hs.151547	ESTs	3.03	DU145, MB-MDA-435s, HT29
304978	AA617735		EST singleton (not in UniGene) with exon	3.03	CALU6, BT474, MB-MDA-435s
305554	AA774567	Hs.121774	EST	3.03	EB, NCI-H460, Caco2
302574	U66199	Hs.249165	fibroblast growth factor 11	3.03	HT29, DU145, PC3
336202			CH22_FGENES.719_6	3.02	NCI-H69, NCI-H23, NCI-H23
302893	AL117539	Hs.173515	H sapiens mRNA; cDNA DKFZp586H021 (from		3.02 EB, DU145, CALU6
315166	AI343966	Hs.158528	ESTs	3.01	Caco2, EB, NCI-H69
335606			CH22_FGENES.582_3	3.01	NCI-H23, NCI-H520, NCI-H345
330058			CH.17_p2 gjl6634847	3.01	OVCA-R, HT29, LnCap
303179	AA071215		EST cluster (not in UniGene) with exon h	3.01	MCF7, RPWE-2, MB-MDA-453
307625	AI299617		EST singleton (not in UniGene) with exon	3	MB-MDA-231, LnCap, BT474
323074	AL119445	Hs.203213	ESTs	3	NCI-H23, NCI-H520, NCI-H460
336232			CH22_FGENES.736_7	3	HT29, BT474, MB-MDA-231
334915			CH22_FGENES.457_4	3	NCI-H345, PRSC_con, NCI-H69
329116			CH.X_hs gjl5868650	3	NCI-H69, PRSC_con, RPWE-2
333495			CH22_FGENES.168_5	3	OVCA-R, NCI-H69, NCI-H345
303756	AI738488	Hs.115838	ESTs	2.99	HT29, PRSC_con, DU145
332134	AA610123	Hs.139240	DKFZP564F1422 protein	2.99	EB, A549, MCF7
322916	AW367294	Hs.154091	ESTs	2.99	DU145, DU145, OVCA-R
318050	AI052093	Hs.133132	ESTs	2.99	NCI-H345, DU145, NCI-H520
301019	AI147356	Hs.98722	ESTs	2.99	NCI-358, NCI-H69, MB-MDA-435s
315213	AA587773	Hs.136494	ESTs	2.98	MB-MDA-231, BT474, LnCap
339251			CH22_BA354I12.GENSCAN.7-5	2.98	NCI-H69, PRSC_log, HT29
303835	T05645		EST cluster (not in UniGene) with exon h	2.97	BT474, NCI-H345, LnCap
300070	AI174603	Hs.256832	ESTs	2.97	DU145, A549, OVCA-R
320954	AB028953	Hs.204121	KIAA1030 protein	2.97	LnCap, DU145, PC3
327624			CH.04_hs gjl5867871	2.97	EB, DU145, LnCap
329029			CH.X_hs gjl6525302	2.96	NCI-H69, PRSC_log, LnCap
317040	AA868584	Hs.126154	ESTs	2.96	DU145, EB, LnCap
328016			CH.06_hs gjl5902482	2.96	NCI-H345, PRSC_con, DU145
312674	AI762475	Hs.151327	ESTs; Moderately similar to IIII ALU SUB	2.96	OVCA-R, NCI-H69, NCI-H69
332301	R70253	Hs.127826	ESTs	2.96	OVCA-R, DU145, MB-MDA-231
300951	AI732374	Hs.105834	ESTs; Weakly similar to 25 kDa trypsin i	2.95	NCI-358, NCI-H460, Caco2
318226	AI078446	Hs.134125	ESTs	2.95	NCI-H460, NCI-H23, NCI-358
311349	AW292933	Hs.254110	ESTs	2.94	EB, DU145, OVCA-R
312757	AI285970	Hs.183817	ESTs	2.94	DU145, LnCap, LnCap
316507	AI381515	Hs.158381	ESTs	2.94	PRSC_con, PRSC_log, RPWE-2
302278	AF018080	Hs.173730	Mediterranean fever	2.93	EB, NCI-H69, DU145
311016	AW173166	Hs.243468	ESTs	2.93	NCI-H345, LnCap, LnCap
323864	AA340724	Hs.214028	ESTs	2.92	EB, Caco2, HT29
336632			CH22_FGENES.13-2	2.92	NCI-H69, NCI-H345, MB-MDA-231
328886			CH.07_hs gjl6588003	2.92	HT29, PC3, LnCap
301859	T61587		EST cluster (not in UniGene) with exon h	2.92	LnCap, EB, EB
323775	AA329856	Hs.143022	ESTs	2.92	PRSC_con, PRSC_log, RPWE-2
315426	AI391486	Hs.128171	ESTs	2.92	CALU6, EB, A549
322264	AF086242		EST cluster (not in UniGene)	2.92	Caco2, OVCA-R, DU145
315135	AA627561	Hs.192446	ESTs	2.91	EB, HT29, DU145
327982			CH.06_hs gjl5868216	2.91	LnCap, MB-MDA-453, NCI-H69
314530	AI052358	Hs.131741	ESTs	2.91	NCI-H460, NCI-H520, RPWE-2
315003	AA527650	Hs.156037	ESTs	2.9	PRSC_con, RPWE-2, MB-MDA-231
339032			CH22_DA59H18.GENSCAN.25-1	2.9	NCI-H69, PRSC_con, RPWE-2
308379	AI623950	Hs.2186	eukaryotic translation elongation factor	2.89	BT474, MB-MDA-231, HT29
312133	T87714	Hs.221665	ESTs	2.88	Caco2, MB-MDA-453, MCF7
307992	AI434166		EST singleton (not in UniGene) with exon	2.88	NCI-H520, MCF7, NCI-H23
308010	AI439190	Hs.181165	eukaryotic translation elongation factor	2.88	Caco2, NCI-H69, NCI-H345
320154	AA336019	Hs.119559	ESTs	2.88	MB-MDA-453, DU145, EB
331496	N34929	Hs.171984	ESTs	2.86	MB-MDA-453, PC3, MCF7
320016	H57622	Hs.194574	ESTs	2.86	PRSC_con, RPWE-2, PRSC_log
317923	AW450544	Hs.220751	ESTs	2.86	NCI-H345, PRSC_con, PRSC_log
301822	X17033	Hs.1142	Integrin; alpha 2 (CD49B; alpha 2 subuni	2.86	PC3, BT474, CALU6
311759	AA705075	Hs.169536	Rhesus blood group-associated glycoprote	2.85	DU145, HT29, MB-MDA-231
315083	AI221325	Hs.210655	ESTs	2.84	PRSC_con, RPWE-2, NCI-H345
317759	AI908455	Hs.202460	ESTs; Weakly similar to hypothetical L1	2.83	HT29, MB-MDA-231, BT474
313980	AI633205	Hs.159914	ESTs	2.83	Caco2, MB-MDA-453, A549
310941	AI453402	Hs.173705	ESTs; Weakly similar to IIII ALU CLASS C	2.83	NCI-H345, MCF7, Caco2
313593	AI911488	Hs.213724	ESTs	2.83	LnCap, Caco2, NCI-H460
314973	AW273128	Hs.254669	EST	2.82	BT474, LnCap, RPWE-2

310950	AI582758	Hs.170561	ESTs	2.82	EB, MB-MDA-453, LnCap
323626	AL039822	Hs.207604	ESTs	2.82	PC3, HT29, CALU6
325410			CH.12_hs gl 5866921	2.81	MB-MDA-453, PRSC_con, NCI-358
313911	AI565458	Hs.116385	ESTs	2.81	PRSC_con, EB, RPWE-2
334244			CH22_FGENES.365_5	2.81	OVCA-R, PC3, MB-MDA-453
309333	AW025709		EST singleton (not in UniGene) with exon	2.81	NCI-H460, NCI-H23, NCI-358
328467			CH.07_hs gl 5868434	2.81	EB, OVCA-R, HT29
318563	AW250501		EST cluster (not in UniGene)	2.81	BT474, NCI-H23, MB-MDA-231
326412			CH.19_hs gl 5867362	2.81	BT474, PRSC_log, RPWE-2
303407	AA309616		EST cluster (not in UniGene) with exon h	2.8	CALU6, NCI-H345, DU145
328462			CH.07_hs gl 5868433	2.8	BT474, CALU6, MCF7
335157			CH22_FGENES.501_7	2.8	NCI-H69, NCI-H345, PRSC_log
313458	AA007259	Hs.255853	ESTs	2.79	OVCA-R, DU145, LnCap
310416	AI695047	Hs.202395	ESTs	2.79	DU145, MB-MDA-435s, PC3
317709	AI435973	Hs.128056	ESTs	2.79	NCI-H460, NCI-358, DU145
321415	AI377596	Hs.3337	transmembrane 4 superfamily member 1	2.79	A549, PC3, OVCA-R
313693	AW469180	Hs.170651	ESTs	2.79	OVCA-R, MCF7, EB
309438	AW102802	Hs.225787	ESTs; Moderately similar to hypothetical	2.79	PC3, OVCA-R, DU145
308961	AI870248		EST singleton (not in UniGene) with exon	2.78	BT474, MB-MDA-231, EB
329107			CH.X_hs gl 5868626	2.78	DU145, MCF7, MB-MDA-435s
313975	AW025024	Hs.65114	keratin 18	2.78	Caco2, EB, DU145
330901	AA157818	Hs.238380	Human endogenous retroviral protease mRN	2.78	PC3, NCI-H520, BT474
311749	R06249	Hs.13911	ESTs	2.78	OVCA-R, MB-MDA-453, MCF7
329853			CH.14_p2 gl 6682295	2.78	BT474, BT474, HT29
322340	AF088076		EST cluster (not in UniGene)	2.77	NCI-H345, Caco2, LnCap
326806			CH.20_hs gl 6469835	2.77	NCI-H69, NCI-H345, MB-MDA-231
314661	AA436432		EST cluster (not in UniGene)	2.77	NCI-H460, MB-MDA-435s, CALU6
322135	AF075082		EST cluster (not in UniGene)	2.77	NCI-358, NCI-H460, Caco2
331849	AA417078	Hs.193767	ESTs	2.77	DU145, EB, CALU6
301056	AI797955	Hs.208076	ESTs; Weakly similar to D(4) DOPAMINE RE	2.76	NCI-H69, RPWE-2, PRSC_con
327739			CH.05_hs gl 5867942	2.76	EB, PC3, LnCap
308016	AI445116		EST singleton (not in UniGene) with exon	2.76	LnCap, HT29, MB-MDA-231
331549	N56866	Hs.237507	EST	2.76	MB-MDA-453, MCF7, OVCA-R
331851	AA418599	Hs.98303	caveolin 3	2.75	MB-MDA-231, NCI-H345, BT474
315023	AA533505	Hs.185844	ESTs	2.75	PRSC_con, OVCA-R, EB
335565			CH22_FGENES.579_1	2.75	OVCA-R, EB, A549
306137	AA916176		EST singleton (not in UniGene) with exon	2.74	EB, LnCap, DU145
332240	N54803		yv31d2.s1 Soares fetal liver spleen 1NFL		
			3' similar to contains L1.t3 L1 repetit	2.74	DU145, EB, CALU6
313246	N90762	Hs.159454	ESTs	2.74	NCI-H69, NCI-H345, PRSC_log
303642	AW299459		EST cluster (not in UniGene) with exon h	2.74	EB, A549, Caco2
325513			CH.12_hs gl 6017035	2.74	MB-MDA-231, NCI-H345, BT474
337236			CH22_FGENES.639-2	2.74	MCF7, MB-MDA-453, NCI-H69
311555	AW407892	Hs.244807	ESTs	2.74	BT474, NCI-H345, NCI-H69
339266			CH22_BA354I12.GENSCAN.10-4	2.73	CALU6, DU145, OVCA-R
300127	AW028615	Hs.235224	ESTs; Weakly similar to KIAA0422 [H.sapi	2.73	NCI-H345, RPWE-2, PRSC_log
311741	R00099	Hs.193642	ESTs	2.72	LnCap, PC3, OVCA-R
310915	AW449673	Hs.201893	ESTs	2.72	DU145, EB, MB-MDA-435s
324982	T31689	Hs.98518	ESTs	2.71	PRSC_con, PRSC_log, RPWE-2
305030	AA629988		EST singleton (not in UniGene) with exon	2.71	DU145, DU145, NCI-358
315396	AW296107	Hs.152686	ESTs	2.69	OVCA-R, Caco2, EB
319098	AI908374		EST cluster (not in UniGene)	2.69	RPWE-2, LnCap, PC3
309119	AI927384	Hs.228499	EST; Moderately similar to PK-120 precu	2.69	LnCap, NCI-H23, NCI-358
312095	AW444937	Hs.233482	ESTs	2.68	Caco2, OVCA-R, HT29
324316	AI291330		EST cluster (not in UniGene)	2.68	NCI-H460, Caco2, PRSC_log
331367	AA425688	Hs.41641	ESTs; Weakly similar to CAGH4 [H.sapiens	2.68	MB-MDA-435s, NCI-H520, NCI-H460
339116			CH22_DA59H18.GENSCAN.49-4	2.68	DU145, EB, CALU6
324297	AI565566	Hs.168587	ESTs	2.68	PRSC_con, OVCA-R, PRSC_log
318728	Z30201		EST cluster (not in UniGene)	2.68	LnCap, Caco2, PC3
304813	AA584540		EST singleton (not in UniGene) with exon	2.68	BT474, OVCA-R, RPWE-2
312393	N34376	Hs.191659	ESTs; Weakly similar to lill ALU CLASS E	2.68	NCI-H345, PRSC_con, EB
330671	AB002302	Hs.92236	KIAA0304 gene product	2.67	NCI-358, OVCA-R, Caco2
305406	AA723860		EST singleton (not in UniGene) with exon	2.66	OVCA-R, EB, MCF7
330957	H08778	Hs.133521	ESTs	2.66	EB, PC3, OVCA-R
300350	AI871129	Hs.172597	ESTs; Weakly similar to zinc finger prot	2.66	NCI-H23, NCI-H520, NCI-H460
322302	W76021		EST cluster (not in UniGene)	2.66	DU145, OVCA-R, PC3
321891	AW157424	Hs.165954	ESTs	2.66	EB, OVCA-R, Caco2
300124	AI217394	Hs.242447	ESTs	2.65	PRSC_con, A549, HT29
302747	AF062275		EST cluster (not in UniGene) with exon h	2.65	NCI-H23, BT474, MCF7
308741	AI802780	Hs.209002	ESTs; Weakly similar to lill ALU SUBFAMI	2.65	PC3, EB, OVCA-R
310802	AI631546	Hs.159732	ESTs	2.65	PRSC_con, PRSC_log, NCI-H69
300694	AA063406		EST cluster (not in UniGene) with exon h	2.65	BT474, EB, MCF7
311395	R23313		EST cluster (not in UniGene)	2.64	EB, OVCA-R, DU145
336538			CH22_FGENES.840_2	2.64	DU145, NCI-H460, NCI-358
316473	AA829961		EST cluster (not in UniGene)	2.64	LnCap, OVCA-R, EB
328134			CH.06_hs gl 5868039	2.64	LnCap, EB, CALU6

329330		CH.X_hs gij5868806	2.64	EB, CALU6, DU145
316664	AI042101	EST cluster (not in UniGene)	2.64	NCI-H345, MB-MDA-231, PRSC_log
328015		CH.06_hs gij5902482	2.63	BT474, HT29, MB-MDA-231
308991	AI879831	EST singleton (not in UniGene) with exon	2.63	BT474, EB, NCI-H23
323899	AL042966	EST cluster (not in UniGene)	2.62	DU145, A549, CALU6
321708	AA476817	EST cluster (not in UniGene)	2.62	EB, A549, CALU6
301752	T75247	EST cluster (not in UniGene) with exon h	2.62	HT29, BT474, NCI-H345
309351	AW057547	EST singleton (not in UniGene) with exon	2.62	NCI-H23, PRSC_con, LnCap
314412	AI864270	Hs.155654 ESTs	2.62	CALU6, MB-MDA-231, BT474
309441	AW103055	Hs.244230 EST	2.62	BT474, MB-MDA-231, MB-MDA-453
335993		CH22_FGENES.656_6	2.61	NCI-H460, NCI-358, NCI-H520
318196	AI056776	Hs.133397 ESTs	2.6	EB, CALU6, HT29
322880	AA310521	Hs.50848 ESTs; Weakly similar to KIAA0862 protein	2.6	DU145, A549, PC3
300558	AI540051	Hs.122638 ESTs	2.6	OVCA-R, NCI-H69, MCF7
318594	AA918320	Hs.224581 ESTs	2.6	PC3, MB-MDA-453, DU145
308554	AI698132	Hs.201923 EST	2.6	LnCap, EB, NCI-H345
335108		CH22_FGENES.494_14	2.6	NCI-H69, NCI-H345, MB-MDA-231
312483	AI417526	Hs.184636 ESTs	2.59	PC3, DU145, OVCA-R
311981	AW452773	Hs.257612 EST	2.59	NCI-H460, MB-MDA-453, NCI-H23
319359	F13458	EST cluster (not in UniGene)	2.59	LnCap, NCI-H460, MB-MDA-231
300230	AI377746	Hs.158846 ESTs	2.59	HT29, NCI-358, NCI-H345
316504	AW135854	Hs.132458 ESTs	2.59	DU145, EB, CALU6
322337	AA249804	EST cluster (not in UniGene)	2.59	NCI-H69, NCI-H345, NCI-H345
301775	AW247670	EST cluster (not in UniGene) with exon h	2.59	NCI-H345, RPWE-2, PRSC_log
301089	AA666396	Hs.220727 ESTs	2.58	PRSC_log, PRSC_con, RPWE-2
331213	T88698	Hs.163862 ESTs	2.58	DU145, EB, OVCA-R
321121	W23285	EST cluster (not in UniGene)	2.58	NCI-H69, MB-MDA-435s, PC3
316634	AW241910	Hs.122254 ESTs	2.58	MCF7, HT29, BT474
322141	AF075092	EST cluster (not in UniGene)	2.58	PC3, OVCA-R, HT29
312108	T82331	Hs.127453 ESTs	2.58	A549, CALU6, Caco2
339071		CH22_DA59H18.GENSCAN.34-1	2.58	CALU6, DU145, EB
311666	AW389509	Hs.223747 ESTs	2.57	OVCA-R, MB-MDA-231, BT474
318662	AI285898	Hs.115367 ESTs	2.57	OVCA-R, DU145, EB
317010	AA863395	EST cluster (not in UniGene)	2.57	NCI-H520, PRSC_con, NCI-358
324710	AI742028	Hs.120884 ESTs; Weakly similar to RAS-RELATED PROT	2.57	LnCap, DU145, MB-MDA-453
327888		CH.06_hs gij5868149	2.56	NCI-H345, MB-MDA-435s, RPWE-2
336149		CH22_FGENES.706_5	2.56	NCI-H69, PC3, A549
312816	H74319	Hs.188620 ESTs	2.56	EB, Caco2, NCI-H460
327999		CH.06_hs gij5867994	2.56	NCI-358, NCI-H520, NCI-H23
316761	AI911173	Hs.213722 ESTs	2.55	NCI-H345, NCI-H460, MB-MDA-231
336958		CH22_FGENES.367-1	2.55	HT29, CALU6, CALU6
325043	W27919	Hs.32944 Inositol polyphosphate-4-phosphatase; ty	2.55	NCI-H460, NCI-H23, HT29
315417	AW452360	Hs.186770 ESTs	2.55	NCI-H345, NCI-H69, PRSC_con
331603	N78656	Hs.161535 EST	2.55	NCI-H345, PRSC_con, PRSC_log
309403	AW082954	EST singleton (not in UniGene) with exon	2.55	BT474, MB-MDA-231, MCF7
337289		CH22_FGENES.672-8	2.54	BT474, HT29, MB-MDA-231
314242	AI570943	Hs.246280 ESTs	2.54	Caco2, MB-MDA-435s, MB-MDA-453
328053		CH.06_hs gij5902482	2.54	MB-MDA-231, DU145, MB-MDA-453
307215	AI193189	EST singleton (not in UniGene) with exon	2.53	HT29, CALU6, MB-MDA-231
327566		CH.03_hs gij5867811	2.53	NCI-H69, NCI-H520, NCI-H345
326338		CH.17_hs gij6056311	2.53	PC3, A549, DU145
318115	AI384027	Hs.159130 ESTs; Moderately similar to IIII ALU SUB	2.53	DU145, EB, PC3
307437	AI245683	EST singleton (not in UniGene) with exon	2.52	NCI-H23, NCI-H520, NCI-358
322059	AA412371	Hs.121344 ESTs	2.52	EB, DU145, OVCA-R
322505	AF147315	EST cluster (not in UniGene)	2.52	PRSC_con, RPWE-2, NCI-H69
314032	AW081897	Hs.193211 ESTs	2.52	NCI-H345, LnCap, DU145
336125		CH22_FGENES.701_12	2.51	NCI-H69, LnCap, DU145
312765	AI692908	Hs.181873 ESTs	2.51	NCI-H23, NCI-358, NCI-H520
335523		CH22_FGENES.572_3	2.51	HT29, BT474, OVCA-R
327585		CH.03_hs gij5867825	2.51	HT29, NCI-H460, MB-MDA-453
323183	AW393850	EST cluster (not in UniGene)	2.51	MB-MDA-231, LnCap, RPWE-2
314418	AI478722	Hs.232275 ESTs; Moderately similar to IIII ALU SUB	2.51	EB, DU145, DU145
313361	AI359782	Hs.137312 ESTs	2.5	CALU6, HT29, DU145
305632	AA805276	EST singleton (not in UniGene) with exon	2.5	MB-MDA-453, NCI-H460, NCI-H23
331689	W90131	Hs.184675 ESTs	2.5	NCI-H69, EB, A549
323438	AI540243	Hs.113817 ESTs	2.5	NCI-H345, PRSC_con, MB-MDA-231
315742	AI821724	Hs.143198 H sapiens PAC clone DJ0872F07 from 7q31	2.5	MCF7, MB-MDA-453, MB-MDA-435s
305971	AA886874	EST singleton (not in UniGene) with exon	2.5	NCI-358, NCI-H23, NCI-H520
336633		CH22_FGENES.13-3	2.5	NCI-H69, NCI-H345, PRSC_log
304746	AA577793	EST singleton (not in UniGene) with exon	2.49	NCI-H69, BT474, MB-MDA-231
327925		CH.06_hs gij5868172	2.49	NCI-358, NCI-358, NCI-H460
336055		CH22_FGENES.683_4	2.49	EB, HT29, MB-MDA-231
328888		CH.07_hs gij6588003	2.48	MB-MDA-435s, MB-MDA-453, PRSC_log
311244	AW016694	Hs.197689 ESTs	2.48	NCI-H345, MCF7, PC3
327155		CH.01_hs gij5867549	2.48	NCI-H69, MB-MDA-231, NCI-H345
334907		CH22_FGENES.453_2	2.48	DU145, NCI-H345, MB-MDA-231

314887	AA910236	Hs.139469	ESTs	2.48	DU145, A549, A549
339435			CH22_DJ579N16.GENSCAN.18-10	2.48	NCI-H69, MCF7, BT474
334172			CH22_FGENES.349_5	2.48	NCI-H69, NCI-H345, PRSC_log
320767	AA299525		EST cluster (not in UniGene)	2.48	NCI-358, NCI-H23, NCI-H460
336772			CH22_FGENES.156-1	2.47	NCI-358, NCI-358, NCI-H23
326957			CH.21_hs gij6469836	2.47	BT474, RPWE-2, PRSC_con
308505	AI686615	Hs.200778	EST; Weakly similar to SALIVARY PROLINE-	2.47	MCF7, MB-MDA-453, MB-MDA-435s
321325	AB033100		EST cluster (not in UniGene)	2.47	EB, CALU6, A549
313149	AW291092	Hs.201058	ESTs	2.47	NCI-H345, PRSC_con, RPWE-2
338325			CH22_EM:AC005500.GENSCAN.307-7	2.46	BT474, LnCap, EB
307877	AI368880		EST singleton (not in UniGene) with exon	2.46	NCI-H23, PRSC_log, NCI-H520
311525	AI799444	Hs.247095	ESTs; Moderately similar to IIII ALU SUB	2.46	PRSC_con, PRSC_log, NCI-H345
337023			CH22_FGENES.433-12	2.46	OVCA-R, CALU6, PRSC_con
300916	AI361798	Hs.164675	ESTs	2.45	LnCap, DU145, CALU6
302919	AL137382		EST cluster (not in UniGene) with exon h	2.45	LnCap, MB-MDA-231, CALU6
320303	AL079289	Hs.137154	H sapiens mRNA full length insert cDNA c	2.45	BT474, MB-MDA-231, MB-MDA-453
318359	AI097439	Hs.135548	ESTs	2.45	NCI-H460, MB-MDA-453, NCI-H345
314384	AA535840	Hs.162203	ESTs; Weakly similar to alternatively sp	2.45	OVCA-R, PC3, EB
326763			CH.20_hs gij6598307	2.45	NCI-H69, NCI-H345, RPWE-2
319900	AW408392		EST cluster (not in UniGene)	2.45	Caco2, NCI-H460, NCI-H23
314451	AA586368	Hs.190232	ESTs	2.45	PRSC_con, NCI-H345, MB-MDA-231
300641	AW237699	Hs.118346	ESTs	2.44	NCI-H345, PRSC_log, PRSC_con
324368	AW299374		EST cluster (not in UniGene)	2.44	PC3, DU145, OVCA-R
336510			CH22_FGENES.834_5	2.44	NCI-H69, RPWE-2, PRSC_con
326876			CH.20_hs gij6682507	2.44	NCI-H23, NCI-H460, NCI-H520
307753	AI340509	Hs.182428	ribosomal protein S2	2.44	NCI-H23, NCI-H460, Caco2
317071	M78728	Hs.132694	ESTs	2.44	NCI-H345, NCI-H69, RPWE-2
313877	AA767869	Hs.250113	ESTs; Moderately similar to thyroid horm component TRAP150 [H.sapiens]	2.44	DU145, LnCap, CALU6
315974	AW029203	Hs.191952	ESTs	2.43	EB, DU145, OVCA-R
322970	AI885052	Hs.142287	ESTs; Weakly similar to IIII ALU CLASS F	2.43	NCI-H345, RPWE-2, EB
317733	AI028257	Hs.132317	ESTs	2.43	CALU6, RPWE-2, OVCA-R
313599	AA748749	Hs.136742	ESTs	2.42	NCI-H460, NCI-358, NCI-H520
323014	AA305198		EST cluster (not in UniGene)	2.42	PRSC_con, NCI-H460, RPWE-2
324980	AA969121	Hs.254296	ESTs	2.41	MCF7, OVCA-R, PC3
301326	AA883831	Hs.252924	ESTs	2.41	PRSC_con, PRSC_log, RPWE-2
308695	AI763350		EST singleton (not in UniGene) with exon	2.41	RPWE-2, NCI-H69, NCI-H345
330166			CH.02_p2 gij6648220	2.41	CALU6, DU145, A549
317552	AW451400	Hs.127019	ESTs	2.41	NCI-358, NCI-358, NCI-H23
320572	AI929508	Hs.159590	lymphocyte antigen 6 complex; locus H	2.41	CALU6, HT29, A549
315618	AI287341	Hs.154029	ESTs; Weakly similar to TRANSCRIPTION FA2.41	2.41	OVCA-R, Caco2, MB-MDA-231
331610	N91109	Hs.54681	ESTs	2.41	NCI-H23, NCI-H520, NCI-358
311731	AW393528	Hs.246875	ESTs	2.41	NCI-H69, NCI-H345, PRSC_con
318571	Z43383	Hs.8053	ESTs	2.4	NCI-358, NCI-H23, NCI-H520
334958			CH22_FGENES.465_27	2.4	DU145, PRSC_con, RPWE-2
323570	AL038623	Hs.208752	ESTs; Weakly similar to IIII ALU SUBFAMI	2.4	OVCA-R, EB, BT474
301685	W67730		EST cluster (not in UniGene) with exon h	2.4	MB-MDA-231, NCI-H345, EB
303849	AW163324		EST cluster (not in UniGene) with exon h	2.4	RPWE-2, PRSC_log, NCI-H345
325702			CH.14_hs gij5867028	2.4	NCI-H23, NCI-H460, NCI-H520
313074	N48261	Hs.127171	ESTs	2.4	MB-MDA-231, RPWE-2, PRSC_log
308994	AI880051		EST singleton (not in UniGene) with exon	2.4	RPWE-2, EB, PRSC_con
330338			CH.08_p2 gij5457162	2.4	DU145, EB, LnCap
327274			CH.01_hs gij5867470	2.4	OVCA-R, DU145, MB-MDA-231
325953			CH.16_hs gij5867140	2.4	MB-MDA-453, MB-MDA-435s, MCF7
333281			CH22_FGENES.128_7	2.4	NCI-H23, HT29, DU145
314778	AW079559	Hs.152258	ESTs	2.39	EB, CALU6, Caco2
317005	AI800251	Hs.197773	ESTs	2.38	MB-MDA-231, BT474, HT29
334257			CH22_FGENES.367_5	2.38	HT29, NCI-358, MB-MDA-231
324783	AA640770		EST cluster (not in UniGene)	2.38	EB, OVCA-R, MB-MDA-453
300949	AA534325	Hs.162183	ESTs	2.38	NCI-H69, NCI-H345, PRSC_log
314957	AW029274	Hs.208368	ESTs; Moderately similar to IIII ALU SUB	2.38	LnCap, DU145, DU145
324350	AW292501	Hs.157174	ESTs; Weakly similar to similar to SH3-b	2.38	HT29, NCI-H23, NCI-H23
338235			CH22_EM:AC005500.GENSCAN.260-16	2.38	NCI-H69, NCI-H460, NCI-H23
300937	AW297302	Hs.255631	ESTs	2.38	PRSC_log, PRSC_con, PRSC_con
317439	AW451327	Hs.170623	ESTs	2.38	A549, DU145, EB
324745	AI742120	Hs.116506	ESTs; Weakly similar to IIII ALU SUBFAMI	2.38	NCI-358, NCI-H460, BT474
338306			CH22_EM:AC005500.GENSCAN.302-2	2.38	NCI-H69, PRSC_con, PRSC_log
318765	Z42071	Hs.23961	ESTs	2.38	LnCap, NCI-H23, NCI-H520
310254	AI239811	Hs.157491	ESTs	2.37	OVCA-R, DU145, EB
305116	AA649244		EST singleton (not in UniGene) with exon	2.37	CALU6, MB-MDA-435s, MB-MDA-453
324016	AL045285	Hs.246849	ESTs; Moderately similar to IIII ALU SUB	2.37	EB, DU145, OVCA-R
322774	AA131111		EST cluster (not in UniGene)	2.37	OVCA-R, EB, A549
335745			CH22_FGENES.601_16	2.37	PRSC_log, PRSC_con, NCI-H69
300972	AI979100	Hs.211518	ESTs	2.37	NCI-H69, NCI-H345, PRSC_log
338809			CH22_EM:AC005500.GENSCAN.531-10	2.37	NCI-H23, NCI-H69, NCI-H520
316983	AI480204	Hs.177131	ESTs	2.37	NCI-H345, PRSC_con, PRSC_log

321308	AI247480	Hs.117029	ESTs	2.37	BT474, NCI-H69, HT29
323578	AA299492	Hs.168166	ESTs	2.37	LnCap, EB, MB-MDA-453
335747			CH22_FGENES.601_20	2.36	NCI-H69, LnCap, PRSC_con
322362	AF039697		EST cluster (not in UniGene)	2.36	DU145, PRSC_con, NCI-H345
314430	N76302	Hs.78110	ESTs; Weakly similar to F17A9.2 [C.elega	2.36	DU145, MB-MDA-453, CALU6
304831	AA586422		EST singleton (not in UniGene) with exon	2.36	NCI-H23, NCI-H460, CALU6
337432			CH22_FGENES.765-1	2.36	MB-MDA-231, BT474, HT29
305984	AA887654		EST singleton (not in UniGene) with exon	2.36	DU145, HT29, CALU6
313486	AW134523	Hs.247186	ESTs	2.36	DU145, A549, CALU6
309028	AI889109	Hs.212032	EST	2.36	NCI-358, NCI-H520, NCI-H23
318292	AI679966	Hs.150603	ESTs	2.35	NCI-H460, Caco2, NCI-H23
334198			CH22_FGENES.354_4	2.35	NCI-H69, PRSC_log, PRSC_con
314458	AI217440	Hs.143873	ESTs	2.35	Caco2, A549, PC3
333346			CH22_FGENES.139_15	2.35	CALU6, DU145, LnCap
325408			CH.12_hs gjl5866921	2.35	NCI-H460, NCI-H520, NCI-H23
313758	AA076743	Hs.129770	ESTs	2.35	NCI-H23, MB-MDA-435s, NCI-H345
309825	AW293701		EST singleton (not in UniGene) with exon	2.35	NCI-H460, NCI-H23, NCI-H520
303536	R55497	Hs.183941	ESTs; Moderately similar to H beta 58 ho	2.35	DU145, CALU6, NCI-H520
331534	N51583	Hs.133756	EST	2.35	NCI-H23, NCI-H520, NCI-358
325164	T16981	Hs.21963	ESTs	2.34	NCI-H345, PRSC_log, NCI-H460
327710			CH.04_hs gjl5867860	2.34	BT474, MB-MDA-231, NCI-H345
306351	AA961356		EST singleton (not in UniGene) with exon	2.34	BT474, MB-MDA-231, MB-MDA-435s
304968	AA614308		EST singleton (not in UniGene) with exon	2.34	CALU6, HT29, MB-MDA-453
334015			CH22_FGENES.313_7	2.34	HT29, MB-MDA-231, BT474
318315	AI091370	Hs.134852	ESTs	2.33	CALU6, NCI-H520, DU145
306809	AI057134		EST singleton (not in UniGene) with exon	2.33	PC3, DU145, EB
337697			CH22_EM:AC000097.GENSCAN.86-1	2.33	RPWE-2, PRSC_log, NCI-H345
329630			CH.11_p2 gjl6729060	2.33	NCI-H520, NCI-H23, NCI-H460
326577			CH.19_hs gjl5867317	2.33	NCI-H460, NCI-358, NCI-H23
333428			CH22_FGENES.149_1	2.33	NCI-H345, PRSC_con, RPWE-2
301080	AI479391	Hs.155405	ESTs; Weakly similar to IIII ALU SUBFAMI	2.33	OVCA-R, MCF7, MCF7
324829	AA714311		EST cluster (not in UniGene)	2.33	NCI-H460, NCI-358, NCI-H23
302776	AJ133798		EST cluster (not in UniGene) with exon h	2.32	NCI-H23, NCI-H460, NCI-H520
325801			CH.14_hs gjl6552451	2.32	PRSC_log, MCF7, NCI-H23
332122	AA609698	Hs.112389	ESTs	2.32	DU145, HT29, PC3
314167	AA243633	Hs.208983	ESTs	2.32	DU145, MCF7, PC3
324023	AA669615	Hs.214226	ESTs	2.31	DU145, NCI-H345, EB
320503	NM_00589		EST cluster (not in UniGene)	2.31	A549, OVCA-R, PC3
312217	T98289		EST cluster (not in UniGene)	2.31	NCI-H23, Caco2, NCI-H69
321304	AA078293		EST cluster (not in UniGene)	2.31	DU145, OVCA-R, EB
323517	AA527359	Hs.154366	ESTs	2.31	NCI-H345, DU145, EB
336455			CH22_FGENES.829_13	2.31	NCI-H345, PRSC_con, RPWE-2
313352	AW292127	Hs.144758	ESTs	2.31	MCF7, DU145, OVCA-R
331457	H93135	Hs.41840	ESTs	2.31	Caco2, NCI-H460, NCI-H23
333054			CH22_FGENES.73_8	2.31	NCI-H69, NCI-358, NCI-H23
308598	AI719237		EST singleton (not in UniGene) with exon	2.31	OVCA-R, CALU6, Caco2
327059			CH.21_hs gjl6531965	2.3	NCI-H460, LnCap, LnCap
334120			CH22_FGENES.333_1	2.3	NCI-H69, RPWE-2, MB-MDA-435s
324154	AI457449	Hs.192817	ESTs	2.3	NCI-H460, MB-MDA-453, NCI-358
326509			CH.19_hs gjl6682496	2.3	NCI-H345, CALU6, OVCA-R
316855	AW291384	Hs.254974	ESTs	2.3	NCI-H345, NCI-H460, BT474
337918			CH22_EM:AC005500.GENSCAN.66-4	2.3	RPWE-2, NCI-H345, PRSC_log
317471	AI825351	Hs.144084	ESTs	2.29	HT29, OVCA-R, DU145
331023	N32599	Hs.5856	ESTs	2.29	OVCA-R, LnCap, A549
332231	N48008	Hs.102629	EST	2.29	CALU6, DU145, EB
309912	AW339671		EST singleton (not in UniGene) with exon	2.29	MB-MDA-435s, PRSC_con, NCI-358
316427	AI241019	Hs.145644	ESTs	2.29	Caco2, HT29, EB
313329	AW293704	Hs.122658	ESTs	2.29	OVCA-R, DU145, Caco2
335019			CH22_FGENES.474_7	2.29	HT29, CALU6, MB-MDA-231
324394	F20654	Hs.152128	ESTs; Moderately similar to IIII ALU SUB	2.29	NCI-H345, MB-MDA-231, RPWE-2
339357			CH22_BA354112.GENSCAN.31-2	2.29	NCI-H69, OVCA-R, BT474
322128	AI346033		EST cluster (not in UniGene)	2.28	NCI-H23, NCI-H520, NCI-H460
301310	AI239457	Hs.130794	ESTs	2.28	OVCA-R, DU145, MB-MDA-231
300623	AI929130	Hs.118261	ESTs; Moderately similar to finger prote	2.28	BT474, RPWE-2, PRSC_con
323409	AL135534		EST cluster (not in UniGene)	2.27	NCI-H345, NCI-358, Caco2
308406	AI634885		EST singleton (not in UniGene) with exon	2.27	OVCA-R, EB, HT29
322518	AI133446		EST cluster (not in UniGene)	2.27	DU145, MB-MDA-435s, OVCA-R
338381			CH22_EM:AC005500.GENSCAN.330-10	2.27	NCI-H69, PRSC_con, PRSC_log
316003	AA704584	Hs.119993	ESTs	2.27	NCI-358, NCI-H520, NCI-H23
307090	AI161024		EST singleton (not in UniGene) with exon	2.27	NCI-H345, DU145, RPWE-2
300356	AA758411	Hs.121335	ESTs	2.27	LnCap, NCI-H460, Caco2
331887	AA431328	Hs.98660	ESTs	2.27	NCI-358, NCI-H520, CALU6
330951	H02566	Hs.191268	H sapiens mRNA; cDNA DKFZp434N174 (from	2.27	OVCA-R, BT474, BT474
305547	AA773111		EST singleton (not in UniGene) with exon	2.27	LnCap, DU145, BT474
312457	AA776743	Hs.191589	ESTs	2.26	NCI-H345, RPWE-2, PRSC_con
333929			CH22_FGENES.300_2	2.26	HT29, CALU6, EB

319845	AA649011	Hs.187902	ESTs	2.26	LnCap, DU145, MCF7
306739	AI028393		EST singleton (not in UniGene) with exon	2.26	MB-MDA-435s, NCI-358, CALU6
306919	AI096832		EST singleton (not in UniGene) with exon	2.26	HT29, BT474, PC3
333312			CH22_FGENES.138_4	2.26	OVCA-R, DU145, PC3
334955			CH22_FGENES.465_24	2.25	RPWE-2, PRSC_con, NCI-H345
312295	AA578233	Hs.173863	ESTs	2.25	OVCA-R, DU145, NCI-H345
307643	AI302124		EST singleton (not in UniGene) with exon	2.25	CALU6, CALU6, OVCA-R
324252	AA421989		EST cluster (not in UniGene)	2.25	OVCA-R, EB, A549
309767	AW271805		EST singleton (not in UniGene) with exon	2.25	DU145, NCI-H460, CALU6
311492	AW410240	Hs.4437	ribosomal protein L28	2.25	NCI-H69, NCI-H460, NCI-H520
312260	H05392	Hs.230597	EST	2.25	Caco2, EB, DU145
327125			CH.21_hs gij6531971	2.25	HT29, NCI-358, BT474
316919	AA845382	Hs.204520	ESTs	2.24	NCI-H23, NCI-H345, NCI-H520
316361	AI433833	Hs.164159	ESTs; Weakly similar to IIII ALU SUBFAMI	2.24	DU145, EB, PC3
315772	AW515373	Hs.158893	ESTs	2.24	OVCA-R, EB, LnCap
320236	H03688		EST cluster (not in UniGene)	2.24	NCI-358, DU145, NCI-H23
315444	AW138821	Hs.221737	ESTs	2.24	NCI-358, CALU6, PRSC_con
333903			CH22_FGENES.294_1	2.24	MB-MDA-231, BT474, A549
335234			CH22_FGENES.515_3	2.24	NCI-H69, PRSC_con, PRSC_log
333727			CH22_FGENES.256_1	2.23	MB-MDA-231, NCI-H69, BT474
332002	AA482009	Hs.105104	ESTs	2.23	EB, NCI-H520, HT29
329611			CH.10_p2 gij3962478	2.23	BT474, HT29, MB-MDA-231
310559	AI783594	Hs.155718	ESTs	2.22	BT474, MCF7, MB-MDA-231
327315			CH.01_hs gij5867508	2.22	NCI-H69, EB, EB
323170	U83527		EST cluster (not in UniGene)	2.22	EB, DU145, LnCap
331522	N49309	Hs.117012	ESTs	2.22	A549, LnCap, DU145
313261	AA730472	Hs.142805	ESTs	2.22	OVCA-R, PC3, LnCap
312740	R97191	Hs.134106	ESTs	2.22	BT474, MCF7, OVCA-R
325055	Z44631	Hs.21658	ESTs	2.22	MB-MDA-453, DU145, CALU6
337895			CH22_EM:AC005500.GENSCAN.56-2	2.22	NCI-H345, PRSC_log, PRSC_con
307140	AI185762		EST singleton (not in UniGene) with exon	2.22	NCI-H520, NCI-H460, EB
321643	W76005	Hs.32094	ESTs	2.21	EB, NCI-H345, PRSC_con
302683	X85153		EST cluster (not in UniGene) with exon h	2.21	BT474, MB-MDA-231, MCF7
322644	AA340904		EST cluster (not in UniGene)	2.21	NCI-H460, NCI-H23, NCI-H520
330415	D83777	Hs.75137	KIAA0193 gene product	2.21	CALU6, A549, Caco2
302334	AF120491		EST cluster (not in UniGene) with exon h	2.21	NCI-H69, NCI-H345, PC3
326710			CH.20_hs gij5867593	2.21	NCI-H520, NCI-358, NCI-H23
323561	AA825426	Hs.238832	ESTs; Weakly similar to IIII ALU SUBFAMI	2.21	NCI-H345, DU145, NCI-H69
337706			CH22_EM:AC000097.GENSCAN.87-11	2.21	MB-MDA-435s, NCI-358, NCI-H520
339309			CH22_BA354112.GENSCAN.22-7	2.21	BT474, HT29, PC3
330436	HG2724-H		Oncogene TIs/Chop, Fusion Activated	2.21	PRSC_con, NCI-H69, Caco2
312360	AI922972	Hs.196073	ESTs	2.21	OVCA-R, MB-MDA-435s, DU145
301855	AF053356		multiple UniGene matches	2.2	NCI-H69, HT29, NCI-H23
331192	T55182	Hs.152571	ESTs; Highly similar to IGF-II mRNA-bind	2.2	OVCA-R, PC3, CALU6
315872	AW051819	Hs.204516	ESTs	2.2	LnCap, OVCA-R, EB
337904			CH22_EM:AC005500.GENSCAN.56-17	2.2	OVCA-R, LnCap, EB
308258	AI565612		EST singleton (not in UniGene) with exon	2.2	DU145, MB-MDA-231, CALU6
320965	H18166		EST cluster (not in UniGene)	2.2	DU145, EB, LnCap
333910			CH22_FGENES.295_3	2.2	DU145, MB-MDA-231, EB
300707	AA080921		EST cluster (not in UniGene) with exon h	2.2	BT474, MCF7, HT29
336011			CH22_FGENES.668_9	2.19	NCI-H460, BT474, NCI-H345
325712			CH.14_hs gij6682473	2.19	NCI-H460, NCI-H23, NCI-358
322738	AF201832		EST cluster (not in UniGene)	2.19	PC3, RPWE-2, PRSC_con
335339			CH22_FGENES.535_16	2.19	HT29, PRSC_log, MCF7
320733	AA738436	Hs.134407	ESTs	2.19	DU145, EB, Caco2
319412	AA679426	Hs.187505	ESTs	2.19	NCI-H345, PRSC_log, PRSC_con
337132			CH22_FGENES.526-3	2.19	NCI-H69, NCI-H345, PRSC_con
301544	AI951651	Hs.224290	ESTs	2.19	PRSC_con, MB-MDA-231, NCI-H23
325285			CH.11_hs gij5866903	2.18	PRSC_con, PRSC_log, MB-MDA-231
338280			CH22_EM:AC005500.GENSCAN.290-11	2.18	PC3, NCI-358, HT29
311421	AI701635	Hs.207077	ESTs	2.18	RPWE-2, NCI-H345, NCI-358
330638	X89576	Hs.159581	matrix metalloproteinase 17 (membrane-in	2.18	HT29, MB-MDA-435s, MB-MDA-453
326603			CH.20_hs gij6056312	2.18	CALU6, DU145, HT29
319055	AA412305		EST cluster (not in UniGene)	2.18	A549, OVCA-R, MB-MDA-435s
335451			CH22_FGENES.562_9	2.18	DU145, LnCap, CALU6
317989	AI203009	Hs.130664	ESTs	2.18	NCI-H345, NCI-H69, NCI-H520
322024	AA334384		EST cluster (not in UniGene)	2.18	Caco2, PC3, NCI-H520
300734	AW205197	Hs.240951	ESTs	2.18	NCI-358, A549, EB
304022	T02990		EST singleton (not in UniGene) with exon	2.18	NCI-H23, NCI-358, NCI-H460
330082			CH.19_p2 gij6015314	2.18	NCI-H23, Caco2, Caco2
312516	AA363245	Hs.189831	ESTs	2.18	BT474, HT29, MB-MDA-231
333932			CH22_FGENES.300_5	2.17	PC3, Caco2, EB
308115	AI479071		EST singleton (not in UniGene) with exon	2.17	BT474, OVCA-R, OVCA-R
320184	U91510	Hs.123036	CD39-like 1	2.17	NCI-H520, NCI-358, NCI-H23
324432	AA464510		EST cluster (not in UniGene)	2.17	CALU6, RPWE-2, HT29
320882	AI832098		EST cluster (not in UniGene)	2.17	OVCA-R, PC3, BT474

312251	H03952	EST cluster (not in UniGene)	2.17	NCI-H460, NCI-H23, NCI-358
315049	AW340486	Hs.121210 ESTs	2.17	NCI-H520, NCI-358, NCI-H23
305018	AA627127	EST singleton (not in UniGene) with exon	2.17	MB-MDA-231, MB-MDA-453, EB
303807	AI792785	Hs.130434 ESTs	2.16	NCI-H345, PRSC_con, PRSC_log
317792	AI653389	Hs.196121 ESTs	2.16	NCI-H345, PRSC_con, LnCap
321668	AA872730	Hs.125229 ESTs	2.16	OVCA-R, PC3, MCF7
328863		CH.07_hs gjl6381929	2.16	PRSC_con, NCI-H345, NCI-H460
319373	R00371	EST cluster (not in UniGene)	2.16	PRSC_con, RPWE-2, NCI-H345
320069	T86541	Hs.189732 ESTs	2.16	NCI-H23, NCI-358, NCI-H345
320235	AF064090	Hs.129708 tumor necrosis factor (ligand) superfam	2.16	NCI-H23, NCI-H460, NCI-H520
338880		CH22_DJ32110.GENSCAN.6-2	2.16	BT474, MCF7, OVCA-R
318314	AI091349	Hs.161133 ESTs	2.16	NCI-H23, NCI-H520, NCI-H460
332696	D86973	Hs.75354 GCN1 (general control of amino-acid synt	2.16	A549, PC3, DU145
331352	AA406133	Hs.7482 KIAA0682 gene product	2.16	PC3, EB, MB-MDA-231
339019		CH22_DA59H18.GENSCAN.21-15	2.15	LnCap, EB, OVCA-R
306975	AI127042	EST singleton (not in UniGene) with exon	2.15	MB-MDA-435s, NCI-H520, NCI-358
318069	AI024557	Hs.131540 ESTs	2.15	Caco2, Caco2, BT474
312997	AW205686	Hs.135130 ESTs	2.15	NCI-H460, NCI-H23, NCI-358
331372	AA433935	Hs.55044 DKFZP586H2123 protein	2.15	PRSC_con, HT29, CALU6
335049		CH22_FGENES.481_5	2.15	NCI-H69, NCI-H345, PRSC_log
324280	AA429772	Hs.191610 ESTs	2.15	MB-MDA-453, MB-MDA-435s, MCF7
330363		CH.X_p2 gjl3126882	2.15	NCI-H23, NCI-H460, NCI-358
322896	AW470296	Hs.144830 ESTs	2.15	HT29, CALU6, EB
321981	AA948204	Hs.127361 ESTs	2.15	MB-MDA-231, DU145, HT29
333294		CH22_FGENES.130_6	2.14	EB, DU145, MB-MDA-453
330170		CH.02_p2 gjl6648220	2.14	HT29, MB-MDA-453, PC3
312973	AI123346	Hs.135241 ESTs	2.14	LnCap, DU145, EB
311104	AI627352	Hs.201449 ESTs	2.14	NCI-H520, NCI-H23, LnCap
325086	T10019	Hs.4194 ESTs	2.14	NCI-H460, NCI-H23, NCI-358
317182	AW183524	Hs.192298 ESTs	2.14	HT29, BT474, MB-MDA-435s
323644	AA310711	Hs.124340 ESTs	2.14	RPWE-2, PRSC_con, PRSC_log
308092	AI474896	EST singleton (not in UniGene) with exon	2.14	BT474, MCF7, MB-MDA-231
322265	AF086244	EST cluster (not in UniGene)	2.14	NCI-H345, RPWE-2, PRSC_con
303521	AA746272	EST cluster (not in UniGene) with exon h	2.14	DU145, MB-MDA-453, EB
312102	AW439340	Hs.189720 ESTs	2.14	NCI-H23, NCI-H460, MB-MDA-435s
316559	AI249468	Hs.228251 EST	2.14	NCI-H460, NCI-358, NCI-H23
338486		CH22_EM:AC005500.GENSCAN.382-8	2.14	NCI-H520, NCI-H23, NCI-H69
301302	AI825444	Hs.210956 ESTs	2.14	BT474, HT29, MB-MDA-231
310591	AI650372	Hs.195979 ESTs	2.14	CALU6, CALU6, Caco2
316231	AA732301	EST cluster (not in UniGene)	2.14	NCI-H23, NCI-H520, NCI-358
326559		CH.19_hs gjl5867310	2.14	DU145, NCI-H460, NCI-H23
324062	AA525291	Hs.204099 ESTs; Weakly similar to !!!! ALU SUBFAM1	2.13	OVCA-R, DU145, EB
323844	AI811303	Hs.143490 ESTs	2.13	MB-MDA-453, MCF7, MB-MDA-435s
333895		CH22_FGENES.293_2	2.13	CALU6, LnCap, DU145
308264	AI567114	Hs.171454 EST	2.13	DU145, CALU6, MB-MDA-453
306081	AA908472	EST singleton (not in UniGene) with exon	2.13	HT29, BT474, MB-MDA-231
333101		CH22_FGENES.79_6	2.13	NCI-H345, NCI-H69, PRSC_log
328544		CH.07_hs gjl5868486	2.13	NCI-H23, NCI-H69, PRSC_log
333355		CH22_FGENES.141_6	2.13	DU145, EB, CALU6
323397	AI524519	Hs.239699 ESTs	2.13	EB, NCI-H460, NCI-H345
305697	AA814956	EST singleton (not in UniGene) with exon	2.13	NCI-H520, NCI-H460, NCI-358
327809		CH.05_hs gjl5867968	2.13	HT29, PC3, OVCA-R
325092	T10115	Hs.92423 ESTs	2.13	HT29, NCI-358, MB-MDA-231
322299	AI971935	Hs.252784 ESTs	2.13	PRSC_con, DU145, DU145
312145	AA029526	Hs.126706 ESTs	2.12	OVCA-R, A549, MB-MDA-435s
323704	AA319421	Hs.193577 ESTs	2.12	Caco2, LnCap, OVCA-R
328971		CH.08_hs gjl6478806	2.12	NCI-358, NCI-H23, NCI-H520
325338		CH.11_hs gjl5866883	2.12	LnCap, NCI-H69, NCI-H345
331332	AA282554	Hs.89034 ESTs	2.12	NCI-H520, NCI-H23, Caco2
327159		CH.01_hs gjl5867550	2.12	EB, DU145, PC3
335180		CH22_FGENES.505_2	2.12	LnCap, NCI-H69, A549
338062		CH22_EM:AC005500.GENSCAN.162-3	2.12	PRSC_con, PRSC_log, NCI-H69
318350	AI636018	Hs.135538 ESTs	2.12	EB, HT29, DU145
312070	AW293140	Hs.108790 ESTs	2.11	Caco2, NCI-H23, A549
328314		CH.07_hs gjl5868371	2.11	HT29, NCI-H23, NCI-H460
315869	AI033547	Hs.132826 ESTs	2.11	BT474, CALU6, MCF7
339246		CH22_BA354112.GENSCAN.5-9	2.11	CALU6, CALU6, BT474
329921		CH.16_p2 gjl6165205	2.11	BT474, MB-MDA-231, HT29
324981	Z25333	Hs.4947 ESTs	2.11	A549, NCI-H460, NCI-H520
331291	AA159323	Hs.109929 ESTs	2.11	NCI-H345, A549, PRSC_con
332729	AA058907	Hs.83190 fatty acid synthase	2.11	NCI-358, LnCap, MB-MDA-453
325448		CH.12_hs gjl5866941	2.11	DU145, MCF7, CALU6
314929	AW188286	Hs.143612 ESTs	2.1	EB, BT474, MB-MDA-231
301063	AI057634	Hs.124596 ESTs	2.1	NCI-H23, NCI-H460, BT474
301952	AB029016	Hs.117333 KIAA1093 protein	2.1	OVCA-R, A549, CALU6
326309		CH.17_hs gjl5867277	2.1	MB-MDA-435s, NCI-H69, MB-MDA-453

315406	AI823453	Hs.146625	ESTs	2.1	OVCA-R, DU145, EB
302376	AB007867	Hs.200480	KIAA0407 protein	2.1	OVCA-R, Caco2, HT29
312181	AA417281	Hs.191595	ESTs	2.1	OVCA-R, A549, DU145
334254			CH22_FGENES.366_4	2.1	LnCap, OVCA-R, DU145
318073	AW167087	Hs.131562	ESTs	2.1	A549, CALU6, EB
304724	AA569881	Hs.65114	keratin 18	2.1	NCI-H23, NCI-H520, NCI-H460
332359	W87704	Hs.211558	ESTs	2.1	MB-MDA-435s, PRSC_con, NCI-H460
331884	AA431302	Hs.98721	EST; Weakly similar to N-copine [H.sapie	2.1	NCI-H345, MB-MDA-231, PRSC_con
308226	AI559106	Hs.181165	eukaryotic translation elongation factor	2.1	EB, CALU6, OVCA-R
324279	AA501412	Hs.191688	ESTs; Weakly similar to Pro-Pol-dUTPase	2.09	OVCA-R, LnCap, PC3
337203			CH22_FGENES.591-3	2.09	NCI-H69, NCI-H345, MB-MDA-231
322346	AA227618	Hs.10882	HMG-box containing protein 1	2.09	HT29, BT474, MB-MDA-231
304470	AA426654	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	2.09	NCI-H23, CALU6, NCI-H520
325977			CH.16_hs gi 6249602	2.09	NCI-H23, NCI-H520, HT29
304696	AA554758		EST singleton (not in UniGene) with exon	2.09	MB-MDA-435s, NCI-H23, BT474
317412	AI301528	Hs.132604	ESTs	2.09	Caco2, EB, NCI-358
315570	AI860360	Hs.160316	ESTs	2.08	PRSC_con, PRSC_log, NCI-H345
327341			CH.01_hs gi 6017016	2.08	MB-MDA-231, PRSC_con, NCI-H69
327431			CH.02_hs gi 5867754	2.08	NCI-H23, NCI-358, NCI-H520
314685	AI870811	Hs.158709	ESTs; Weakly similar to KIAA0938 protein	2.08	MB-MDA-453, MCF7, OVCA-R
328624			CH.07_hs gi 5868246	2.08	MCF7, NCI-358, RPWE-2
303596	AW303377		EST cluster (not in UniGene) with exon h	2.08	RPWE-2, PRSC_con, PRSC_log
336717			CH22_FGENES.81-1	2.08	BT474, HT29, MCF7
317370	AW204139	Hs.174424	ESTs; Weakly similar to p140mDia [M.musc	2.08	NCI-H23, NCI-H460, NCI-H69
331287	AA149061	Hs.172971	ESTs	2.08	OVCA-R, EB, NCI-H345
304211	N62228		EST singleton (not in UniGene) with exon	2.08	BT474, MCF7, MB-MDA-231
315613	AW137420	Hs.192311	ESTs	2.08	PRSC_con, PRSC_log, PRSC_log
325636			CH.14_hs gi 5867002	2.08	NCI-358, NCI-H460, MB-MDA-453
336406			CH22_FGENES.823_21	2.08	HT29, EB, DU145
301714	F06529		EST cluster (not in UniGene) with exon h	2.08	LnCap, PRSC_log, PRSC_con
300496	R45159	Hs.221804	ESTs	2.08	PRSC_con, LnCap, RPWE-2
318970	R21114	Hs.21383	ESTs	2.08	NCI-H23, NCI-H520, NCI-H460
334115			CH22_FGENES.330_15	2.08	BT474, NCI-H69, HT29
308082	AI473682		EST singleton (not in UniGene) with exon	2.08	MB-MDA-435s, NCI-H345, MB-MDA-231
308282	AI569456		EST singleton (not in UniGene) with exon	2.08	LnCap, EB, PRSC_con
313038	AW451618	Hs.124195	ESTs	2.07	NCI-H345, PRSC_con, LnCap
317974	AW444468	Hs.144900	ESTs	2.07	NCI-358, NCI-H23, NCI-H520
324063	AW292740	Hs.254815	ESTs	2.07	Caco2, NCI-358, NCI-H520
334759			CH22_FGENES.428_8	2.07	CALU6, HT29, NCI-H520
307864	AI367417		EST singleton (not in UniGene) with exon	2.07	NCI-H460, NCI-358, NCI-H23
304356	AA196027	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	2.07	HT29, MCF7, MB-MDA-435s
303929	AW470753		EST singleton (not in UniGene) with exon	2.07	NCI-H345, PRSC_con, RPWE-2
331857	AA421160	Hs.9456	SWI/SNF related; matrix assocd; actin de	2.07	EB, A549, PC3
322814	AI824495	Hs.211038	ESTs	2.06	PRSC_con, RPWE-2, Caco2
303650	AA430709		EST cluster (not in UniGene) with exon h	2.06	RPWE-2, NCI-H345, PRSC_con
333403			CH22_FGENES.144_21	2.06	OVCA-R, CALU6, PC3
313663	AI953261	Hs.169813	ESTs	2.06	NCI-H345, OVCA-R, NCI-H23
338594			CH22_EM:AC005500.GENSCAN.435-4	2.06	DU145, LnCap, EB
334676			CH22_FGENES.418_29	2.06	NCI-H69, PRSC_log, PRSC_con
310046	AI198032	Hs.210356	ESTs	2.06	MB-MDA-435s, NCI-H23, Caco2
309169	AI949216		EST singleton (not in UniGene) with exon	2.06	CALU6, EB, NCI-358
329752			CH.14_p2 gi 6065777	2.06	CALU6, HT29, DU145
325085	T10001	Hs.4188	ESTs	2.06	EB, OVCA-R, MB-MDA-435s
332062	AA521016	Hs.185375	ESTs	2.06	OVCA-R, MB-MDA-453, MCF7
302074	AA382871	Hs.132794	phosphate cytidylyltransferase 1; cholin	2.06	LnCap, EB, NCI-H69
326344			CH.17_hs gi 6525295	2.06	HT29, BT474, MB-MDA-453
330855	AA079318		zm98c2.s1 Stratagene colon HT29 (#937221		
			IMAGE:545954 3', mRNA seq	2.06	RPWE-2, LnCap, PRSC_con
302525	AF024690	Hs.248056	G protein-coupled receptor 43	2.05	NCI-358, NCI-H23, DU145
331903	AA436673	Hs.29417	H sapiens mRNA; cDNA DKFZp586B0323 (from	2.05	Caco2, DU145, A549
316322	AW296618	Hs.120637	ESTs	2.05	BT474, MB-MDA-453, OVCA-R
321525	H78875		EST cluster (not in UniGene)	2.05	NCI-H23, PRSC_con, NCI-H520
305071	AA640579		EST singleton (not in UniGene) with exon	2.05	MB-MDA-231, BT474, HT29
326033			CH.17_hs gi 5867178	2.05	HT29, DU145, BT474
334730			CH22_FGENES.424_5	2.05	BT474, EB, OVCA-R
305335	AA704235		EST singleton (not in UniGene) with exon	2.05	MCF7, OVCA-R, MB-MDA-453
320521	N31464	Hs.24743	ESTs	2.05	MB-MDA-453, MB-MDA-231, PC3
333515			CH22_FGENES.172_5	2.04	NCI-H345, RPWE-2, PRSC_con
311020	AI918672	Hs.213783	ESTs	2.04	NCI-H460, NCI-H23, NCI-H520
324323	AA393739		EST cluster (not in UniGene)	2.04	OVCA-R, PC3, LnCap
305486	AA748889		EST singleton (not in UniGene) with exon	2.04	NCI-H345, PRSC_log, CALU6
312162	T91823		EST cluster (not in UniGene)	2.04	NCI-H520, NCI-H23, NCI-358
330980	H28794	Hs.6659	ESTs	2.04	MCF7, MB-MDA-453, MB-MDA-435s
317463	AA927290	Hs.130462	ESTs	2.04	NCI-H23, Caco2, NCI-H69
303460	AA700155	Hs.117900	ESTs	2.04	DU145, EB, CALU6
337435			CH22_FGENES.766-2	2.03	NCI-H345, OVCA-R, LnCap

305464	AA742425	EST singleton (not in UniGene) with exon	2.03	CALU6, NCI-H520, NCI-358
307918	AI383496	EST singleton (not in UniGene) with exon	2.03	NCI-H23, BT474, MB-MDA-231
322209	H89360	EST cluster (not in UniGene)	2.03	DU145, OVCA-R, MB-MDA-453
310295	AW205198	Hs.149146 ESTs	2.03	NCI-H23, NCI-H460, NCI-358
325886		CH.16_hs gij5867087	2.03	NCI-H345, NCI-H345, RPWE-2
329719		CH.14_p2 gij6065785	2.03	NCI-H69, RPWE-2, PRSC_con
309247	AI972768	EST singleton (not in UniGene) with exon	2.03	LnCap, PRSC_con, RPWE-2
328277		CH.07_hs gij6004471	2.03	LnCap, RPWE-2, A549
307296	AI205705	Hs.147222 EST	2.03	NCI-H460, NCI-358, NCI-H23
327203		CH.01_hs gij5867447	2.03	HT29, BT474, MB-MDA-231
306866	AI086683	EST singleton (not in UniGene) with exon	2.03	BT474, NCI-H345, HT29
333339		CH22_FGENES.139_8	2.03	HT29, DU145, CALU6
323115	AI921875	EST cluster (not in UniGene)	2.03	BT474, BT474, MB-MDA-231
304811	AA584361	EST singleton (not in UniGene) with exon	2.03	NCI-H23, NCI-358, NCI-H460
323372	AL135125	Hs.13913 ESTs	2.02	DU145, EB, A549
312854	AA828713	EST cluster (not in UniGene)	2.02	NCI-H345, PRSC_con, PRSC_log
307904	AI381019	EST singleton (not in UniGene) with exon	2.02	HT29, MCF7, MB-MDA-453
332099	AA608983	af5d4.s1 Soares_testis_NHT H sapiens cDN	2.02	PRSC_con, NCI-H345, RPWE-2
324634	AI684571	Hs.175831 ESTs	2.02	NCI-H460, Caco2, NCI-358
335721		CH22_FGENES.599_24	2.02	NCI-H69, PRSC_log, NCI-H345
312452	AI692643	Hs.172749 ESTs	2.02	HT29, Caco2, MB-MDA-231
325396		CH.12_hs gij5866921	2.01	HT29, NCI-H520, NCI-H460
328770		CH.07_hs gij6017031	2.01	NCI-H23, NCI-H460, NCI-358
335585		CH22_FGENES.581_24	2.01	MB-MDA-453, DU145, MCF7
335634		CH22_FGENES.584_14	2.01	NCI-H23, NCI-H460, NCI-H69
338271		CH22_EM:AC005500.GENSCAN.287-1	2.01	MCF7, DU145, PC3
328607		CH.07_hs gij5868233	2.01	NCI-H460, NCI-H23, NCI-358
307050	AI147341	Hs.146734 EST	2.01	NCI-H520, NCI-H23, NCI-358
334946		CH22_FGENES.465_13	2.01	CALU6, BT474, DU145
319793	R56360	EST cluster (not in UniGene)	2.01	NCI-H460, HT29, NCI-358
307223	AI193698	Hs.184776 ribosomal protein L23a	2.01	NCI-358, NCI-H520, NCI-H23
312627	AA344698	Hs.133169 ESTs	2.01	PC3, LnCap, MB-MDA-231
329221		CH.X_hs gij5868727	2.01	NCI-H345, NCI-H69, NCI-358
305145	AA653589	EST singleton (not in UniGene) with exon	2.01	LnCap, EB, OVCA-R
328428		CH.07_hs gij5868417	2.01	NCI-H69, MB-MDA-453, BT474
305990	AA888866	Hs.125919 EST	2.01	NCI-H520, NCI-358, NCI-H23
319368	R00003	Hs.133171 ESTs	2	OVCA-R, LnCap, PC3
324805	AA927002	Hs.131350 ESTs	2	NCI-H460, NCI-H23, NCI-358
301138	AA719179	Hs.189419 ESTs	2	NCI-H69, NCI-H23, PRSC_con
304675	AA541740	EST singleton (not in UniGene) with exon	2	NCI-H460, NCI-H520, MB-MDA-231
326194		CH.17_hs gij5867213	2	HT29, NCI-358, BT474

Table 5: H chip – B survivor vs Met query – up in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

Pkey	Ex Accn	UniG_ID	Complete_Title	Ratio Met/B surv.
102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	5.56
128530	AA504343	Hs.183475	Homo sapiens clone 25061 mRNA sequence	4.62
129093	AA262710	Hs.108614	KIAA0627 protein	4.23
124690	R05818	Hs.173830	ESTs	3.96
115558	AA393806	Hs.1010	regulator of mitotic spindle assembly 1	3.39
134261	AA227678	Hs.8084	Humn DNA sequence from clone 465N24 on c3.22	
104792	AA029288	Hs.29147	ESTs; Highly similar to ZINC FINGER PROT	3.17
133770	M69197	Hs.242279	haptoglobin-related protein	3.07

Table 6: H chip – B survivor vs Met query – down in Mets

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Ex Accn	UnlG_ID	Complete_Title	Ratio Met/B surv.
100116	D00654	Hs.77443	actin; gamma 2; smooth muscle; enteric	0.07
101923	S75256		HNL=neutrophil lipocalin [human, ovarian	0.2
129982	M87789	Hs.140	immunoglobulin gamma 3 (Gm marker)	0.2
130064	T67053	Hs.181125	immunoglobulin lambda gene cluster	0.2

Table 7: I chip – B survivor vs Met query – up in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

Pkey	Ex_Accn	UniG_ID	Title	Ratio Met/B surv
319379	T91443	Hs.193963	ESTs	19.65
321920	N63915			11.9
324302	AA543008	Hs.136806	ESTs; Weakly similar to IIII ALU SUBFAM I	9.31
314522	AI732331	Hs.187750	ESTs; Moderately similar to IIII ALU CLA	5.79
331433	H68097	Hs.161023	EST	4.79
324643	AI436356	Hs.130729	ESTs	4.59
332471	AA416967	Hs.120980	nuclear receptor co-repressor 2	4.58
314915	AA573072	Hs.187748	ESTs; Weakly similar to IIII ALU SUBFAM I	4.3
321354	AA078493		EST cluster (not in UniGene)	4.26
322309	AF086372		EST cluster (not in UniGene)	3.89
325100	T10265	Hs.116122	ESTs; Weakly similar to coded for by C.	3.81
314071	AA192455	Hs.188690	ESTs	3.74
315178	AW362945	Hs.162459	ESTs	3.66
330987	H40988	Hs.131965	ESTs; Weakly similar to IIII ALU SUBFAM I	3.51
337898			CH22_EM:AC005500.GENSCAN.56-5	3.21
319403	T98413		EST cluster (not in UniGene)	3.2
331469	N22273	Hs.39140	ESTs	3.15
331549	N56866	Hs.237507	EST	3.14
331644	T99544	Hs.173734	ESTs; Weakly similar to IIII ALU CLASS B	3.14
313220	AI971981	Hs.118241	ESTs	3.04

Table 8: I chip – B survivor vs Met query – down in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

Pkey	Ex_Accn	UniG_ID	Title	Ratio Met/B surv
333658			CH22_FGENES.241_4	0.06
333657			CH22_FGENES.241_2	0.07
333654			CH22_FGENES.240_2	0.07
332859			CH22_FGENES.27_2	0.07
333656			CH22_FGENES.240_4	0.07
304480	AA430373		EST singleton (not in UniGene) with exon	0.08
333737			CH22_FGENES.261_1	0.09
308601	AI719930		EST singleton (not in UniGene) with exon	0.1
334030			CH22_FGENES.320_2	0.1
333637			CH22_FGENES.229_2	0.13
302347	AF039400	Hs.194659	chloride channel; calcium activated; fam	0.16
333653			CH22_FGENES.239_2	0.16
333635			CH22_FGENES.228_2	0.19
333647			CH22_FGENES.235_2	0.19
307588	AI285535		EST singleton (not in UniGene) with exon	0.2
337954			CH22_EM:AC005500.GENSCAN.96-3	0.2
333588			CH22_FGENES.206_2	0.21
320244	AA296922	Hs.129778	gastrointestinal peptide	0.22
333642			CH22_FGENES.231_2	0.23
337951			CH22_EM:AC005500.GENSCAN.94-1	0.23
333730			CH22_FGENES.258_1	0.23
333646			CH22_FGENES.234_2	0.24

Table 9: H chip – B survivor vs Met query – up in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

Pkey	Ex Accn	UniGID	Complete_Title	Median Mets AI vs Median B-Sur AI
100655	HG2841-HT2970		Albumin, Alt. Splice 5	11.98
124875	R70506	Hs.207693	ESTs; Weakly similar to IIII ALU SUBFAMI	9.21
102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	6.73
100654	HG2841-HT2969		Albumin, Alt. Splice 3, Missplicing In Alloalbumin Venezia	6.18
118828	N79496	Hs.50824	EST	5.93
128046	AA873285	Hs.137947	ESTs	5.9
128896	D14446	Hs.107	fibrinogen-like 1	5.17
127917	AA211895	Hs.118831	EST; Highly similar to dJ1163J1.2.1 [H.s	5.11
125090	T91518		ye20f05.s1 Stratagene lung (#937210) Hom	4.47
118579	N68905		small inducible cytokine A5 (RANTES)	4.23
123526	AA608657		ESTs; Moderately similar to IIII ALU SUB	4.21
128062	AA379500	Hs.193155	ESTs	4.14
119174	R71234		yi54c08.s1 Soares placenta Nb2HP Homo sa	4.11
128530	AA504343	Hs.183475	Homo sapiens clone 25061 mRNA sequence	4.09
119404	T92950		ye27c10.s1 Stratagene lung (#937210) Hom	3.98
118475	N66845	Hs.165411	ESTs; Weakly similar to IIII ALU CLASS B	3.96
129974	K00629	Hs.199300	Human kpnl repeat mma (cdna clone pcd-k	3.87
108888	AA135606	Hs.189384	ESTs; Weakly similar to IIII ALU SUBFAMI	3.85
123963	C13961	Hs.210115	EST	3.8
123523	AA608588	Hs.193634	ESTs	3.76
128230	AA984074	Hs.176757	ESTs	3.75
124090	H09570	Hs.143032	ESTs; Weakly similar to neuronal thread	3.67
124690	R05818	Hs.173830	ESTs	3.58
134261	AA227678	Hs.8084	Human DNA sequence from clone 465N24 on	3.57
126917	AA176225	Hs.193929	ESTs	3.52
126050	H27267	Hs.75860	hydroxyacyl-Coenzyme A dehydrogenase/3-k	3.45
126649	AA856990	Hs.125058	ESTs	3.42
115096	AA255991	Hs.175319	ESTs	3.4
129906	H39216	Hs.239970	ESTs; Weakly similar to ZNF91L [H.sapien	3.38
123022	AA480909		aa28f10.s1 NCI_CGAP_GCB1 Homo sapiens cD	3.38
106145	AA424791	Hs.5734	KIAA0679 protein	3.38
125191	W67257	Hs.138871	ESTs; Weakly similar to IIII ALU CLASS B	3.36
108836	AA132061	Hs.222727	ESTs; Weakly similar to ubiquitous TPR m	3.3
128710	J04813	Hs.104117	cytochrome P450; subfamily IIIA (niphedi	3.27
123460	AA598981	Hs.251122	EST	3.25
133735	AC002045	Hs.251928	nuclear pore complex interacting protein	3.24
124696	R06273	Hs.186467	ESTs; Moderately similar to IIII ALU SUB	3.24
120748	AA303153	Hs.237994	EST; Weakly similar to IIII ALU SUBFAMIL	3.21
133770	M69197	Hs.242279	haptoglobin-related protein	3.17
128336	AI242720	Hs.146043	ESTs; Weakly similar to alternatively sp	3.14
135357	AA235803	Hs.79572	cathepsin D (lysosomal aspartyl protease	3.12
128088	R02443	Hs.186467	ESTs; Moderately similar to IIII ALU SUB	3.08
124055	F10904	Hs.100516	Homo sapiens clone 23605 mRNA sequence	3.06
124896	R82063	Hs.101594	EST	3.06
127598	AA610677	Hs.168851	ESTs	3.04
116802	H44061	Hs.194026	ESTs	3.01

Table 10: H chip – B survivor vs Met query – Down in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

Pkey	Ex Accn	Unig_ID	Complete_Title	Ratio Met/B surv.
100116	D00654	Hs.77443	actin; gamma 2; smooth muscle; enteric	0.09
130064	T67053	Hs.181125	immunoglobulin lambda gene cluster	0.11
129982	M87789	Hs.140	immunoglobulin gamma 3 (Gm marker)	0.12
131219	C00476	Hs.24395	small inducible cytokine subfamily B (Cy	0.13
133806	M12759	Hs.76325	Human Ig J chain gene	0.17
132982	L02326	Hs.198118	immunoglobulin lambda-like polypeptide 2	0.18
131713	X57809	Hs.181125	immunoglobulin lambda gene cluster	0.18
131791	S71043	Hs.32225	immunoglobulin alpha 1	0.2
133725	V00563	Hs.179543	immunoglobulin mu	0.22
101923	S75256		HNL=neutrophil lipocalin [human, ovarian	0.23
101461	M22430	Hs.76422	phospholipase A2; group IIA (platelets;	0.24
103448	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	0.24

Table 11: H chip – Met vs Normal query – up in Mets

		Pkey:	Unique Eos probeset identifier number			
		ExAccn:	Exemplar Accession number, Genbank accession number			
		UnigeneID:	Unigene number			
		Unigene Title:	Unigene gene title			
Pkey	Ex Accn	UniG_ID	Complete_Title	Median Mets AI vs Median Normal AI		
100655	HG2841-HT2970		Albumin, Alt. Splice 5	15.91		
102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	6.83		
124875	R70506	Hs.207693	ESTs; Weakly similar to IIII ALU SUBFAMI	6.68		
100654	HG2841-HT2969		Albumin, Alt. Splice 3, Missplicing In Alloalbumin Venezia	5.28		
124059	F13673	Hs.99769	ESTs	5.11		
128896	D14446	Hs.107	fibrinogen-like 1	5.05		
134453	X70683	Hs.83484	SRY (sex determining region Y)-box 4	4.82		
131564	AA491465	Hs.28792	ESTs	4.78		
127917	AA211895	Hs.118831	EST; Highly similar to dJ1163J1.2.1 [H.s	4.76		
115096	AA255991	Hs.175319	ESTs	4.67		
104558	R56678	Hs.88959	Human DNA sequence from clone 967N21 on	4.63		
123526	AA608657		ESTs; Moderately similar to IIII ALU SUB	4.61		
125090	T91518		ye20f05.s1 Stratagene lung (#937210) Hom	4.59		
129666	M77349	Hs.118787	transforming growth factor, beta-induced	4.58		
118828	N79496	Hs.50824	EST	4.56		
128046	AA873285	Hs.137947	ESTs	4.45		
133421	AA436560	Hs.7327	claudin 1	4.09		
129158	J05257	Hs.109	dipeptidase 1 (renal)	4.04		
128062	AA379500	Hs.193155	ESTs	4.03		
124696	R06273	Hs.186467	ESTs; Moderately similar to IIII ALU SUB	4.01		
118475	N66845	Hs.165411	ESTs; Weakly similar to IIII ALU CLASS B	3.96		
104755	AA024482	Hs.9029	DKFZP434G032 protein	3.83		
104978	AA088458	Hs.19322	ESTs	3.74		
118579	N68905		small inducible cytokine A5 (RANTES)	3.7		
123796	AA620390	Hs.247444	ESTs	3.62		
127240	AA888387	Hs.243845	ESTs; Moderately similar to IIII ALU SUB	3.61		
104105	AA422123	Hs.42457	ESTs	3.55		
129349	D86974	Hs.110613	KIAA0220 protein	3.54		
119329	T51832		ESTs; Moderately similar to IIII ALU SUB	3.53		
114617	AA084148	Hs.110659	ESTs	3.52		
123143	AA487595		aa95e2.s1 Stratagene fetal retina 93722	3.48		
103119	X63629	Hs.2877	cadherin 3; P-cadherin (placental)	3.48		
119404	T92950		ye27c10.s1 Stratagene lung (#937210) Hom	3.47		
123963	C13961	Hs.210115	EST	3.47		
116480	C14088	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	3.4		
108836	AA132061	Hs.222727	ESTs; Weakly similar to ubiquitous TPR m	3.39		
120748	AA303153	Hs.237994	EST; Weakly similar to IIII ALU SUBFAMIL	3.38		
133770	M69197	Hs.242279	haptoglobin-related protein	3.38		
132358	X60486	Hs.46423	H4 histone family; member G	3.37		
127759	AI369384		arylsulfatase D	3.37		
129095	L12350	Hs.108623	thrombospondin 2	3.37		
128261	AI061213	Hs.13179	ESTs; Moderately similar to IIII ALU SUB	3.36		
126908	AA169866		ESTs; Weakly similar to IIII ALU SUBFAMI	3.36		
128954	N32118	Hs.209100	DKFZP434C171 protein	3.34		
119174	R71234		yi54c08.s1 Soares placenta Nb2HP Homo sa	3.33		
106687	AA463234	Hs.119387	KIAA0792 gene product	3.32		
128230	AA984074	Hs.176757	ESTs	3.3		
126649	AA856990	Hs.125058	ESTs	3.25		
124620	N74051	Hs.194092	ESTs; Weakly similar to IIII ALU SUBFAMI	3.24		
135427			AFFX control: human alu repeats	3.23		
129967	H99653	Hs.138618	ESTs	3.22		
125191	W67257	Hs.138871	ESTs; Weakly similar to IIII ALU CLASS B	3.2		
124684	R02401	Hs.221078	ESTs	3.2		
128010	AA856953	Hs.23348	S-phase kinase-associated protein 2 (p45	3.17		
119423	T99544	Hs.173734	ESTs; Weakly similar to IIII ALU CLASS B	3.16		
123022	AA480909		aa28f10.s1 NCL_CGAP_GCB1 Homo sapiens cD	3.15		
103654	Z70759		H.sapiens mitochondrial 16S rRNA gene (p	3.13		
128336	AI242720	Hs.146043	ESTs; Weakly similar to alternatively sp	3.12		
124690	R05818	Hs.173830	ESTs	3.1		
129791	F02778	Hs.173887	KIAA0876 protein	3.07		
114472	AA028924	Hs.177407	ESTs; Weakly similar to IIII ALU SUBFAMI	3.07		
115429	AA284139	Hs.89295	EST	3.06		
130020	AA433930	Hs.240443	ESTs; Weakly similar to HNK-1 sulfotrans	3.06		
126050	H27267	Hs.75860	hydroxyacyl-Coenzyme A dehydrogenase/3-k	3.05		

129906	H39216	Hs.239970	ESTs; Weakly similar to ZNF91L [H.sapien	3.04
123422	AA598484	Hs.238476	EST	3.03
103059	X57351	Hs.174195	Interferon induced transmembrane protein	3.02
124253	H69742	Hs.102201	ESTs	3.02
123523	AA608588	Hs.193634	ESTs	3.02
132669	AA188378	Hs.54602	ESTs; Weakly similar to 60S RIBOSOMAL PR3.02	
123196	AA489250	Hs.59403	serine palmitoyltransferase; subunit II	3.01
122948	AA477483		zu44h2.s1 Soares ovary tumor NbHOT Homo	3.01
119053	R11501		yf28f1.s1 Soares fetal liver spleen 1NFL	3.01
125953	H40829		yo05d11.r1 Soares adult brain N2b5HB55Y	3
119155	R61715	Hs.138237	ESTs	3

Table 12: H chip – Met vs Normal query – down in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

Pkey	Ex Accn	UniG_ID	Complete_Title	Median Mets AI vs Median Normal AI
103466	Y00339	Hs.155097	carbonic anhydrase II	0.01
104258	AF007216	Hs.5462	solute carrier family 4; sodium bicarbon	0.02
108999	AA156064	Hs.72115	ESTs	0.04
101046	K01160		Accession not listed in Genbank	0.04
133565	H57056	Hs.204831	ESTs	0.05
101346	L76465	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	0.05
123137	AA487468	Hs.100686	ESTs; Weakly similar to secreted cement	0.05
134534	X73501	Hs.84905	H. Sapiens mRNA for cytokeratin 20	0.05
118823	N79237	Hs.50813	ESTs; Weakly similar to long chain fatty	0.06
102095	U11313	Hs.75760	sterol carrier protein 2	0.06
111855	R37362	Hs.21351	ESTs	0.06
129105	AA224351	Hs.108681	ESTs	0.07
130320	U19495	Hs.237356	stromal cell-derived factor 1	0.07
113778	W15263	Hs.5422	ESTs	0.07
116786	H25836	Hs.83429	tumor necrosis factor (ligand) superfam	0.07
100116	D00654	Hs.77443	actin; gamma 2; smooth muscle; enteric	0.07
104636	AA004415	Hs.106106	ESTs	0.07
107032	AA599472	Hs.247309	succinate-CoA ligase; GDP-forming; beta	0.08
106605	AA457718	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	0.08
128906	AA487557	Hs.10706	ESTs	0.08
130016	AA055811	Hs.143131	transmembrane glycoprotein	0.08
113523	T90037	Hs.16686	ESTs	0.08
102638	U67319	Hs.9216	caspase 7; apoptosis-related cysteine pr	0.09
124308	H93575	Hs.227146	Homo sapiens mRNA; cDNA DKFZp564J142 (fr	0.09
129519	AA298786	Hs.112242	ESTs	0.09
134749	L10955	Hs.89485	carbonic anhydrase IV	0.09
130366	L11708	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	0.09
109272	AA195718	Hs.86030	ESTs	0.09
102124	U14528	Hs.29981	solute carrier family 26 (sulfate transp	0.1
132711	N73702	Hs.238927	ESTs	0.1
131861	D11925	Hs.184245	KIAA0929 protein Msx2 interacting nuclea	0.1
133806	M12759	Hs.76325	Human Ig J chain gene	0.1
102571	U60115		Homo sapiens skeletal muscle LIM-protein	0.1
114846	AA234929	Hs.44343	ESTs	0.11
131328	V01512	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	0.11
106569	AA455983	Hs.117816	sorcin	0.11
103542	Z11793	Hs.3314	selenoprotein P; plasma; 1	0.11
128915	C02386	Hs.107139	ESTs	0.11
120914	AA377254	Hs.97107	EST	0.11
130867	J04093	Hs.2056	UDP glycosyltransferase 1	0.11
110837	N30796	Hs.17424	ESTs; Weakly similar to semaphorin F [H.	0.12
101877	M97496	Hs.778	guanylate cyclase activator 1B (retina)	0.12
132617	AA171913	Hs.5338	carbonic anhydrase XII	0.12
129113	AA147646	Hs.108740	DKFZP586A0522 protein	0.12
133435	T23983	Hs.7365	ESTs	0.13
132836	F09557	Hs.57929	slit (Drosophila) homolog 3	0.13
125832	AA628600	Hs.117587	ESTs	0.13
104613	AA001049	Hs.24713	Homo sapiens mRNA; cDNA DKFZp586G0123 (f	0.13
132903	AA235404	Hs.5985	Homo sapiens clone 25186 mRNA sequence	0.13
119479	W32094	Hs.55501	ESTs	0.14
131273	AA421139	Hs.173542	ESTs	0.14
106674	AA461303	Hs.7946	DKFZP586D1519 protein	0.14
108980	AA151676	Hs.33455	peptidyl arginine delminase; type II	0.14
103211	X73079	Hs.205126	polymeric immunoglobulin receptor	0.14
131219	C00476	Hs.24395	small inducible cytokine subfamily B (Cy	0.15
116459	AA621399	Hs.64193	ESTs	0.15
130219	R77539	Hs.15285	ESTs	0.15
113863	W68388	Hs.21288	ESTs; Weakly similar to KIAA0704 protein	0.15
101564	M32886	Hs.117816	sorcin	0.15
109502	AA233837	Hs.44755	ESTs; Weakly similar to membrane glycopr	0.15
107222	D51235	Hs.82689	tumor rejection antigen (gp96) 1	0.15
135237	AA454930	Hs.9691	ESTs	0.15

112483	R66534	Hs.28403	ESTs	0.15	
132387	R70914	Hs.8997	heat shock 70kD protein 1	0.15	
130343	AA490262	Hs.15485	ESTs; Weakly similar to APICAL-LIKE PROT	0.16	
105496	AA256323	Hs.25264	DKFZP434N126 protein	0.16	
104037	AA372630	Hs.100347	differentially expressed in hematopoietic	0.16	
101461	M22430	Hs.76422	phospholipase A2; group IIA (platelets;	0.16	
116551	D20458	Hs.229071	EST	0.16	
133889	AA099391	Hs.211582	myosin; light polypeptide kinase	0.16	
103653	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	0.16	
101070	L02785	Hs.1650	down-regulated in adenoma	0.17	
131501	AA121127	Hs.181307	H3 histone; family 3A	0.17	
133515	X98311	Hs.74466	carcinoembryonic antigen-related cell ad	0.17	
108604	AA099820	Hs.49696	ESTs	0.17	
132982	L02326	Hs.198118	immunoglobulin lambda-like polypeptide 2	0.17	
131676	C20785	Hs.30514	ESTs	0.17	
134675	AA250745	Hs.87773	protein kinase; cAMP-dependent; catalyti	0.17	
133441	M82962	Hs.179704	meprin A; alpha (PABA peptide hydrolase)	0.18	
130455	X17059	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	0.18	
131734	D62965	Hs.31297	ESTs	0.18	
100749	HG3521-HT3715		Ras-Related Protein Rap1b	0.18	
116724	F13665	Hs.65641	ESTs	0.18	
129265	X68277	Hs.171695	dual specificity phosphatase 1	0.18	
102347	U37518	Hs.83429	tumor necrosis factor (ligand) superfam	0.18	
114542	AA055768	Hs.122576	ESTs	0.18	
123900	AA621223	Hs.112953	EST	0.19	
121780	AA422086	Hs.124660	ESTs	0.19	
115662	AA405715	Hs.64179	hypothetical protein	0.19	
113803	W42789	Hs.31446	ESTs	0.19	
105493	AA256268	Hs.10283	ESTs	0.19	
113195	T57112		yc20g11.s1 Stratagene lung (#937210) Hom	0.19	
129462	D84239	Hs.111732	IgG Fc binding protein	0.19	
133664	X86693	Hs.75445	hevin	0.2	
126180	R18070	Hs.3712	ubiquinol-cytochrome c reductase; Rieske	0.2	
100687	HG3115-HT3291		Golli-Mbp (Gb:L18862)	0.2	
130064	T67053	Hs.181125	immunoglobulin lambda gene cluster	0.2	
101367	M12963	Hs.73843	alcohol dehydrogenase 1 (class I); alpha	0.2	
132254	L20826	Hs.430	plastin 1 (I isoform)	0.2	
105646	AA282147	Hs.5888	ESTs	0.2	
132883	AA047151	Hs.5897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f	0.21	0.21
132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma	0.21	
108931	AA147186	Hs.250746	ESTs	0.22	
131421	X64177	Hs.2667	metallothionein 1H	0.22	
107295	T34527	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	0.22	
103576	Z26317	Hs.2631	desmoglein 2	0.22	
105173	AA182030	Hs.8364	ESTs	0.22	
134843	H60595	Hs.90061	progesterone binding protein	0.22	
102009	U02680	Hs.82643	protein tyrosine kinase 9	0.23	
123997	D51171	Hs.78902	voltage-dependent anion channel 2	0.23	
106609	AA458652	Hs.32181	ESTs	0.23	
101300	L40391	Hs.6445	Homo sapiens (clone s153) mRNA fragment	0.23	
129717	AA481670	Hs.12150	ESTs; Weakly similar to retinal short-ch	0.23	
108565	AA085342	Hs.1526	ATPase; Ca++ transporting; cardiac muscl	0.23	
121314	AA402799	Hs.182538	ESTs	0.23	
124803	R45480	Hs.164866	cyclin K	0.23	
130208	AA620556	Hs.15250	peroxisomal D3;D2-enoyl-CoA isomerase	0.23	
132888	AA490775	Hs.5920	UDP-N-acetylglucosamine-2-epimerase/N-ac	0.23	
132720	Z69881	Hs.5541	ATPase; Ca++ transporting; ubiquitous	0.23	
102239	U26726	Hs.1376	hydroxysteroid (11-beta) dehydrogenase 2	0.23	
115764	AA421562	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	0.24	
130558	H96654	Hs.15984	ESTs; Weakly similar to gene pp21 protei	0.24	
122666	AA455052	Hs.99387	ESTs	0.24	
134495	D63477	Hs.84087	KIAA0143 protein	0.24	
124017	F02202	Hs.100960	ESTs	0.24	
106925	AA491261	Hs.37558	Homo sapiens clone 23923 mRNA sequence	0.24	
115187	AA261805	Hs.44021	ESTs	0.24	
105309	AA233790	Hs.4104	ESTs; Weakly similar to cDNA EST-yk386g7	0.24	
124457	N50114	Hs.128704	ESTs	0.24	
130616	AA233763	Hs.16726	Homo sapiens mRNA; cDNA DKFZp564A132 (fr	0.25	0.25
105795	AA369245	Hs.17448	ESTs; Weakly similar to IIII ALU SUBFAMI	0.25	
134579	N23222	Hs.85963	CD36 antigen (collagen type I receptor;	0.25	

Table 13: H chip – Met vs Normal query – up in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

Pkey	Ex Accn	UniG_ID	Complete Title	Ratio Met/Normal	
102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	8.457	
111307	N73988	Hs.37477	ESTs; Weakly similar to CGI-141 protein	6.05	
103119	X63629	Hs.2877	cadherin 3; P-cadherin (placental)	5.207	
131564	AA491465	Hs.28792	ESTs	5.136	
119729	W69747	Hs.94806	KIAA1062 protein	4.667	
124059	F13673	Hs.99769	ESTs	4.398	
123987	C21171	Hs.95497	ESTs; Weakly similar to GLUCOSE TRANSPOR	4.292	4.292
128817	N47524	Hs.28491	spermidine/spermine N1-acetyltransferase	3.964	
133770	M69197	Hs.242279	haptoglobin-related protein	3.823	
130412	AA406554	Hs.241572	golgi autoantigen; golgin subfamily a; 5	3.719	
104755	AA024482	Hs.9029	DKFZP434G032 protein	3.702	
132676	AA283035	Hs.54813	ESTs	3.645	
134453	X70683	Hs.83484	SRY (sex determining region Y)-box 4	3.581	
124690	R05818	Hs.173830	ESTs	3.446	
106949	AA496805	Hs.177425	KIAA0964 protein	3.42	
130724	AA370091	Hs.179680	ESTs	3.402	
128992	R49693	Hs.107708	ESTs	3.32	
133421	AA436560	Hs.7327	claudin 1	3.255	
103047	X55990	Hs.73839	ribonuclease; RNase A family; 3 (eosinop	3.229	
102990	X51441	Hs.181062	serum amyloid A1	3.149	
115429	AA284139	Hs.89295	EST	3.114	
129158	J05257	Hs.109	dipeptidase 1 (renal)	3.019	
123533	AA608751	Hs.244904	ESTs; Weakly similar to IIII ALU SUBFAMI	3.011	

Table 14: H chip – Met vs Normal query – down in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

PkeyY	Ex Accn	UniG_ID	Complete_Title	Ratio Met/Normal
103466	Y00339	Hs.155097	carbonic anhydrase II	0.012
104258	AF007216	Hs.5462	solute carrier family 4; sodium bicarbon	0.025
108999	AA156064	Hs.72115	ESTs	0.034
101046	K01160		Accession not listed in Genbank	0.041
133565	H57056	Hs.204831	ESTs	0.042
101346	L76465	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	0.043
102095	U11313	Hs.75760	sterol carrier protein 2	0.054
111855	R37362	Hs.21351	ESTs	0.055
130320	U19495	Hs.237356	stromal cell-derived factor 1	0.058
123137	AA487468	Hs.100686	ESTs; Weakly similar to secreted cement	0.06
107222	D51235	Hs.82689	tumor rejection antigen (gp96) 1	0.06
102638	U67319	Hs.9216	caspase 7; apoptosis-related cysteine pr	0.063
128906	AA487557	Hs.10706	ESTs	0.065
129105	AA224351	Hs.108681	ESTs	0.069
110837	N30796	Hs.17424	ESTs; Weakly similar to semaphorin F [H.	0.069
100116	D00654	Hs.77443	actin; gamma 2; smooth muscle; enteric	0.071
116786	H25836	Hs.83429	tumor necrosis factor (ligand) superfami	0.074
130867	J04093	Hs.2056	UDP glycosyltransferase 1	0.075
132836	F09557	Hs.57929	slit (Drosophila) homolog 3	0.076
131861	D11925	Hs.184245	KIAA0929 protein Msx2 interacting nuclea	0.081
106674	AA461303	Hs.7946	DKFZP586D1519 protein	0.084
109272	AA195718	Hs.86030	ESTs	0.088
132711	N73702	Hs.238927	ESTs	0.091
106569	AA455983	Hs.117816	sorcin	0.092
104636	AA004415	Hs.106106	ESTs	0.093
118823	N79237	Hs.50813	ESTs; Weakly similar to long chain fatty	0.094
134534	X73501	Hs.84905	H. Sapiens mRNA for cytokeratin 20	0.095
119479	W32094	Hs.55501	ESTs	0.096
113778	W15263	Hs.5422	ESTs	0.098
128482	U83908	Hs.100407	programmed cell death 4	0.102
124653	N92884	Hs.109641	ESTs	0.106
133407	AA093348	Hs.7306	secreted frizzled-related protein 1	0.108
135237	AA454930	Hs.9691	ESTs	0.109
116250	AA480975	Hs.44829	ESTs	0.111
132617	AA171913	Hs.5338	carbonic anhydrase XII	0.112
131273	AA421139	Hs.173542	ESTs	0.113
116710	F10577	Hs.70312	ESTs	0.114
131791	S71043	Hs.32225	immunoglobulin alpha 1	0.114
112483	R66534	Hs.28403	ESTs	0.115
132017	W67251	Hs.37331	Homo sapiens vav 3 oncogene (VAV3) mRNA	0.116
124308	H93575	Hs.227146	Homo sapiens mRNA; cDNA DKFZp564J142 (fr	0.117
114846	AA234929	Hs.44343	ESTs	0.119
116551	D20458	Hs.229071	EST	0.12
105299	AA233511	Hs.194720	ATP-binding cassette; sub-family G (WHIT	0.122
130366	L11708	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	0.122
133806	M12759	Hs.76325	Human Ig J chain gene	0.122
104776	AA026349	Hs.31412	ESTs	0.125
129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1	0.125
131272	AA423884	Hs.139033	paternally expressed gene 3	0.127
105774	AA348014	Hs.23412	ESTs	0.128
134604	M22995	Hs.865	RAP1A; member of RAS oncogene family	0.128
134711	X04011	Hs.88974	cytochrome b-245; beta polypeptide (chro	0.128
129113	AA147646	Hs.108740	DKFZP586A0522 protein	0.133
123995	D51119	Hs.100090	tetraspan 3	0.133
129168	T90621	Hs.109052	chromosome 14 open reading frame 2	0.133
123891	AA621103	Hs.99216	ESTs; Moderately similar to IIII ALU SUB	0.135
132694	M60830	Hs.5509	ecotropic viral integration site 2B	0.135
135342	W60097	Hs.99120	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	0.135
131510	AA207114	Hs.27842	ESTs; Weakly similar to similar to 1-acy	0.137
133652	AA287383	Hs.7540	ESTs	0.137
134749	L10955	Hs.89485	carbonic anhydrase IV	0.139
106586	AA456598	Hs.256269	ESTs	0.139

106893	AA489636	Hs.25253	ESTs	0.139	
101070	L02785	Hs.1650	down-regulated in adenoma	0.14	
114293	Z40718	Hs.20196	adenylate cyclase 9	0.14	
113966	W86600	Hs.9842	ESTs	0.141	
101185	L19872	Hs.170087	aryl hydrocarbon receptor	0.145	
131492	AA393876	Hs.1255	nuclear receptor subfamily 2; group F; m	0.145	
133889	AA099391	Hs.211582	myosin; light polypeptide kinase	0.145	
120914	AA377254	Hs.97107	EST	0.147	
118771	N74690	Hs.50547	ESTs	0.149	
105496	AA256323	Hs.25264	DKFZP434N126 protein	0.151	
131011	R41771	Hs.22146	ESTs	0.153	
106210	AA428239	Hs.10338	ESTs	0.154	
114069	Z38161	Hs.197335	plasma glutamate carboxypeptidase	0.154	
133011	AA042990	Hs.171921	sema domain; immunoglobulin domain (Ig);	0.154	
115967	AA446887	Hs.42911	ESTs	0.154	
102571	U60115		Homo sapiens skeletal muscle LIM-protein	0.155	
100687	HG3115-HT3291		Golli-Mbp (Gb:L18862)	0.155	
132903	AA235404	Hs.5985	Homo sapiens clone 25186 mRNA sequence	0.155	
125832	AA628600	Hs.117587	ESTs	0.155	
130064	T67053	Hs.181125	immunoglobulin lambda gene cluster	0.157	
123264	AA491003	Hs.99824	BCE-1 protein	0.159	
130919	AA291710	Hs.21276	collagen; type IV; alpha 3 (Goodpasture	0.159	
103542	Z11793	Hs.3314	selenoprotein P; plasma; 1	0.161	
101478	M23379	Hs.758	RAS p21 protein activator (GTPase activa	0.162	
108921	AA142913	Hs.71721	ESTs	0.164	
100642	HG2743-HT3926		Caldesmon 1, Alt. Splice 6, Non-Muscle	0.167	
132109	AA599801	Hs.40098	ESTs	0.167	
115719	AA416997	Hs.59622	ESTs	0.169	
128915	C02386	Hs.107139	ESTs	0.171	
117634	N36421	Hs.107854	ESTs; Weakly similar to SODIUM- AND CHLO	0.172	
129462	D84239	Hs.111732	IgG Fc binding protein	0.174	
131328	V01512	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	0.176	
130343	AA490262	Hs.15485	ESTs; Weakly similar to APICAL-LIKE PROT	0.177	
115764	AA421562	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	0.177	
122261	AA436830	Hs.98902	ESTs	0.179	
106605	AA457718	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	0.179	
109991	H09813	Hs.12896	KIAA1034 protein	0.181	
101300	L40391	Hs.6445	Homo sapiens (clone s153) mRNA fragment	0.181	
123080	AA485303	Hs.205126	polymeric immunoglobulin receptor	0.182	
130016	AA055811	Hs.143131	transmembrane glycoprotein	0.186	
122666	AA455052	Hs.99387	ESTs	0.188	
105453	AA252893	Hs.9001	ESTs	0.189	
108980	AA151676	Hs.33455	peptidyl arginine deiminase; type II	0.19	
100248	D31888	Hs.78398	KIAA0071 protein	0.192	
130036	AA195260	Hs.206738	ESTs; Moderately similar to !!!! ALU SUB	0.192	
110882	N36001	Hs.17348	ESTs; Weakly similar to !!!! ALU SUBFAMI	0.193	
131676	C20785	Hs.30514	ESTs	0.195	
111029	N54792	Hs.24697	cytidine monophosphate-N-acetylneuramini	0.196	
131257	AA256042	Hs.24908	ESTs	0.196	
133348	T23517	Hs.7149	ESTs	0.196	
133784	AA214305	Hs.76173	ESTs	0.196	
113863	W68388	Hs.21288	ESTs; Weakly similar to KIAA0704 protein	0.197	
103158	X67235	Hs.118651	hematopoietically expressed homeobox	0.198	
102347	U37518	Hs.83429	tumor necrosis factor (ligand) superfamI	0.2	
111351	N90223	Hs.23392	ESTs	0.2	
123495	AA599850	Hs.106747	ESTs; Weakly similar to similar to BPTI/	0.2	
123802	AA620448	Hs.61408	Homo sapiens clone 24760 mRNA sequence	0.2	
129243	H88033	Hs.109727	KIAA0733 protein	0.2	
130219	R77539	Hs.15285	ESTs	0.2	
131171	H04644	Hs.167619	ESTs; Weakly similar to !!!! ALU SUBFAMI	0.2	
133746	U44378	Hs.75862	MAD (mothers against decapentaplegic; Dr	0.2	
116459	AA621399	Hs.64193	ESTs	0.201	
109613	F03031	Hs.27519	ESTs	0.202	
133435	T23983	Hs.7365	ESTs	0.202	
103002	X52001	Hs.1408	endothelin 3	0.204	
125153	W38294		Accession not listed in Genbank	0.204	
131919	AA121266	Hs.34641	ESTs	0.204	
100749	HG3521-HT3715		Ras-Related Protein Rap1b	0.205	
105085	AA147537	Hs.4811	ESTs	0.208	
124571	N67470	Hs.173074	DKFZP564O1863 protein	0.21	
129519	AA298786	Hs.112242	ESTs	0.21	
116724	F13665	Hs.65641	ESTs	0.21	
132932	T15482	Hs.6093	ESTs	0.21	
113803	W42789	Hs.31446	ESTs	0.211	
110792	N24899	Hs.6630	ESTs	0.212	
105178	AA187490	Hs.21941	ESTs	0.212	

107295	T34527	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	0.212	
115262	AA279112	Hs.88594	ESTs	0.213	
115839	AA429038	Hs.40541	ESTs	0.213	
103211	X73079	Hs.205126	polymeric immunoglobulin receptor	0.214	
108604	AA099820	Hs.49696	ESTs	0.215	
105173	AA182030	Hs.8364	ESTs	0.217	
108539	AA084677	Hs.54558	ESTs; Weakly similar to protein B [H.sap	0.217	
109984	H09594	Hs.10299	ESTs	0.217	
133536	Y00264	Hs.177486	amyloid beta (A4) precursor protein (pro	0.217	
129965	T71333	Hs.13854	ESTs	0.219	
114542	AA055768	Hs.122576	ESTs	0.219	
132982	L02326	Hs.198118	immunoglobulin lambda-like polypeptide 2	0.22	
101809	M86849		Homo sapiens connexin 26 (GJB2) mRNA, co	0.222	
105795	AA369245	Hs.17448	ESTs; Weakly similar to III ALU SUBFAMI	0.222	
132119	H99211	Hs.40334	ESTs	0.222	
132733	R25385	Hs.123654	KIAA0824 protein	0.222	
109415	AA227219	Hs.110826	trinucleotide repeat containing 9	0.222	
113083	T40530	Hs.8241	ESTs; Weakly similar to heat shock prote	0.223	
107053	AA600147	Hs.5741	ESTs; Weakly similar to NADH-cytochrome	0.224	
103653	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	0.225	
104613	AA001049	Hs.24713	Homo sapiens mRNA; cDNA DKFZp586G0123 (f	0.225	0.225
126180	R18070	Hs.3712	ubiquinol-cytochrome c reductase; Rieske	0.227	
132015	D11900	Hs.3731	ESTs	0.227	
130616	AA233763	Hs.16726	Homo sapiens mRNA; cDNA DKFZp564A132 (fr	0.227	0.227
132883	AA047151	Hs.5897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f	0.23	0.23
123169	AA488892	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprot	0.233	
115187	AA261805	Hs.44021	ESTs	0.234	
116787	H28581	Hs.15641	ESTs	0.234	
113195	T57112		yc20g11.s1 Stratagene lung (#937210) Hom	0.235	
130707	W45457	Hs.203559	ESTs	0.235	
124803	R45480	Hs.164866	cyclin K	0.235	
116844	H64938	Hs.38331	ESTs	0.235	
102759	U81607	Hs.788	A kinase (PRKA) anchor protein (gravin)	0.238	
130584	AA009839	Hs.180841	tumor necrosis factor receptor superfami	0.238	
133240	D31161	Hs.68613	ESTs	0.238	
132952	AA425154	Hs.61426	ESTs	0.239	
132720	Z69881	Hs.5541	ATPase; Ca++ transporting; ubiquitous	0.24	
131734	D62965	Hs.31297	ESTs	0.24	
111890	R38678	Hs.12365	ESTs	0.241	
102325	U35139	Hs.50130	necdin (mouse) homolog	0.244	
104968	AA084602	Hs.29669	ESTs	0.244	
105674	AA284755	Hs.214742	CDW52 antigen (CAMPATH-1 antigen)	0.244	
120519	AA258585	Hs.129887	cadherin 19 (NOTE: redefinition of symbo	0.244	
134675	AA250745	Hs.87773	protein kinase; cAMP-dependent; catalyti	0.244	
130642	M63438	Hs.156110	Immunoglobulin kappa variable 1D-8	0.245	
134418	R78190	Hs.82933	ESTs; Weakly similar to cDNA EST EMBL:TO	0.245	
115137	AA257976	Hs.56156	ESTs	0.245	
131713	X57809	Hs.181125	immunoglobulin lambda gene cluster	0.246	
108931	AA147186	Hs.250746	ESTs	0.246	
106609	AA458652	Hs.32181	ESTs	0.248	
115559	AA393810	Hs.41067	ESTs	0.25	
133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec	0.25	
134088	D43636	Hs.79025	KIAA0096 protein	0.25	
134487	R38185	Hs.83954	Homo sapiens unknown mRNA	0.25	

Table 15: I chip – Met vs Normal query – up in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

Pkey	Ex_Accn	UniG_ID	Title	Ratio Met/Normal
319379	T91443	Hs.193963	ESTs	18.71
321920	N63915		EST cluster (not in UniGene)	11.9
314522	AI732331	Hs.187750	ESTs; Moderately similar to IIII ALU CLA	7.23
315720	AW291875	Hs.163900	ESTs	6.06
308010	AI439190	Hs.181165	eukaryotic translation elongation factor	5.76
313774	AW136836	Hs.144583	ESTs	5.01
300734	AW205197	Hs.240951	ESTs	3.98
337895			CH22_EM:AC005500.GENSCAN.56-2	3.98
312339	AA524394		EST cluster (not in UniGene)	3.66
331644	T99544	Hs.173734	ESTs; Weakly similar to IIII ALU CLASS B	3.53
324643	AI436356	Hs.130729	ESTs	3.52
324302	AA543008	Hs.136806	ESTs; Weakly similar to IIII ALU SUBFAM I	3.41
314912	AI431345	Hs.161784	ESTs	3.33
319403	T98413		EST cluster (not in UniGene)	3.32
308676	AI761036		EST singleton (not in UniGene) with exon	3.27
331858	AA421163	Hs.163848	ESTs	3.22
315178	AW362945	Hs.162459	ESTs	3.21
321354	AA078493		EST cluster (not in UniGene)	3.18
337898			CH22_EM:AC005500.GENSCAN.56-5	3.16
322682	AI110679		EST cluster (not in UniGene)	3.15
313197	AI738851	Hs.222487	ESTs	3.1
308991	AI879831		EST singleton (not in UniGene) with exon	3.08
310016	AW449612	Hs.152475	ESTs	3.05

Table 16: I chip – Met vs Normal query – down in Mets

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title

Pkey	Ex_Accn	UniG_ID	title	Ratio Met/Normal
303041	AF127035		EST cluster (not in UniGene) with exon h	0.02
302360	AJ010901	Hs.198267	mucin 4; tracheobronchial	0.03
301948	AA344647	Hs.116724	aldo-keto reductase family 1; member B11	0.03
336091			CH22_FGENES.689_3	0.04
333657			CH22_FGENES.241_2	0.04
333658			CH22_FGENES.241_4	0.04
333737			CH22_FGENES.261_1	0.05
333656			CH22_FGENES.240_4	0.05
302347	AF039400	Hs.194659	chloride channel; calcium activated; fam	0.06
336084			CH22_FGENES.688_13	0.06
330385	AA449749	Hs.31386	ESTs; Highly similar to secreted apoptos	0.06
304487	AA434241		EST singleton (not in UniGene) with exon	0.07
302292	AF067797		EST cluster (not in UniGene) with exon h	0.07
334030			CH22_FGENES.320_2	0.07
332859			CH22_FGENES.27_2	0.07
333654			CH22_FGENES.240_2	0.07
303270	AL120518	Hs.105352	ESTs	0.08
320352	Y13323	Hs.145296	disintegrin protease	0.08
333637			CH22_FGENES.229_2	0.08
324094	AA382603		EST cluster (not in UniGene)	0.08
320590	U67058	Hs.168102	Human proteinase activated receptor-2 mR	0.08
330622	X63597	Hs.2996	sucrase-isomaltase	0.08
331441	H75860	Hs.39720	ESTs	0.08
308601	AI719930		EST singleton (not in UniGene) with exon	0.09
323770	AA722425		EST cluster (not in UniGene)	0.09
335188			CH22_FGENES.507_3	0.09
333730			CH22_FGENES.258_1	0.09
304480	AA430373		EST singleton (not in UniGene) with exon	0.09
336081			CH22_FGENES.688_10	0.1
332071	AA598594	Hs.112475	ESTs	0.1
318538	N28625	Hs.74034	caveolin 1; caveolae protein; 22kD	0.1
311331	AI679622	Hs.32225	immunoglobulin alpha 1	0.1
319668	NM_002731		EST cluster (not in UniGene)	0.11
332567	N23730	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	0.11
319395	AW062570	Hs.13809	ESTs	0.11
315594	AI983437	Hs.155145	ESTs	0.11
321539	N98619	Hs.62461	ARP2 (actin-related protein 2; yeast) ho	0.12
333647			CH22_FGENES.235_2	0.12
333588			CH22_FGENES.206_2	0.12
321286	AI380940		EST cluster (not in UniGene)	0.12
320727	U96044		EST cluster (not in UniGene)	0.13
335687			CH22_FGENES.596_2	0.13
324611	AA743462	Hs.165337	ESTs	0.14
335115			CH22_FGENES.496_2	0.14
324660	AA541644	Hs.186044	ESTs	0.14
337951			CH22_EM:AC005500.GENSCAN.94-1	0.14
302332	AI833168	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	0.14
300921	AW293224	Hs.232165	ESTs	0.14
333646			CH22_FGENES.234_2	0.14
335116			CH22_FGENES.496_3	0.14
320211	AL039402	Hs.125783	DEME-6 protein	0.15
336092			CH22_FGENES.689_6	0.15
330673	D57823	Hs.92962	Sec23 (S. cerevisiae) homolog A	0.16
303042	AF129532		EST cluster (not in UniGene) with exon h	0.16
337954			CH22_EM:AC005500.GENSCAN.96-3	0.16
336645			CH22_FGENES.26-1	0.16
335651			CH22_FGENES.590_2	0.16
314499	AL044570	Hs.147975	ESTs	0.17
336124			CH22_FGENES.701_9	0.17
315199	AA877996	Hs.125376	ESTs	0.17
324525	AW044647	Hs.196284	ESTs	0.17
320825	NM_004751		EST cluster (not in UniGene)	0.18

302049	AA377072	Hs.129792	Homo sapiens Chromosome 16 BAC clone CIT	0.18
336083			CH22_FGENES.688_12	0.18
333653			CH22_FGENES.239_2	0.18
323243	W44372		EST cluster (not in UniGene)	0.19
316610	AW087973	Hs.126731	ESTs	0.19
315033	AI493046	Hs.146133	ESTs	0.19
330551	U39840	Hs.105440	hepatocyte nuclear factor 3; alpha	0.19
333642			CH22_FGENES.231_2	0.19
301281	AA843986	Hs.190586	ESTs	0.2
333626			CH22_FGENES.224_2	0.21
303792	C75094	Hs.199839	ESTs; Highly similar to NG22 [H.sapiens]	0.21
332325	T79428	Hs.191264	ESTs	0.21
321223	AA431366		EST cluster (not in UniGene)	0.21
333635			CH22_FGENES.228_2	0.22
314645	AI808999	Hs.207570	ESTs	0.22
322929	AI365585	Hs.146246	ESTs	0.22
324718	AI557019	Hs.116467	ESTs	0.22
335652			CH22_FGENES.590_3	0.22
307783	AI347274		EST singleton (not in UniGene) with exon	0.22
331344	AA357927	Hs.70208	ESTs	0.22
336088			CH22_FGENES.688_17	0.23
320802	D83824	Hs.185055	BENE protein	0.23
335692			CH22_FGENES.596_7	0.23
333593			CH22_FGENES.210_2	0.23
335667			CH22_FGENES.590_18	0.24
314853	AA729232	Hs.153279	ESTs	0.24
320244	AA296922	Hs.129778	gastrointestinal peptide	0.24
300601	AI762130	Hs.165619	ESTs	0.24
305080	AA641485		EST singleton (not in UniGene) with exon	0.25
335189			CH22_FGENES.507_4	0.25

Table 17: B survivor vs Mets – Up in B survivor

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

Pkey	Ex Accn	UniG_ID	Complete Title	Ratio BS/Met	
101006	J04132	Hs.97087	CD3Z antigen; zeta polypeptide (TT3 com	7.28	
114173	Z39050	Hs.21963	ESTs	6.13	
130284	X82206	Hs.153961	ARP1 (actin-related protein 1; yeast) ho	5.77	
100787	HG3872-HT4142		Immunoglobulin Gamma Heavy Chain, V(6)Dj c Regions (Gb:U13200)	5.63	
132461	AA405775	Hs.49005	hypothetical protein	5.62	
133806	M12759	Hs.76325	Human Ig J chain gene	5.46	
133747	D86972	Hs.75863	KIAA0218 gene product	5.45	
123328	AA496968	Hs.105403	EST	5.28	
132671	X76302	Hs.54649	putative nucleic acid binding protein RY	5.25	
132018	AA293194	Hs.3737	ESTs	5.22	
100186	D17516	Hs.4748	adenylate cyclase activating polypeptide	5.14	
107155	AA621202	Hs.7946	DKFZP586D1519 protein	5.1	
103566	Z22555	Hs.180616	CD36 antigen (collagen type I receptor;	5.06	
113355	T79203	Hs.14480	ESTs	4.99	
129040	U38864	Hs.108139	zinc finger protein 212	4.96	
130214	H78003	Hs.15266	ESTs	4.93	
129550	AA480991	Hs.113025	ESTs	4.92	
129704	W81301	Hs.12064	ubiquitin specific protease 22	4.91	
116425	AA609574	Hs.51483	ESTs	4.77	
105166	AA179787	Hs.30570	polyglutamine binding protein 1	4.65	
118765	N74442	Hs.183696	ESTs	4.6	
108999	AA156064	Hs.72115	ESTs	4.57	
112756	R93908	Hs.35258	ESTs	4.54	
111655	R16884	Hs.187462	ESTs	4.48	
119392	T90672	Hs.238859	ESTs	4.42	
131957	AA609008	Hs.183232	ESTs	4.41	
129275	D82061	Hs.109993	Ke6 gene; mouse; human homolog of	4.4	
113634	T95085	Hs.125182	ESTs	4.4	
127187	AA297138	Hs.207422	ESTs	4.32	
101147	L13266	Hs.105	glutamate receptor; ionotropic; N-methyl	4.3	
134901	S78873	Hs.90875	RAB interacting factor	4.26	
100896	HG4593-HT4998		Sodium Channel 1	4.24	
100687	HG3115-HT3291		Golli-Mbp (Gb:L18862)	4.21	
129758	AA599552	Hs.183770	Homo sapiens mRNA; cDNA DKFZp566P2346 (f	4.19	
105440	AA252243	Hs.22851	ESTs	4.16	
131551	AA127867	Hs.28608	ESTs	4.15	
113761	T99373	Hs.189786	ESTs	4.09	
105897	AA401091		ESTs	4.07	
129495	AA382529	Hs.239676	ESTs	4.06	
103436	X98206		H.sapiens mRNA for UV-B repressed sequen	4.03	
104673	AA007633	Hs.20010	ESTs	4.03	
128886	L36720	Hs.106880	bystin-like	4.02	
100702	HG3236-HT3413		Neurofibromatosis 2 Tumor Suppressor (Gb:L27065)	3.99	
123547	AA608820	Hs.124085	KIAA0921 protein	3.98	
134877	AA455241	Hs.90527	ESTs	3.97	
123650	AA609332	Hs.180696	ESTs	3.94	
106482	AA451672	Hs.108824	ESTs; Weakly similar to cDNA EST yk415c1	3.94	
101909	S69265		Homo sapiens mRNA for PLE21 protein; com	3.93	
108390	AA075070		zm86b6.s1 Stratagene ovarian cancer (#93 LYMPHOCYTE ANTIGEN LY-6A.2/LY-6E.1 PREC	3.93	
135403	U06643	Hs.99923	lectin; galactoside-binding; soluble; 7	3.89	
121038	AA398536	Hs.97365	ESTs	3.88	
128496	T83496	Hs.100610	ESTs	3.86	
108785	AA128946		ESTs	3.86	
119838	W79499	Hs.58580	ESTs	3.85	
130109	L12060	Hs.1497	retinoic acid receptor; gamma	3.84	
134538	U79288	Hs.85053	KIAA0513 gene product	3.83	
110310	H38209	Hs.32728	EST	3.81	
110433	H49425	Hs.32992	ESTs	3.78	
111834	R36138	Hs.152458	ESTs	3.76	
130903	N27086	Hs.21068	ESTs	3.74	
105142	AA164851	Hs.15380	ESTs; Weakly similar to HERV-E envelope	3.73	

130248	U84569	Hs.153452	chromosome 21 open reading frame 2	3.73	
130645	AA020942	Hs.17200	STAM-like protein containing SH3 and ITA	3.73	
123378	AA521043	Hs.185832	ESTs	3.73	
103985	AA313880		EST185737 Colon carcinoma (HCC) cell lin	3.73	
112397	R60822	Hs.26805	EST	3.72	
100980	J03069	Hs.72931	v-myc avian myelocytomatosis viral oncog	3.72	
102609	U64863	Hs.158297	programmed cell death 1	3.7	
108974	AA151402	Hs.46531	ESTs	3.7	
130192	Y12661	Hs.171014	VEGF nerve growth factor inducible	3.69	
131318	X51699	Hs.2558	bone gamma-carboxyglutamate (gla) protei	3.68	
113759	T99364	Hs.16074	Homo sapiens mRNA; cDNA DKFZp564I153 (fr	3.66	
133712	L19267	Hs.198836	dystrophin myotonic-containng WD repea	3.65	
134229	R15108	Hs.8037	ESTs	3.65	
134241	AA300265	Hs.80540	KIAA0195 gene product	3.65	
124699	R06413	Hs.112278	arrestin; beta 1	3.62	
107343	U03115	Hs.103945	Human V beta T-cell receptor (TCRBV) gen	3.62	
128511	AA425636	Hs.10082	potassium intermediate/small conductance	3.62	
105466	AA253412	Hs.21489	ESTs	3.61	
131377	R41389	Hs.26159	ESTs	3.6	
119135	R49548	Hs.169681	death effector domain-containing	3.6	
132982	L02326	Hs.198118	immunoglobulin lambda-like polypeptide 2	3.59	
128514	H84261	Hs.100843	ESTs; Weakly similar to similar to GTP-b	3.56	
102396	U41804	Hs.54411	putative T1/ST2 receptor binding protein	3.55	
134945	R50247	Hs.91600	ESTs	3.55	
134913	X60483	Hs.91031	H4 histone family; member D	3.54	
102053	U07664	Hs.37035	homeo box HB9	3.52	
121569	AA412686	Hs.97955	ESTs	3.52	
132560	AA005315	Hs.204524	ESTs; Weakly similar to KIAA0747 protein	3.51	
118456	N66580	Hs.161496	EST; Weakly similar to HC1 ORF [M.muscul	3.51	
111518	R08160	Hs.222529	ESTs; Weakly similar to IIII ALU SUBFAMI	3.51	
116795	H38858	Hs.251783	EST	3.5	
130377	AA378316	Hs.155182	KIAA1036 protein	3.5	
121774	AA421758	Hs.98361	ESTs	3.49	
123413	AA521448	Hs.103845	ESTs	3.49	
133798	AA444115	Hs.76277	ESTs; Weakly similar to salivary proline	3.49	
135183	X93996	Hs.239663	myeloid/lymphoid or mixed-lineage leukem	3.48	
132479	AA477715	Hs.4953	golgi autoantigen; golgin subfamily a; 3	3.47	
117191	H99394	Hs.40339	EST	3.47	
130942	X87852	Hs.21432	H.sapiens mRNA for SEX gene	3.46	
130700	D55696	Hs.18069	protease; cysteine; 1 (legumain)	3.43	
131301	T17386	Hs.164501	ESTs	3.43	
100818	HG4018-HT4288		Opioid-Binding Cell Adhesion Molecule	3.43	
103393	X94612	Hs.41749	protein kinase; cGMP-dependent; type II	3.43	
131337	AA228116	Hs.170204	KIAA0551 protein	3.42	
133403	X68688	Hs.72991	zinc finger protein 33b (KOX 31)	3.42	
124728	R16231	Hs.106620	Homo sapiens clone 23950 mRNA sequence	3.41	
123168	AA488881	Hs.105218	EST	3.39	
123324	AA496932	Hs.105399	KIAA0809 protein	3.38	
106947	AA496685	Hs.37936	suppressor of variegation 3-9 (Drosophil	3.38	
116717	F11065	Hs.79363	ESTs	3.36	
102794	U88629	Hs.173334	ELL-RELATED RNA POLYMERASE II; ELONGATIO	3.34	
117503	N31963	Hs.44286	ESTs	3.33	
112220	R50295	Hs.25703	ESTs	3.33	
106340	AA441792	Hs.22857	chord domain-containing protein 1	3.33	
106308	AA436186	Hs.30662	ESTs	3.32	
130894	D16105	Hs.210	leukocyte tyrosine kinase	3.31	
120039	W92548	Hs.94985	ESTs	3.31	
131428	U17838	Hs.26719	PR domain containing 2; with ZNF domain	3.3	
113285	T66830	Hs.182712	ESTs	3.3	
109458	AA232648	Hs.87068	ESTs	3.29	
132134	AA242904	Hs.40637	proline-rich Gla (G-carboxyglutamic acid	3.29	
118964	N93330	Hs.54937	Homo sapiens clone 24722 unknown mRNA; p	3.29	
127621	AI218205	Hs.116204	ESTs	3.29	
135149	U40002	Hs.95351	lipase; hormone-sensitive	3.28	
114371	Z41835	Hs.27810	ESTs	3.28	
130043	AA055404	Hs.193953	ESTs; Weakly similar to IIII ALU SUBFAMI	3.27	
121347	AA405181	Hs.97972	ESTs	3.25	
105754	AA302657	Hs.192028	ESTs	3.25	
121327	AA404286	Hs.173125	peptidylprolyl isomerase F (cyclophilin	3.25	
111204	N68295	Hs.37982	ESTs	3.25	
120949	AA397830	Hs.98347	ESTs; Weakly similar to GLIOMA PATHOGENE	3.25	
130024	U15197	Hs.241560	Human histo-blood group ABO protein mRNA	3.24	
125005	T61449	Hs.193727	ESTs	3.24	
121067	AA398662	Hs.97302	ESTs	3.24	
120996	AA398281	Hs.143684	ESTs	3.23	
117101	H94043	Hs.24341	DKFZP586I1419 protein	3.23	

130708	U40490	Hs.18136	nicotinamide nucleotide transhydrogenase	3.23	
130270	L40399	Hs.153820	hypothetical protein	3.22	
131605	AA256220	Hs.29383	ESTs	3.22	
100854	HG4194-HT4464		Sodium/Hydrogen Exchanger 5	3.22	
123026	AA481072	Hs.99743	ESTs	3.21	
108328	AA070204		zm68b3.s1 Stratagene neuroepithelium (#9	3.2	
104259	AF007833	Hs.159265	Homo sapiens kruppel-related zinc finger	3.2	
133711	J04130	Hs.75703	small inducible cytokine A4 (homologous	3.2	
112261	R52145	Hs.25894	ESTs; Highly similar to hypothetical pro	3.19	
119529	W38053		Accession not listed in Genbank	3.19	
122386	AA446221	Hs.6092	F-box protein containing leucine-rich re	3.19	
109157	AA179161	Hs.73562	ESTs	3.19	
119903	W85707	Hs.75936	erythrocyte membrane protein band 4.9 (d	3.18	
127452	AA491317		aa65c01.r1 NCI_CGAP_GCB1 Homo sapiens cD	3.18	
124229	H62793	Hs.221892	ESTs	3.18	
129221	AA417126	Hs.109571	translocase of inner mitochondrial membr	3.17	
133185	AA481404	Hs.6686	ESTs	3.16	
121479	AA411911	Hs.98110	ESTs	3.16	
133872	T79868	Hs.180903	hypothetical protein	3.16	
132504	U12897	Hs.5022	Imprinted in Prader-Willi syndrome	3.16	
103089	X60382	Hs.179729	collagen; type X; alpha 1 (Schmid metaph	3.15	
129654	AA019943	Hs.118463	H.sapiens mRNA for unknown liver orphan	3.15	
117295	N22360	Hs.43153	ESTs	3.15	
107349	U48224	Hs.158321	beaded filament structural protein 2; ph	3.14	
103451	X99459	Hs.154782	adaptor-related protein complex 3; sigma	3.14	
114854	AA235056	Hs.120244	ESTs	3.14	
121044	AA398551	Hs.97374	ESTs	3.13	
128582	U22963	Hs.101840	major histocompatibility complex; class	3.13	
112598	R78565	Hs.138395	EST	3.13	
113170	T54342	Hs.222506	ESTs	3.13	
111714	R23146	Hs.23466	ESTs	3.13	
111809	R33616	Hs.24688	EST	3.12	
115249	AA278961	Hs.71124	ESTs	3.11	
103228	X75546	Hs.230	fibromodulin	3.11	
129944	L00389	Hs.1361	cytochrome P450; subfamily I (aromatic c	3.11	
107927	AA028915	Hs.237709	EST	3.11	
130297	H94949	Hs.171955	trophinin-assisting protein (tastin)	3.1	
125742	H81181	Hs.183654	ESTs; Weakly similar to unknown [S.cerev	3.1	
134802	L35546	Hs.89709	glutamate-cysteine ligase (gamma-glutamy	3.1	
112560	R72293	Hs.6179	Homo sapiens mRNA; cDNA DKFZp586K2322 (f	3.1	
129266	AA343881	Hs.209061	sudD (suppressor of bimD6; Aspergillus n	3.09	
126982	AA211419		small inducible cytokine A5 (RANTES)	3.09	
131594	H29723	Hs.29261	ESTs; Weakly similar to serine protease	3.08	
134910	AA431320	Hs.9100	ESTs	3.08	
103505	Y09912	Hs.33102	transcription factor AP-2 beta (activati	3.08	
110525	H57330	Hs.37430	EST	3.07	
123276	AA491270	Hs.187946	ESTs	3.06	
130519	H91819	Hs.10669	ESTs; Moderately similar to KIAA0400 [H.	3.06	
126621	AA192638		zq01h08.r1 Stratagene muscle 937209 Homo	3.05	
134327	AF006041	Hs.178743	death-associated protein 6	3.04	
103513	Y10209		H.sapiens mRNA for CD3L protein	3.04	
131243	R16667	Hs.24752	spectrin SH3 domain binding protein 1	3.04	
115187	AA261805	Hs.44021	ESTs	3.04	
107543	Z43703	Hs.4552	Homo sapiens HRIHFB2157 mRNA; partial cd	3.04	
134051	S67070	Hs.78846	heat shock 27kD protein 2	3.04	
113461	T86737	Hs.193536	ESTs	3.03	
130490	X57522	Hs.158164	ATP-binding cassette; sub-family B (MDR/	3.03	
128843	AA234141	Hs.203004	katanin p80 (WD40-containing) subunit B	3.03	
100941	HG862-HT862		Transition Protein 2	3.03	
122268	AA436855	Hs.178202	ESTs	3.02	
107425	W26719	Hs.30204	ESTs	3.02	
130930	U19261		TNF receptor-associated factor 1	3.02	
132958	W90398	Hs.6147	KIAA1075 protein	3.02	
100973	J02888	Hs.73956	NAD(P)H menadione oxidoreductase 2; diox	3.01	
104924	AA058532	Hs.28774	ESTs	3.01	
129998	Y10055	Hs.162808	phosphoinositide-3-kinase; catalytic; de	3.01	
130023	X13461	Hs.239600	calmodulin-like 3	3.01	
129536	M33493	Hs.184504	trypsin; alpha	3	
112015	R42836	Hs.23198	ESTs	3	
103036	X54925	Hs.83169	matrix metalloproteinase 1 (interstitial	2.99	
100756	HG3565-HT3768		Zinc Finger Protein (Gb:M88357)	2.99	
103425	X97301		H.sapiens mRNA for Ptg-11 protein	2.99	
118291	N63076	Hs.138746	EST	2.98	
125877	H15229		ym30g04.r1 Soares infant brain 1N1B Homo	2.98	
			repetitive element.; mRNA sequence.	2.98	
101371	M13232	Hs.36989	coagulation factor VII (serum prothrombi	2.98	

102958	X15675	Hs.93174	Human endogenous retrovirus pHE.1 (ERV9)	2.97	
121183	AA400138	Hs.97703	ESTs	2.97	
119241	T12559	Hs.221382	ESTs	2.96	
115067	AA253458	Hs.91299	postmeiotic segregation increased 2-like	2.96	
126196	AA084394		zn05g10.s1 Stratagene hNT neuron (#93723	2.96	
111642	R16153	Hs.128740	ESTs; Highly similar to DNB-5 (H.sapiens	2.95	
100898	HG4638-HT5050		Spliceosomal Protein Sap 49	2.95	
129370	AA287879	Hs.110796	ESTs; Moderately similar to GTP-binding	2.94	
128915	C02386	Hs.107139	ESTs	2.94	
101868	M96233	Hs.82891	glutathione S-transferase M4	2.94	
124394	N29724		gamma2-adaptin	2.93	
103559	Z19585	Hs.75774	thrombospondin 4	2.93	
107882	AA025630	Hs.17801	ESTs; Moderately similar to serine/proli	2.93	
134919	T99639	Hs.91142	KH-type splicing regulatory protein (FUS	2.92	
110293	H30258	Hs.37165	collagen; type IX; alpha 2	2.92	
132433	AA082546	Hs.48516	ESTs	2.92	
127347	AA428350		ESTs	2.92	
121976	AA429807	Hs.98632	ESTs	2.91	
133025	AA135492	Hs.6318	ESTs; Highly similar to peroxisomal shor	2.91	
133413	S72043	Hs.73133	metallothionein 3 (growth inhibitory fac	2.91	
111694	R22035	Hs.23331	ESTs	2.91	
128369	F12681	Hs.205300	ESTs	2.9	
102464	U49260	Hs.3828	mevalonate (diphospho) decarboxylase	2.9	
135358	C21431	Hs.99486	ESTs; Weakly similar to aralar1 (H.sapie	2.9	
108661	AA113287	Hs.65905	ESTs; Weakly similar to PTB-ASSOCIATED S	2.9	
102185	U20230		Human guanyl cyclase C gene, partial cds	2.89	
122071	AA431787	Hs.98762	EST	2.89	
102040	U06088	Hs.159479	galactosamine (N-acetyl)-6-sulfate sulfa	2.89	
115689	AA410645	Hs.199014	ESTs	2.88	
135110	T15817	Hs.193788	nitric oxide synthase 2A (inducible; hep	2.88	
118729	N73717	Hs.161526	EST	2.88	
129518	AA369807	Hs.112238	ESTs	2.88	
125788	R74309	Hs.44499	small EDRK-rich factor 2	2.87	
128650	U57971	Hs.103124	ATPase; Ca++ transporting; plasma membra	2.87	
125936	H30751	Hs.182859	lifeguard	2.87	
100779	HG3731-HT4001		Immunoglobulin Heavy Chain, VdJc Regions (Gb:L23566)	2.87	
104451	M13299	Hs.102119	blue cone pigment	2.86	
133539	M21574	Hs.74615	platelet-derived growth factor receptor;	2.86	
119506	W37833	Hs.55563	ESTs	2.86	
126568	AA190515		zp85d12.r1 Stratagene HeLa cell s3 93721	2.86	
134184	X53742	Hs.79732	fibulin 1	2.86	
127633	AI339609	Hs.152733	potassium voltage-gated channel; Isk-rel	2.86	
128716	AA045978	Hs.173611	NADH dehydrogenase (ubiquinone) Fe-S pro	2.86	
107135	AA620782	Hs.23247	ESTs	2.85	
117748	N47317	Hs.141858	ESTs	2.85	
124030	F04143	Hs.151032	Homo sapiens clone 23856 unknown mRNA; p	2.85	
135120	AA449841	Hs.108300	NOT3 (negative regulator of transcriptio	2.84	
102156	U17977		HSU17977 Humn fibroblast cDNA H sapiens	2.84	
129418	AA401401	Hs.11127	PET112 (yeast homolog)-like	2.84	
103222	X74795	Hs.77171	minichromosome maintenance deficient (S.	2.84	
125145	W38001		Accession not listed in Genbank	2.83	
100560	HG2228-HT2305		Crystallin, Beta B	2.83	
105370	AA236476	Hs.22791	ESTs; Weakly similar to transmembrane pr	2.83	
127036	AI468598		ESTs	2.83	
128788	AA029073	Hs.105685	ESTs	2.83	
119523	W38041		Accession not listed in Genbank	2.82	
126436	N31224	Hs.211579	melanoma adhesion molecule	2.82	
126559	R15866	Hs.170263	tumor protein 53-binding protein; 1	2.82	
118183	N59287	Hs.48361	EST	2.82	
101298	L40387	Hs.118633	2'-5'-oligoadenylate synthetase-like	2.81	
131830	U33054	Hs.32959	G protein-coupled receptor kinase 2 (Dro	2.81	
124173	H41281	Hs.107619	ESTs	2.81	
102295	U32581		Homo sapiens KIAA0421 mRNA; partial cds	2.81	
129719	N66396	Hs.167766	ESTs; Moderately similar to Pro-a2(XI) [2.81	
126573	AA482023	Hs.155218	E1B-55kDa-associated protein 5	2.81	
125477	AI270093	Hs.234642	aquaporin 3	2.81	
106492	AA451896	Hs.7922	ESTs; Weakly similar to contains similar	2.8	
			p19; an RNA polymerase II elongation fa	2.8	
132881	T86118	Hs.58875	ESTs	2.8	
114733	AA133778	Hs.95734	ESTs	2.79	
104618	AA001611	Hs.186494	ESTs	2.79	
134137	F10045	Hs.79347	KIAA0211 gene product	2.79	
133212	U82979	Hs.67846	leukocyte Ig-like receptor; subfamily B	2.78	
100882	HG4460-HT4729		Immunoglobulin Heavy Chain, VdJc Regions (Gb:L23564)	2.78	
104756	AA024622	Hs.15813	solute carrier family 22 (organic cation	2.78	
129861	N69507	Hs.129849	DKFZP564M182 protein	2.78	

120824	AA347548	Hs.96876	ESTs	2.78
100684	HG3107-HT3283		Plasma Membrane Calcium Pump Hpmca2a	2.78
121789	AA423970	Hs.178111	ESTs	2.78
101647	M59941	Hs.118200	colony stimulating factor 2 receptor; be	2.78
113722	T97957	Hs.202948	ESTs; Weakly similar to alternatively sp	2.77
115107	AA256371	Hs.186645	ESTs	2.77
111464	R05518	Hs.19521	ESTs	2.77
108446	AA079120		zm95e1.s1 Stratagene colon HT29 (#937221	2.77
123921	AA621329	Hs.250671	Hu DNA seq frm clone 1163J1 on chr 22q13 prot (similar to mouse Celsr1; rat MEGF	2.77
134445	M59488	Hs.83384	S100 calcium-binding protein; beta (neur	2.76
114132	Z38688	Hs.24192	ESTs	2.76
120500	AA256430	Hs.132525	ESTs	2.76
101860	M95610	Hs.37165	collagen; type IX; alpha 2	2.76
134430	H52105	Hs.8309	KIAA0747 protein	2.76
124152	H27216	Hs.107635	ESTs	2.76
132268	AA058833	Hs.23445	ESTs; Weakly smlr to similar to M. muscu	2.76
116257	AA481493	Hs.88537	ESTs	2.76
102438	U46570	Hs.7733	tetralcopeptide repeat domain 1	2.75
122393	AA446334	Hs.99064	ESTs	2.75
107653	AA010210	Hs.47041	ESTs	2.75
123674	AA609473	Hs.105187	ESTs; Moderately similar to kinesin like	2.75
129858	T66906	Hs.12970	ESTs	2.75
130117	U06641	Hs.150207	UDP glycosyltransferase 2 family; polype	2.75
133464	M13982	Hs.73917	Interleukin 4	2.75
127039	AA233366	Hs.256491	ESTs	2.74
128318	AA418202	Hs.13810	ESTs	2.74
123363	AA504818	Hs.171279	ESTs	2.74
127654	AA649249	Hs.75640	natriuretic peptide precursor A	2.74
132067	L20860	Hs.178382	glycoprotein Ib (platelet); beta polypep	2.74
125664	AA948418	Hs.25744	ESTs; Weakly similar to Ydr412wp [S.cere	2.73
132354	L05187	Hs.211913	small proline-rich protein 1A	2.73
101568	M33764	Hs.75212	ornithine decarboxylase 1	2.73
101438	M20777	Hs.159263	Homo sapiens; alpha-2 (VI) collagen	2.73
116233	AA479082	Hs.61142	ESTs	2.73
122194	AA435882	Hs.97531	ESTs	2.72
113995	W88466	Hs.22010	ESTs	2.72
124251	H68286	Hs.107924	ESTs	2.71
120583	AA281304	Hs.78614	complement component 1; q subcomponent b	2.71
134958	U72507	Hs.234216	Human 40871 mRNA partial sequence	2.71
124280	H85835	Hs.100058	dihydropyrimidinase-like 4	2.71
130113	M64673	Hs.1499	heat shock transcription factor 1	2.71
106588	AA456612	Hs.25682	ESTs; Weakly smlr to PHOSPHATIDYLETHANOL	2.71
132023	F01927	Hs.3743	ESTs; Weakly similar to proline-rich pro	2.7
112284	R53558	Hs.26052	ESTs	2.7
107897	AA026240	Hs.61387	ESTs	2.7
122610	AA453598	Hs.99336	ESTs	2.7
119070	R27788	Hs.52302	ESTs	2.7
103491	Y08836		Homo sapiens mRNA for HRX-like protein	2.7
108225	AA058843	Hs.161620	EST	2.7
105829	AA398290	Hs.21965	ESTs	2.69
127749	AI251757	Hs.145234	ESTs	2.69
128428	AI185718	Hs.143900	ESTs	2.69
108409	AA075578		zm88h3.s1 Stratagene ovarian cancer (#93	2.69
114739	AA134923	Hs.103833	ESTs; Weakly similar to predicted using	2.68
128821	D87002	Hs.135	multiple UniGene matches	2.68
107412	W26105	Hs.8961	ESTs	2.68
117012	H85893	Hs.194387	ESTs; Weakly similar to IIII ALU SUBFAMI	2.68
135262	AA416551	Hs.9732	ESTs	2.68
105367	AA236397	Hs.20304	ESTs	2.68
134771	L13939	Hs.89576	adaptor-related protein complex 1; beta	2.68
105036	AA128617	Hs.25549	ESTs	2.68
125093	T92930	Hs.186750	ESTs	2.68
119340	T61899	Hs.90677	ESTs; Highly similar to CGI-82 protein [2.67
132603	H62900	Hs.53066	hsp70-interacting protein	2.67
113733	T98386	Hs.184548	ESTs	2.67
123564	AA608902	Hs.112612	ESTs	2.66
116059	AA454165	Hs.53455	ESTs	2.66
125803	R79373	Hs.29852	ESTs	2.66
123012	AA479962	Hs.139636	EST	2.66
106080	AA418046	Hs.35124	ESTs	2.66
128809	T59668	Hs.102267	lysyl oxidase	2.66
104354	H08988	Hs.113759	ESTs	2.66
107068	AA609028	Hs.8032	ESTs	2.65
101418	M17754	Hs.1276	BN51 (BHK21) temperature sensitivity com	2.65
135157	AA460138	Hs.95582	SRY (sex-determining region Y)-box 20	2.65

123312	AA496258	Hs.99601	ESTs	2.65	
130034	C00350	Hs.14454	chromosome 2 open reading frame 1	2.65	
103897	AA248870	Hs.55058	ESTs	2.65	
117771	N47961	Hs.46794	ESTs	2.65	
109980	H09529	Hs.98693	DKFZP586J0917 protein	2.64	
121966	AA429653	Hs.98616	EST	2.64	
114233	Z39652	Hs.27457	ESTs	2.64	
129594	R70379	Hs.115396	Human germline IgD chain gene; C-region;	2.63	
102319	U34587	Hs.66578	corticotropin releasing hormone receptor	2.63	
111700	R22212	Hs.23361	ESTs	2.63	
127365	AA001628	Hs.74335	heat shock 90kD protein 1; beta	2.63	
104205	AA496240	Hs.17270	DKFZP434C211 protein	2.63	
124559	N66223	Hs.135928	ESTs; Weakly similar to IIII ALU SUBFAMI	2.63	
106351	AA442772	Hs.191987	ESTs; Weakly similar to IIII ALU SUBFAMI	2.63	
121903	AA427605	Hs.258742	myosin-binding protein C; cardiac	2.62	
116442	AA620310	Hs.184343	ESTs; Weakly similar to KIAA0585 protein	2.62	
127041	F06090		HSC0WG031 normalized infant brain cDNA H	2.62	
132860	U93049	Hs.58435	FYN-binding protein (FYB-120/130)	2.62	
131591	L22454	Hs.180069	nuclear respiratory factor 1	2.61	
118118	N56901	Hs.47995	ESTs	2.61	
134809	X52611	Hs.18387	transcription factor AP-2 alpha (activat	2.61	
117706	N45091	Hs.46472	ESTs	2.61	
127488	AA312179	Hs.178617	ESTs; Weakly similar to CGI-82 protein [2.61	
114891	AA235984	Hs.87469	ESTs	2.6	
116426	AA609668	Hs.71657	ESTs	2.6	
132589	AA432197	Hs.5260	ESTs; Weakly similar to CGI-08 protein [2.6	
128410	AA452788		zx39g11.r1 Soares_total_fetus_Nb2HF8_9w	2.6	
106081	AA418394	Hs.25354	ESTs	2.6	
129919	R02003	Hs.191208	ESTs; Weakly similar to weak similarity	2.59	
124672	R00307	Hs.188504	ESTs	2.59	
122758	AA459013	Hs.99742	X-ray repair complementing defective rep	2.59	
125656	AA040118	Hs.78687	neutral sphingomyelinase (N-SMase) activ	2.59	
130052	J00220	Hs.145288	Human Ig active epsilon1 5' UT; V-D-J re	2.59	
134878	U28055	Hs.250826	macrophage stimulating; pseudogene 9	2.59	
131908	L05624	Hs.3446	mitogen-activated protein kinase kinase	2.59	
126470	AA843339	Hs.193168	ESTs; Weakly similar to CGI-52 protein [2.59	
132353	M31651	Hs.46319	sex hormone-binding globulin	2.58	
119588	W44559	Hs.142525	ESTs	2.58	
131757	D17532	Hs.316	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.58	
118114	N56875	Hs.143212	cystatin F (leukocystatin)	2.58	
128200	A1279952	Hs.158037	ESTs; Weakly similar to transcription re	2.58	
131208	C14586	Hs.24220	Homo sapiens mRNA; cDNA DKFZp566M051 (fr	2.58	2.58
124721	R11131	Hs.154966	ESTs	2.57	
108706	AA121820		Homo sapiens mRNA for KIAA0842 protein;	2.57	
118831	N79592	Hs.50838	ESTs	2.57	
115708	AA412212	Hs.44033	ESTs	2.57	
107233	D59322	Hs.22595	ESTs	2.57	
129559	AA234945	Hs.11360	ESTs	2.57	
126953	AA743849	Hs.127286	ESTs	2.56	
108165	AA055221	Hs.63168	ESTs	2.56	
104069	AA401547	Hs.172694	ESTs	2.56	
112146	R46512	Hs.25374	ESTs	2.56	
108384	AA074891	Hs.124917	ESTs; Highly similar to KIAA0838 protein	2.56	
131779	R49047	Hs.179779	ribosomal protein L37	2.56	
111829	R36070	Hs.25079	EST	2.55	
103424	X97267	Hs.155975	protein tyrosine phosphatase; receptor t	2.55	
100133	D13118	Hs.80986	ATP synthase; H+ transporting; mitochond	2.55	
130208	AA620556	Hs.15250	peroxisomal D3;D2-enoyl-CoA isomerase	2.55	
124649	N92593	Hs.102907	ESTs	2.55	
106511	AA452865	Hs.206713	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	2.55	
128467	AA176446	Hs.180428	ESTs; Weakly similar to hypothetical 43.	2.55	
113524	T90072	Hs.15060	ESTs	2.55	
107821	AA020991	Hs.172856	ESTs	2.55	
111900	R39044	Hs.25318	Homo sapiens clone 25194 mRNA sequence	2.54	
109908	H05255	Hs.203237	EST	2.54	
132069	D87454	Hs.192966	KIAA0265 protein	2.54	
130660	T95262	Hs.17538	ESTs	2.54	
112983	T23443	Hs.7111	ESTs	2.54	
128279	H08885		yl88b08.r1 Soares infant brain 1NIB Homo	2.54	
106415	AA447994	Hs.29188	ESTs	2.53	
116741	H03268	Hs.181746	EST	2.53	
103148	X66362	Hs.2994	PCTAIRE protein kinase 3	2.53	
132336	AA342422	Hs.45073	ESTs	2.53	
129484	R92488	Hs.111989	ESTs	2.53	
110169	H19696	Hs.31612	ESTs; Moderately similar to CAGH4 [H.sap	2.53	
116880	H68380	Hs.144174	EST	2.53	

133511	X04106	Hs.74451	calpain; small polypeptide	2.53	
126037	M85772	Hs.6066	KIAA1112 protein	2.53	
132678	AA599876	Hs.5486	ESTs	2.53	
128751	AA442274	Hs.183176	ESTs	2.52	
133664	X86693	Hs.75445	hevin	2.52	
126977	AA309665		EST180547 Jurkat T-cells V Homo sapiens	2.52	
120697	AA291522	Hs.97250	EST	2.52	
128571	AA416619	Hs.101661	ESTs	2.52	
104422	H86858	Hs.132909	ESTs	2.52	
122372	AA446008	Hs.99044	EST	2.52	
112154	R46769	Hs.25388	ESTs	2.52	
126900	R16034	Hs.12701	ESTs; Highly similar to plasmolipin [H.s	2.51	
115000	AA251342	Hs.144584	ESTs	2.51	
110632	H72344	Hs.171635	ESTs	2.51	
129154	N23673	Hs.108969	mannosidase; alpha; class 2B; member 1	2.51	
107440	W28069	Hs.251993	ESTs; Weakly similar to similar to zinc	2.51	
105694	AA287109	Hs.37883	ESTs	2.51	
106249	AA430388	Hs.13144	ESTs; Weakly similar to ORF YGR038w [S.c	2.51	
134462	U11037	Hs.83620	sel-1 (suppressor of lin-12; C.elegans)-	2.51	
101800	M85276	Hs.105806	granulysin	2.51	
119884	W81606	Hs.58662	Homo sapiens mRNA; cDNA DKFZp564G212 (fr	2.51	
110289	H29829	Hs.31524	ESTs	2.51	
125506	H54273	Hs.154073	UDP-galactose transporter related	2.51	
102954	X15393	Hs.2813	motilin	2.51	
127851	AI469331	Hs.130497	ESTs; Weakly similar to CHLORIDE CONDUCT	2.5	
126179	AI191445	Hs.143855	ESTs; Highly similar to IROQUOIS-CLASS H	2.5	
129443	W69967	Hs.111497	ESTs; Moderately similar to neuronal pro	2.5	
104480	N41486	Hs.99654	protein-O-mannosyltransferase 1	2.5	
115580	AA398695	Hs.144339	Hu DNA seq frm clone 495O10 on chr 6q26- Prot L37A) pseudogene; last exon of gene for a novel prot smlr to worm E04F6.2; ESTs; STSs and GSSs	2.5	
119595	W45031	Hs.55878	EST	2.5	
103336	X85785	Hs.183	Duffy blood group	2.5	
102792	U87964	Hs.227576	GTP binding protein 1	2.49	
129643	L27584	Hs.250712	calcium channel; voltage-dependent; beta	2.49	
134503	U34880	Hs.84183	diphtheria toxin resistance protein reqrd	2.49	
117245	N20989	Hs.42927	ESTs	2.49	
126888	H78745	Hs.1063	small nuclear ribonucleoprotein polypept	2.49	
135313	D63484	Hs.98508	KIAA0150 protein	2.49	
121186	AA400156	Hs.183294	ESTs	2.49	
130651	X04445	Hs.1734	Inhibin; alpha	2.49	
134218	AA227480	Hs.80205	pim-2 oncogene	2.49	
104008	AA334630		EST38874 Embryo, 9 week Homo sapiens cDN	2.49	
129705	X78706	Hs.12068	carbamate acetyltransferase	2.49	
127900	AI143912	Hs.121824	ESTs	2.49	
104609	R96417	Hs.107795	ESTs	2.48	
131628	U47292	Hs.2979	trefoil factor 2 (spasmolytic protein 1)	2.48	
132184	U51003	Hs.419	distal-less homeo box 2	2.48	
130450	U70735	Hs.15591	COP9 subunit 6 (MOV34 homolog; 34 kD)	2.48	
101679	M62628	Hs.163271	Human alpha-1 Ig germline C-region membr	2.48	
120858	AA350147	Hs.96940	EST	2.48	
101012	J04444	Hs.697	cytochrome c-1	2.48	
110453	H52133	Hs.33026	ESTs; Weakly similar to similar to Enter	2.48	
133771	M68891	Hs.760	GATA-binding protein 2	2.48	
102944	X14445	Hs.37092	fibroblast growth fctr 3 (murine mammary	2.48	
113269	T65159	Hs.85044	ESTs	2.48	
107069	AA609045	Hs.11759	ESTs; Weakly similar to IIII ALU CLASS B	2.48	
100476	HG1019-HT1019		Serine Kinase Psk-H1	2.47	
106457	AA449718	Hs.27801	zinc finger protein 278	2.47	
105718	AA291629	Hs.74335	heat shock 90kD protein 1; beta	2.47	
104925	AA058683	Hs.5548	Homo sapiens clone 23765 mRNA sequence	2.47	
109913	H05527	Hs.31588	ESTs	2.47	
103412	X96698	Hs.42957	methyltransferase-like 1	2.47	
102326	U35246	Hs.226025	vacuolar protein sorting 45A (yeast homo	2.47	
116813	H49911	Hs.93102	ESTs	2.47	
123690	AA609566	Hs.112723	EST	2.47	
124714	R09486	Hs.193118	ESTs	2.47	
126154	AI004105	Hs.14232	ESTs; Moderately similar to KIAA0563 pro	2.47	
118880	N90168	Hs.54593	EST	2.47	
122274	AA437094	Hs.184456	ESTs; Weakly similar to IIII ALU SUBFAMI	2.46	
129600	N78980	Hs.11567	ESTs; Moderately similar to unknown [H.s	2.46	
121356	AA405437	Hs.93581	Homo sapiens mRNA; cDNA DKFZp586E171 (fr	2.46	
109560	F01778	Hs.8154	ESTs	2.46	
123342	AA504336	Hs.31659	thyroid hormone receptor-associated prot	2.46	
128032	AI150084	Hs.126678	ESTs	2.46	
129101	H90310	Hs.108665	ESTs; Weakly similar to CELL-CYCLE NUCLE	2.46	

131185	M25753	Hs.23960	cyclin B1	2.46	
121451	AA411008	Hs.98085	EST	2.46	
104328	D81932		HUM424C5B Hu fetal brain (TFujiwara) H s	2.46	
126543	AA723810	Hs.69517	ESTs; Highly similar to differentially e	2.45	
123600	AA609106	Hs.112644	ESTs	2.45	
131020	AA411756	Hs.20594	ESTs; Weakly similar to misato [D.melano	2.45	
134191	W28902	Hs.7979	KIAA0736 gene product	2.45	
130446	X79510	Hs.155693	protein tyrosine phosphatase; non-recept	2.45	
131613	R88228	Hs.29595	JM4 protein	2.45	
118864	N89670	Hs.42148	ESTs; Weakly similar to Su(P) [D.melanog	2.45	
104232	AB002351	Hs.10587	KIAA0353 protein	2.45	
122604	AA453489	Hs.99333	ESTs	2.45	
120626	AA285064	Hs.104485	EST	2.45	
116655	F03866	Hs.68090	ESTs	2.44	
116267	AA485080	Hs.256539	ESTs	2.44	
114944	AA243172	Hs.87619	TED protein	2.44	
127629	AA293279	Hs.29173	ESTs	2.44	
120350	AA211300	Hs.104166	ESTs	2.44	
103620	Z47087	Hs.182643	transcription elongation factor B (SII)	2.44	
131420	Z11737	Hs.2664	flavin containing monooxygenase 4	2.44	
131312	AA399226	Hs.25527	tight junction protein 3 (zona occludens	2.43	
122812	AA461044	Hs.142980	EST	2.43	
135100	AA398926	Hs.251108	Homo sapiens mRNA; chromosome 1 specific	2.43	
113464	T86931	Hs.16295	ESTs	2.43	
100045	M11507		AFFX control: transferrin receptor	2.43	
128975	AA092129	Hs.107538	ESTs; Moderately similar to /prediction	2.43	
103688	AA011479	Hs.154701	ESTs	2.43	
127331	F20186		HSPD05873 HM3 Homo sapiens cDNA clone 05	2.43	2.43
107337	T97111	Hs.191235	ESTs; Weakly similar to Ydr324cp [S.cere	2.43	
122171	AA435750	Hs.98830	EST	2.43	
107601	AA004636	Hs.50223	ESTs	2.43	
119800	W73523	Hs.58314	ESTs	2.43	
104886	AA053348	Hs.144626	growth differentiation factor 11	2.42	
122899	AA469960	Hs.178420	ESTs; Highly similar to WASP interacting	2.42	
125933	AI308037	Hs.84120	ESTs; Weakly similar to nucleoporin p62	2.42	
121664	AA417291	Hs.97978	ESTs	2.42	
125450	AA377194	Hs.238909	ESTs; Weakly similar to POLYPOSIS LOCUS	2.42	
114611	AA081374	Hs.108110	DKFZP547E2110 protein	2.42	
111595	R11492	Hs.191225	ESTs	2.42	
111671	R19368	Hs.229084	EST	2.42	
110687	H93005	Hs.177311	ESTs	2.42	
103019	X53414	Hs.144567	alanine-glyoxylate aminotransferase (oxa	2.42	
119076	R36634	Hs.235534	ESTs	2.42	
130589	AA234308	Hs.16441	DKFZP434H204 protein	2.42	
125975	AA495891	Hs.152290	ESTs; Highly similar to PACAP type-3/VIP	2.42	
106380	AA446188	Hs.16614	ESTs	2.41	
121965	AA429652	Hs.104901	EST	2.41	
121604	AA416788	Hs.98259	EST	2.41	
100885	HG4490-HT4876		Proline-Rich Protein Prb4, Allele	2.41	
117807	N48701	Hs.46523	EST	2.41	
119840	W79525	Hs.58586	ESTs	2.41	
102458	U48861	Hs.54397	cholinergic receptor; nicotinic; beta po	2.41	
116152	AA460920	Hs.215683	ESTs; Moderately similar to IIII ALU SUB	2.41	
126741	AA522512	Hs.29759	Homo sapiens mRNA; cDNA DKFZp586L2123 (f	2.41	2.41
103381	X92715	Hs.3057	zinc finger protein 74 (Cos52)	2.41	
124837	R55630	Hs.233602	KIAA0596 protein	2.41	
129322	AA437153	Hs.110407	ESTs; Weakly similar to coded for by C.	2.4	
129291	AA281930	Hs.110099	core-binding factor; runt domain; alpha	2.4	
124789	R43803	Hs.78110	ESTs; Weakly similar to F17A9.2 [C.elega	2.4	
133253	Y00970	Hs.183088	acrosin	2.4	
118990	N94447	Hs.55047	EST	2.4	
134897	R71427	Hs.9081	phenylalanyl-tRNA synthetase beta-subuni	2.4	
116572	D45654	Hs.65582	DKFZP586C1324 protein	2.4	
104294	D14539	Hs.234774	myeloid/lymphoid or mixed-lineage leukem	2.4	
118764	N74440	Hs.205264	ESTs	2.4	
117437	N27645		yw5e3.s1 Weizmann Olfactory Epithelium H 3' similar to contains L1.t3 L1 repetit	2.4	
111651	R16733	Hs.20499	ESTs	2.39	
109583	F02322	Hs.26135	ESTs	2.39	
125969	R94247	Hs.193879	ESTs	2.39	
130647	AA457216	Hs.214190	interleukin enhancer binding factor 1	2.39	
113708	T97467	Hs.18065	ESTs	2.39	
133469	L03785	Hs.170482	myosin; light polypeptide 5; regulatory	2.39	
118266	N62837	Hs.48647	immunoglobulin-like transcript 7	2.39	
121656	AA417248	Hs.98212	ESTs	2.39	
126530	AI422841	Hs.180086	ESTs	2.39	

123708	AA609648	Hs.207767	EST	2.39	
107875	AA025308	Hs.61182	ESTs	2.39	
111711	R22891	Hs.7093	ESTs	2.39	
131405	U79255	Hs.26468	amyloid beta (A4) precursor protein-bind	2.39	
127454	AA502957	Hs.153590	ESTs	2.39	
132341	AA448419	Hs.45209	ESTs	2.38	
133673	D87673	Hs.75486	heat shock transcription factor 4	2.38	
113213	T58607		ya94a02.s1 Stratagene placenta (#937225)	2.38	
106230	AA429356	Hs.12047	ESTs	2.38	
116692	F09261	Hs.66103	ESTs	2.38	
126197	AA172284	Hs.103657	ESTs; Weakly similar to CH-TOG PROTEIN [2.38	
115966	AA446866	Hs.71371	ESTs	2.38	
132636	U65785	Hs.5417	oxygen regulated protein (150kD)	2.38	
109965	H09077	Hs.30895	EST	2.38	
130203	L14754	Hs.1521	immunoglobulin mu binding protein 2	2.38	
131332	R50487	Hs.25717	ESTs	2.38	
119105	R42357	Hs.91453	ESTs	2.37	
129253	W69316	Hs.109778	ESTs; Weakly similar to similar to beta-	2.37	
113602	T92558	Hs.17036	ESTs	2.37	
118102	N55272	Hs.145798	ESTs	2.37	
100734	HG3432-HT3620		Fibroblast Growth Factor Receptor K-Sam, Alt. Splice 3, K-Sam III	2.37	
111533	R08548	Hs.251651	EST	2.37	
130813	U12259	Hs.198	paired box gene 3 (Waardenburg syndrome	2.37	
119180	R80413	Hs.92520	ESTs	2.37	
109335	AA211443	Hs.86492	ESTs	2.37	
107386	U97698	Hs.159593	mucin 6; gastric	2.36	
122486	AA448328	Hs.115527	ESTs	2.36	
112997	T23548	Hs.167467	ESTs	2.36	
109674	F09051	Hs.21837	ESTs; Weakly similar to KIAA0927 protein	2.36	
128868	AA423827	Hs.106730	hypothetical protein	2.36	
127027	R17261		yg12g07.r1 Soares Infant brain 1NIB H sa	2.36	
123099	AA485931	Hs.79	aminoacylase 1	2.36	
115716	AA416767	Hs.43498	ESTs; Weakly similar to ORF YKL201c [S.c	2.36	
130830	D86982	Hs.20060	KIAA0229 protein	2.36	
109051	AA159920	Hs.72322	ESTs	2.36	
130181	R39552	Hs.151608	Homo sapiens clone 23622 mRNA sequence	2.36	
131114	R46233	Hs.23107	ESTs	2.36	
123589	AA609047	Hs.188922	ESTs	2.36	
130872	U03891		phorbolln (similar to apolipoprotein B m	2.36	
131962	H78550	Hs.2780	jun D proto-oncogene	2.36	
130502	M55067	Hs.1583	neutrophil cytosolic factor 1 (47kD; chr	2.36	
121785	AA423883	Hs.142442	ESTs	2.35	
125405	T97171	Hs.121570	ESTs	2.35	
103682	AA000993		ESTs	2.35	
125649	T77395	Hs.194816	stomatin-like protein 1	2.35	
115452	AA285019	Hs.55263	ESTs; Highly similar to mitochondrial di	2.35	
129338	T56800	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (fr	2.35	2.35
106105	AA421268	Hs.149443	putative tumor suppressor	2.35	
134770	R72079	Hs.89575	CD79B antigen (immunoglobulin-associated	2.35	
119422	T99496	Hs.229598	EST	2.35	
109869	H02849	Hs.30345	EST	2.35	
134314	AA263032	Hs.81634	ATP synthase; H+ transporting; mitochond	2.35	
114989	AA251097	Hs.189119	ESTs	2.35	
122619	AA453755	Hs.191515	ESTs	2.35	
133129	AA428580	Hs.65551	ESTs	2.35	
128465	AA416762	Hs.100221	nuclear receptor subfamily 1; group H; m	2.35	
115636	AA402715	Hs.58389	ESTs	2.35	
130836	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	2.34	
132385	Y10256	Hs.47007	serine/threonine protein-kinase	2.34	
107776	AA018820	Hs.221147	ESTs	2.34	
109791	F10669	Hs.13228	DRE-antagonist modulator; calsenillin	2.34	
124409	N33212	Hs.107197	ESTs	2.34	
131068	AA397916	Hs.22595	ESTs	2.34	
121079	AA398719	Hs.14169	ESTs; Weakly similar to CREB-binding pro	2.34	
124662	N94340	Hs.171835	ESTs; Weakly smlr to PUT PRE-MRNA SPLIC	2.34	2.34
133820	M13686	Hs.177582	surfactant; pulmonary-associated protein	2.34	
129424	M55593	Hs.111301	matrix metalloproteinase 2 (gelatinase A	2.34	
109066	AA161377	Hs.72404	EST	2.34	
100339	D63485	Hs.181359	KIAA0151 gene product	2.34	
100809	HG3991-HT4261		Cpg-Enriched Dna, Clone E18	2.34	
120844	AA349417	Hs.96917	ESTs	2.33	
124927	R96146	Hs.221459	ESTs	2.33	
109779	F10527	Hs.3353	Homo sapiens clone 24940 mRNA sequence	2.33	
101171	L16842	Hs.119251	ubiquinol-cytochrome c reductase core pr	2.33	
110805	N26904	Hs.24048	ESTs; Weakly similar to FK506/rapamycin-	2.33	
125440	A1090982	Hs.31895	ESTs	2.33	

133159	AC000061	Hs.663	cystic fibrosis transmembr conductance re	2.33	
101829	M91368	Hs.129763	solute carrier family 8 (sodium/calcium	2.33	
126492	AA778565	Hs.142505	ESTs	2.33	
102774	U83303	Hs.164021	small inducible cytokine subfamily B (CX	2.33	
130480	N50809	Hs.15760	ESTs; Weakly similar to similar to Yeast	2.33	
126878	AI424759	Hs.238928	ESTs	2.33	
117338	N23889	Hs.43466	ESTs	2.32	
118662	N70877	Hs.13055	ESTs	2.32	
130354	AA416685	Hs.155001	UNC13 (C. elegans)-like	2.32	
108760	AA477330	Hs.12293	ESTs	2.32	
124294	H90573	Hs.102298	EST	2.32	
119428	W02129	Hs.55242	EST	2.32	
132629	Z40942	Hs.5383	ESTs	2.32	
127998	AA854161	Hs.143585	ESTs	2.32	
132728	AA293334	Hs.5566	ESTs; Highly similar to RAS-RELATED PROT	2.32	
120292	AA189116	Hs.96168	ESTs	2.32	
107598	AA004528	Hs.169444	ESTs	2.32	
128164	AI478174	Hs.144846	ESTs	2.32	
105753	AA299789	Hs.15277	ESTs	2.31	
131256	AA262340	Hs.24907	coronin; actin-binding protein; 2B	2.31	
110891	N38863	Hs.234392	platelet-activating factor acetylhydrola	2.31	
116767	H13689	Hs.92530	ESTs	2.31	
100545	HG2147-HT2217		Mucin 3, Intestinal (Gb:M55405)	2.31	
125264	W88995	Hs.167641	ESTs; Weakly similar to C15H9.5 [C.elega	2.31	
118387	N64579		yz51d11.s1 Morton Fetal Cochlea H saplen	2.31	
104335	D83847	Hs.183864	elastase 3B	2.31	
107464	W42944	Hs.171939	ESTs	2.31	
112304	R54798	Hs.26239	ESTs	2.31	
134313	AA136100	Hs.6673	trinucleotide repeat containing 15	2.31	
116322	AA490900	Hs.58643	ESTs; Highly similar to JAK3B [H.sapiens	2.31	
111275	N70970	Hs.35006	ESTs	2.31	
100109	AJ000480	Hs.143513	phosphoprotein regulated by mitogenic pa	2.31	
109338	AA211717	Hs.86507	ESTs	2.31	
134432	AA053022	Hs.8312	ESTs	2.31	
129649	AD000092	Hs.182628	Homo sapiens DNA from chr 19p13.2 cosmid		
			EKLF; GCDH; CRTG; and RAD23A genes; gen	2.31	
122623	AA453990	Hs.99248	ESTs	2.31	
112070	R43976	Hs.236310	EST	2.31	
127683	AA668123	Hs.134170	ESTs	2.31	
104920	AA057620	Hs.30807	ESTs; Highly similar to dJ186O1.1 [H.sap	2.31	
106064	AA417373	Hs.15898	ESTs	2.31	
106782	AA478487		ESTs	2.31	
126709	AA028159	Hs.47234	ESTs	2.3	
105129	AA158386	Hs.186476	ESTs	2.3	
105719	AA291644	Hs.36793	ESTs	2.3	
121698	AA418399	Hs.10351	KIAA0308 protein	2.3	
119069	R27619	Hs.231046	EST	2.3	
130388	U72515	Hs.189583	putative protein similar to nassy (Droso	2.3	
103444	X98801	Hs.74617	dynactin 1 (p150; Glued (Drosophila) hom	2.3	
114604	AA076128		zm18g4.s1 Stratagene pancreas (#93728) H		
			3' similar to SW:RS1A_HUMAN P3927 4S RI	2.3	
103878	AA227635	Hs.202588	ESTs	2.3	
105828	AA398276	Hs.11962	ESTs	2.3	
119778	W72920	Hs.58244	ESTs	2.3	
120401	AA234309	Hs.193011	ESTs	2.3	
116290	AA488691	Hs.57969	phenylalanine-tRNA synthetase	2.3	
130479	R44163	Hs.12457	Homo sapiens clone 23770 mRNA sequence	2.3	
104253	AF002672	Hs.152944	loss of heterozygosity; 11; chromosomal	2.29	
132615	H66367	Hs.53358	ESTs; Weakly similar to IIII ALU SUBFAMI	2.29	
121954	AA429598	Hs.98587	ESTs	2.29	
101336	L49169	Hs.75678	FBJ murine osteosarcoma viral oncogene h	2.29	
127247	AA313802	Hs.6289	growth factor receptor-bound protein 2	2.29	
117300	N22565	Hs.43212	ESTs	2.29	
122229	AA436198	Hs.103902	ESTs	2.29	
125106	T95766	Hs.189760	ESTs	2.29	
128083	R16100	Hs.166476	ESTs	2.29	
131279	AA089853	Hs.25197	STIP1 homology and U-Box containing prot	2.29	
133838	M97796	Hs.180919	inhibitor of DNA binding 2; dominant neg	2.29	
111837	R36447	Hs.24453	ESTs	2.29	
111435	R01620	Hs.19198	ESTs	2.29	
123613	AA609158	Hs.112656	EST	2.29	
133560	AA256365	Hs.7486	protein expressed in thyroid	2.29	
122896	AA469952	Hs.97899	ESTs; Weakly similar to dal2; len:343; C	2.29	
113378	T80627	Hs.14757	ESTs	2.29	
127174	AA293204	Hs.139352	ESTs	2.29	
120153	Z39582	Hs.65777	EST	2.29	

112741	R93080	Hs.35035	ESTs	2.28	
132152	AA044784	Hs.4105	Homo sapiens mRNA; cDNA DKFZp586A0618 (f	2.28	2.28
109790	F10665	Hs.25031	ESTs	2.28	
113776	W04657	Hs.24248	ESTs	2.28	
102934	X13451		Hu mRNA for lymphocyte lineage-restricted	2.28	
126168	AA322034		EST24690 Cerebellum II Homo sapiens cDNA	2.28	2.28
126363	N94706		Human Chromosome 16 BAC clone CIT987SK-A	2.28	
101427	M19508		Human myeloperoxidase gene, exons 1-4	2.28	
132616	AA386264	Hs.5337	Isocitrate dehydrogenase 2 (NADP+); mito	2.28	
105537	AA258813	Hs.27160	ESTs	2.28	
126527	AA548559	Hs.103853	ESTs	2.28	
115359	AA281936	Hs.88914	ESTs	2.28	
108474	AA079667		zm93d1.s1 Stratagene ovarian cncr (#9372	2.28	
120685	AA291066	Hs.105099	ESTs	2.28	
126171	AA704771	Hs.191942	ESTs	2.28	
112858	T02963	Hs.4454	ESTs	2.28	
121817	AA424826	Hs.98475	EST	2.28	
107895	AA026150	Hs.61384	ESTs	2.28	
131161	Z38223	Hs.23735	potassium voltage-gated channel; subfam	2.28	
135173	M72885	Hs.95910	Human GOS2 protein gene; complete cds	2.27	
103182	X69819	Hs.99995	intercellular adhesion molecule 3	2.27	
113889	W72720	Hs.194347	ESTs	2.27	
128984	AA319615	Hs.238030	secretory carrier membrane protein 2	2.27	
101531	M29877	Hs.576	fucosidase; alpha-L- 1; tissue	2.27	
115916	AA436889	Hs.91910	ESTs	2.27	
129892	H96850	Hs.89674	dolichyl-diphosphooligosaccharide-protei	2.27	
103035	X54871	Hs.77690	RAB5B; member RAS oncogene family	2.27	
126479	T78141		ESTs	2.27	
125778	R71976	Hs.161791	ESTs; Weakly similar to !!!! ALU SUBFAM	2.27	
108132	AA053586	Hs.63048	ESTs	2.27	
111017	N53965	Hs.256327	ESTs	2.27	
127165	AA359719	Hs.127121	ESTs	2.27	
126446	AI421309	Hs.118926	DKFZP586K0919 protein	2.26	
107864	AA025061	Hs.61246	ESTs	2.26	
122277	AA437133	Hs.98936	ESTs	2.26	
115604	AA400378	Hs.49391	ESTs	2.26	
105061	AA134824	Hs.4865	ESTs	2.26	
118549	N68163	Hs.49455	EST	2.26	
110509	H56493	Hs.61960	ESTs; Moderately similar to HYPOTHETICAL	2.26	2.26
114088	Z38280	Hs.26971	Human Chromosome 16 BAC clone CIT987SK-2	2.26	
103225	X74837	Hs.2750	mannosidase; alpha; class 1A; member 1	2.26	
125842	AA746654	Hs.5181	proliferation-associated 2G4; 38kD	2.26	
104538	R25069	Hs.175681	ESTs	2.26	
130304	U09368	Hs.154205	zinc finger protein 140 (clone pHZ-39)	2.26	
120680	AA290743	Hs.97242	ESTs	2.26	
124062	H00440	Hs.144524	ESTs; Weakly similar to signal transduce	2.26	
103289	X80915	Hs.1573	growth differentiation factor 5 (cartila	2.26	
109286	AA197273	Hs.191324	ESTs	2.26	
128555	U62739	Hs.101408	branched chain aminotransferase 2; mitoc	2.26	
129439	AA171694	Hs.111461	ceruloplasmin (ferroxidase)	2.26	
109221	AA192755	Hs.85840	ESTs; Weakly similar to stac [H.sapiens]	2.26	
109906	H05084	Hs.28077	ESTs; Highly similar to GDP-mannose pyro	2.26	
130540	U35234	Hs.159534	protein tyrosine phosphatase; receptor t	2.26	
122870	AA465158	Hs.192861	Spi-B transcription factor (Spi-1/PU.1 r	2.26	
120219	Z41124	Hs.66045	EST	2.26	
128021	AI001136	Hs.78223	N-acylaminoacyl-peptide hydrolase	2.26	
121732	AA421047	Hs.98330	ESTs	2.26	
107817	AA020781	Hs.60847	ESTs	2.25	
101069	L02648	Hs.84232	transcobalamin II; macrocytic anemia	2.25	
103065	X58399	Hs.81221	Human L2-9 transcript of unrearranged im	2.25	
118019	N52585	Hs.47517	ESTs	2.25	
122220	AA436011	Hs.98187	ESTs	2.25	
109161	AA179392	Hs.73601	EST	2.25	
128699	K03207	Hs.103972	proline-rich protein BstNI subfamily 4	2.25	
101914	S71824	Hs.167988	neural cell adhesion molecule 1	2.25	
102697	U74667	Hs.6364	Tat interactive protein (60kD)	2.25	
119939	W86753	Hs.82407	ESTs	2.25	
127793	AI298835	Hs.30445	ESTs; Weakly similar to transcription re	2.25	
104450	L77564	Hs.103978	serine/threonine kinase 22B (spermiogene	2.25	
133096	AA136042	Hs.131053	ESTs	2.25	
115416	AA283893	Hs.203866	ESTs	2.25	
117056	H90322	Hs.41387	EST	2.25	
115598	AA400129	Hs.65735	ESTs	2.25	
121267	AA401397	Hs.165296	ESTs; Highly similar to kallikrein-like	2.25	
104778	AA026397	Hs.11039	Homo sapiens clone 24804 mRNA sequenca	2.25	
110926	N48252	Hs.135287	ESTs	2.24	

102795	U88667	Hs.198396	ATP-binding cassette; sub-family A (ABC1	2.24
118643	N70324	Hs.49840	ESTs	2.24
103304	X82240	Hs.2484	T-cell leukemia/lymphoma 1A	2.24
134814	Z48475	Hs.89771	glucokinase (hexokinase 4) regulatory pr	2.24
125912	AA171719	Hs.5233	eukaryotic translation initiation factor	2.24
134365	R32377	Hs.82240	syntaxin 3A	2.24
117224	N20300	Hs.218707	ESTs	2.24
107169	AA621601	Hs.184446	ESTs; Weakly similar to small GTP-bindin	2.24
133948	M59916	Hs.77813	sphingomyelin phosphodiesterase 1; acid	2.24
101426	M19483	Hs.25	ATP synthase; H ⁺ transporting; mitochond	2.24
119922	W86196	Hs.177384	ESTs	2.24
123361	AA504810	Hs.139649	EST	2.24
123915	AA621298	Hs.112967	ESTs	2.24
123540	AA608792	Hs.112591	EST	2.24
124978	T40560	Hs.221759	ESTs	2.24
102354	U38268		Human cytochrome b pseudogene, partial c	2.24
124198	H53099	Hs.198271	NADH dehydrogenase (ubiquinone) 1 alpha	2.24
102160	U18235	Hs.121561	ATP-binding cassette; sub-family A (ABC1	2.24
107520	X76091	Hs.100007	regulatory factor X; 2 (influences HLA c	2.24
131589	U52100	Hs.29191	epithelial membrane protein 2	2.24
126633	AA206993	Hs.154145	guanine nucl binding protein (G protein)	2.23
130887	AA258379	Hs.155986	angiotensin receptor-like 2	2.23
119894	W84670	Hs.58518	EST	2.23
124544	N63837	Hs.40500	similar to S. cerevisiae RER1	2.23
103104	X61587	Hs.75082	ras homolog gene family; member G (rho G	2.23
110119	H17306	Hs.177229	ESTs	2.23
131411	AA464043	Hs.26506	ESTs; Weakly similar to NY-REN-45 antige	2.23
102346	U37359	Hs.227297	meiotic recombination (S. cerevisiae) 11	2.23
106003	AA411167	Hs.8734	ESTs; Moderately similar to IIII ALU CLA	2.23
122564	AA452251	Hs.98669	ESTs	2.23
133688	U42031	Hs.7557	FK506-binding protein 5	2.23
132096	AA131410	Hs.3964	Homo sapiens clone 24877 mRNA sequence	2.23
110038	H11746	Hs.31097	ESTs	2.23
123788	AA620293	Hs.112853	ESTs	2.23
135070	X99350	Hs.93974	forkhead box J1	2.23
104908	AA055841	Hs.154396	ESTs	2.22
128674	AA025001	Hs.169452	ESTs	2.22
100810	HG3992-HT4262		Cpg-Enriched Dna, Clone E35	2.22
120065	W93579	Hs.59478	EST	2.22
122775	AA459692	Hs.112143	ESTs	2.22
125443	H71482	Hs.177592	ribosomal protein; large; P1	2.22
118617	N69666	Hs.183413	ESTs; Moderately similar to IIII ALU SUB	2.22
128001	AI167814	Hs.166664	ESTs	2.22
128160	AI279080	Hs.149971	ESTs; Moderately similar to IIII ALU CLA	2.22
106608	AA458644	Hs.27115	ESTs	2.22
103485	Y08409	Hs.248415	thyroid hormone responsive SPOT14 (rat)	2.22
135008	AA173423	Hs.92918	ESTs; Weakly similar to R07G3.8 [C.elega	2.22
110122	H17333	Hs.159837	EST	2.22
128397	AI393421	Hs.14032	ESTs	2.22
110231	H24359	Hs.28733	ESTs	2.22
123188	AA489092	Hs.177726	ESTs	2.22
131903	AA481723	Hs.3436	deleted in oral cancer (mouse; homolog)	2.22
122649	AA454616	Hs.90336	ATPase; H ⁺ transporting; lysosomal (vacu	2.22
133090	AA448228	Hs.6468	ESTs	2.22
108002	AA037664	Hs.55067	ESTs; Weakly similar to T07F12.1 gene pr	2.22
133120	X64559	Hs.65424	tetranectin (plasminogen-binding protein	2.21
114263	Z40073	Hs.6045	ESTs	2.21
125518	R20148	Hs.193851	ESTs	2.21
128613	U78551	Hs.102482	Homo sapiens gallbladder mucin MUC5B mRN	2.21
102773	U83192	Hs.23731	discs; large (Drosophila) homolog 4	2.21
119526	W38049		Accession not listed in Genbank	2.21
126844	AA299325		EST11903 Uterus tumor I Homo sapiens cDN	2.21
105860	AA399251	Hs.180933	ESTs; Weakly similar to methyl-CpG bindi	2.21
126957	AA733145	Hs.194560	ESTs	2.21
108959	AA150107	Hs.81810	ESTs	2.2
131663	AA423926	Hs.30318	ESTs	2.2
127468	H02941	Hs.8888	ESTs	2.2
104483	N42776	Hs.146233	ESTs	2.2
123848	AA620773	Hs.221996	ESTs	2.2
101623	M55905	Hs.75342	malic enzyme 2; NAD(+)-dependent; mitoch	2.2
120872	AA357993	Hs.96996	ESTs	2.2
135033	AA173241	Hs.93454	ESTs	2.2
122286	AA437259	Hs.104944	EST	2.2
114862	AA235174	Hs.50250	ESTs	2.2
100255	D38047	Hs.78466	proteasome (prosome; macropain) 26S subu	2.2
103063	X58234	Hs.123178	translocase of inner mitochondrial membr	2.2

132777	R56898	Hs.56663	ESTs	2.2
133082	AA457129	Hs.6455	RuvB (E coli homolog)-like 2	2.2
127529	AA558980	Hs.191750	ESTs	2.2
114602	AA075642	Hs.103594	deleted in malignant brain tumors 1	2.2
120722	AA293435	Hs.97277	ESTs	2.2
102675	U72512		Human B-cell receptor associated protein	2.2
128551	H09058	Hs.237323	N-acetylglucosamine-phosphate mutase; DK	2.2
112020	R43001	Hs.22298	EST	2.2
123625	AA609216	Hs.112666	EST	2.2
120315	AA194266	Hs.178393	ESTs	2.2
122081	AA431992	Hs.104920	ESTs	2.19
101798	M85220		Accession not listed in Genbank	2.19
111501	R07444	Hs.163118	ESTs	2.19
132832	D63482	Hs.57734	KIAA0148 gene product	2.19
100544	HG2147-HT2217		Mucin 3, Intestinal (Gb:M55405)	2.19
106835	AA482077	Hs.33713	ESTs; Weakly similar to hypothetical pro	2.19
132934	AA076145	Hs.61053	ESTs	2.19
108762	AA127515	Hs.71787	ESTs; Highly similar to 30S ribosomal pr	2.19
120164	Z39733	Hs.158159	FAT tumor suppressor (Drosophila) homolo	2.19
135395	L08096	Hs.99899	tumor necrosis factor (ligand) superfam	2.19
101717	M69013	Hs.1686	guanine nucleotide binding protein (G pr	2.19
121172	AA400013	Hs.97750	EST	2.18
114861	AA235123	Hs.40719	ESTs	2.18
120851	AA349662	Hs.174248	ESTs	2.18
121083	AA398736	Hs.97653	EST	2.18
107171	AA621624	Hs.28088	Homo sapiens clone 24515 mRNA sequence	2.18
128754	D31446	Hs.10488	Breakpoint cluster region protein; uteri	2.18
100149	D13897	Hs.169249	peptide YY	2.18
132405	AA323787	Hs.4770	KIAA1068 protein	2.18
114666	AA112274		zm27g6.s1 Stratagene pancreas (#93728) H element;contains element LTR8 repetitiv	2.18
127008	AA223879		zr10g05.r1 Stratagene NT2 neuronal precu	2.18
110373	H42896	Hs.29438	ESTs	2.18
119354	T66942	Hs.100651	golgi SNAP receptor complex member 2	2.18
130115	M31627	Hs.149923	X-box binding protein 1	2.18
130514	AA161085	Hs.15871	ESTs; Weakly similar to acid phosphatase	2.18
128848	H08077	Hs.217179	ESTs; Weakly similar to T27A1.5 [C.elega	2.18
110161	H19312	Hs.28096	ESTs	2.18
132367	X82224	Hs.46634	cysteine conjugate-beta lyase; cytoplasm	2.18
125882	H45538	Hs.101448	metastasis associated 1	2.17
113837	W57698	Hs.8888	ESTs	2.17
106376	AA444004	Hs.6084	ESTs	2.17
113755	T99075	Hs.18570	ESTs	2.17
107525	X91817	Hs.102866	transketolase-like 1	2.17
119207	R93186	Hs.84298	CD74 antigen (invar polypept of maj hist	2.17
131862	AA236365		3-phosphoglycerate dehydrogenase	2.17
115514	AA297739	Hs.55609	ESTs; Weakly similar to ISOLEUCYL-TRNA S	2.17
112290	R53940	Hs.26016	ESTs	2.17
126136	H83353		yv82f02.r1 Soares melanocyte 2NbHM Homo	2.17
121574	AA412712	Hs.119325	Huntingtin-interacting protein A	2.17
118530	N67900	Hs.118446	ESTs	2.16
132327	AA203285	Hs.44892	ESTs; Weakly similar to dJ733D15.1 [H.sa	2.16
100564	HG2239-HT2324		Potassium Channel Protein (Gb:Z11585)	2.16
129376	AA022622	Hs.13543	ESTs; Weakly similar to hypothetical pro	2.16
135317	X86012	Hs.98602	Human DNA sequence from intron 22 of the 9.5kb repeated region; int22h-1; involv	2.16
114973	AA250845	Hs.87762	ESTs	2.16
107559	AA001504	Hs.59860	ESTs	2.16
111014	N53787	Hs.191117	ESTs	2.16
101250	L34060	Hs.79133	cadherin 8	2.16
110697	H93721	Hs.20798	ESTs	2.16
126843	AA450166	Hs.22641	ESTs; Moderately similar to predicted pr	2.16
108272	AA063616	Hs.43773	ESTs	2.16
125012	T66935	Hs.104859	ESTs	2.16
111639	R16101	Hs.140834	EST	2.15
123157	AA488443	Hs.100426	DKFZP564A063 protein	2.15
102315	U34252	Hs.2533	aldehyde dehydrogenase 9 (gamma-aminobut	2.15
131897	AA287623	Hs.3426	GTPase; human homolog of E. coli essenti	2.15
121528	AA412253	Hs.238909	ESTs; Weakly similar to POLYPOSIS LOCUS	2.15
122806	AA460707	Hs.106397	ESTs	2.15
125727	H00958	Hs.181641	ESTs	2.15
133279	AA069571	Hs.6957	Homo sapiens clone 24616 mRNA sequence	2.15
103219	X74570	Hs.75268	sialyltransferase 4C (beta-galactosidase	2.15
120881	AA362144	Hs.104601	EST	2.15
134060	D42039	Hs.78871	KIAA0081 protein	2.15
106598	AA457140	Hs.11411	DKFZP566O084 protein	2.15

125576	R66208	yi30h03.r1 Soares placenta Nb2HP H sapie	
		contains Alu repetitive element; contain	2.15
126727	AA037230	Hs.135084 cystatin C (amyloid angiopathy and cereb	2.15
101490	M25629	Hs.123107 kallikrein 1; renal/pancreas/salivary	2.15
129708	AA417181	Hs.120858 ESTs	2.14
100627	HG2702-HT2798	Serine/Threonine Kinase (Gb:Z25424)	2.14
121703	AA418671	Hs.104807 ESTs	2.14
106809	AA479704	Hs.220324 Humn DNA seq frm clone 283E3 on chr 1p36	
		Female Reproductive tract MIFR1; -2; MM	2.14
129525	F03873	Hs.112306 Homo sapiens clone 24955 mRNA sequence;	2.14
100478	HG1067-HT1067	Mucin (Gb:M22406)	2.14
118593	N69020	Hs.207689 EST	2.14
114047	W94427	Hs.3807 ESTs; Weakly similar to PHOSPHOLEMMAN PR	2.14
128823	AA478207	Hs.10632 ESTs; Moderately similar to sex-determin	2.14
100534	HG1980-HT2023	Tubulin, Beta 2	2.14
105757	AA321146	Hs.30596 ESTs	2.14
109617	F03192	Hs.26789 ESTs; Weakly similar to dJ162H14.1 [H.sa	2.14
121547	AA412448	Hs.104777 ESTs	2.14
119420	T98291	Hs.102484 glutathione S-transferase A3	2.14
120274	AA177051	nc02a02.s1 NCI_CGAP_Pr3 Homo sapiens cDN	
		repetitive element; contains element LTR	2.14
132933	AA598702	Hs.6101 bone morphogenetic protein 6	2.14
133405	X07881	Hs.73031 proline-rich protein BstNI subfamily 3	2.14
119811	W73922	Hs.49047 ESTs	2.14
134536	AA457735	Hs.850 IMP (inosine monophosphate) dehydrogenas	2.14
105125	AA157799	Hs.6980 aldo-keto reductase family 7; member A2	2.14
101398	M15881	Hs.1137 uromodulin (uromucoid; Tamm-Horsfall gly	2.14
132751	AA397901	Hs.55993 ESTs	2.13
115777	AA424142	Hs.39384 putative secreted ligand homologous to f	2.13
123193	AA489228	Hs.136956 ESTs	2.13
116875	H67749	Hs.161022 EST	2.13
107271	D60607	Hs.34931 EST	2.13
134551	R44839	Hs.8526 l-beta-1;3-N-acetylglucosaminyltransfera	2.13
113413	T83739	Hs.186512 ESTs	2.13
120522	AA258843	Hs.258748 ESTs	2.13
119965	W87738	Hs.59039 EST	2.13
131283	AA101601	Hs.183986 herpesvirus entry mediator B (poliovirus	2.13
107347	U43628	Hs.102598 mucosal vascular addressin cell adhesion	2.13
116490	C14265	Hs.66450 ESTs	2.13
100563	HG2239-HT2324	Potassium Channel Protein (Gb:Z11585)	2.13
110441	H50302	Hs.19845 ESTs; Highly similar to protein phosphat	2.13
101035	J05158	Hs.73858 carboxypeptidase N; polypeptide 2; 83kD	2.13
132500	AA047297	Hs.50107 ESTs; Moderately similar to CDO [H.sapie	2.13
129807	L34820	Hs.5299 aldehyde dehydrogenase 5 family; member	2.13
106250	AA430466	Hs.28890 ESTs	2.13
113569	T91086	Hs.162070 EST	2.13
122911	AA470087	Hs.239726 ESTs	2.13
107452	W28988	Hs.250746 ESTs	2.12
111824	R35661	Hs.25006 EST	2.12
132831	U53442	Hs.57732 mitogen-activated protein kinase 11	2.12
110244	H26742	Hs.25367 ESTs; Weakly similar to ALR [H.sapiens]	2.12
128918	H85347	Hs.107164 spectrin; beta; non-erythrocytic 1	2.12
133728	M10901	Hs.75772 nuclear receptor subfamily 3; group C; m	2.12
122476	AA448211	Hs.99164 ESTs	2.12
132004	L37360	Hs.37054 ephrin-A3	2.12
113971	W86760	Hs.220682 ESTs	2.12
103386	X92972	Hs.80324 protein phosphatase 6; catalytic subunit	2.12
131120	AA443676	Hs.23133 ESTs; Weakly similar to alcohol sulfotra	2.12
102186	U20285	G protein pathway suppressor 1	2.12
103694	AA018541	Hs.60580 zinc finger protein	2.12
111995	R42333	Hs.20893 ESTs	2.12
124436	N39596	Hs.182584 ESTs	2.12
100306	D50495	Hs.80598 transcription elongation factor A (SII);	2.12
103084	X59932	Hs.77793 c-src tyrosine kinase	2.11
115092	AA255903	Hs.80975 CD39-like 4	2.11
121579	AA416543	Hs.111981 ESTs	2.11
127101	AI349351	Hs.118944 ESTs	2.11
121195	AA400273	Hs.97791 ESTs	2.11
112721	R91484	Hs.30853 ESTs	2.11
113253	T64207	Hs.55296 HLA-B associated transcript-1	2.11
120838	AA348887	Hs.96907 ESTs	2.11
114122	Z38582	Hs.12751 ESTs	2.11
112635	R82298	Hs.29497 ESTs	2.11
103785	AA095600	Hs.225647 ESTs	2.11
128260	AA331445	EST35277 Embryo, 8 week I Homo sapiens c	2.11
122987	AA479155	Hs.103364 ESTs	2.11

110374	H42983	Hs.227263	ESTs	2.11	
116595	D60625	Hs.177656	calmodulin 1 (phosphorylase kinase; delt	2.11	
126117	H78617		yu26a08.r1 Soares fetal liver spleen 1NF	2.11	
116610	D80448	Hs.45177	ESTs	2.11	
111430	R01248	Hs.19165	ESTs	2.11	
106700	AA463929	Hs.28701	ESTs	2.11	
120181	Z40121	Hs.65870	ESTs; Weakly similar to Pro-Pol-dUTPase	2.1	
132545	AA147218	Hs.5105	ESTs	2.1	
105005	AA115253	Hs.28805	ESTs	2.1	
126702	U54602	Hs.2785	keratin 17	2.1	
124096	H10060	Hs.101687	EST	2.1	
132720	Z69881	Hs.5541	ATPase; Ca++ transporting; ubiquitous	2.1	
121926	AA428559	Hs.104895	ESTs	2.1	
125734	AA157445	Hs.227391	DKFZP547E1010 protein	2.1	
122368	AA443963	Hs.104964	EST	2.1	
116910	H72014	Hs.161031	ESTs; Weakly similar to SYNAPTOTAGMIN I	2.1	
113171	T54613	Hs.9761	EST	2.1	
134629	U00951	Hs.87150	Human clone A9A2BR11 (CAC)n/(GTG)n repea	2.1	2.1
105712	AA291293	Hs.25219	ESTs	2.1	
106931	AA495918	Hs.26714	ESTs	2.1	
114278	Z40424	Hs.27728	ESTs	2.1	
116615	D80666	Hs.45203	ESTs	2.09	
100189	D21089	Hs.320	xeroderma pigmentosum; complementation g	2.09	
119500	W37694	Hs.55561	ESTs	2.09	
129605	S72493	Hs.115947	keratin 16 (focal non-epidermolytic palm	2.09	
133912	X62744	Hs.77522	major histocompatibility complex; class	2.09	
129636	N34942	Hs.11782	ESTs	2.09	
106372	AA443941	Hs.4992	tumor suppressing subtransferable candid	2.09	
101885	M98539	Hs.8272	prostaglandin D2 synthase (21kD; brain)	2.09	
132749	AA235989	Hs.55967	short stature homeobox 2	2.09	
135042	X91348	Hs.93522	putative non-coding transcript (DiGeorge	2.09	
109404	AA224594	Hs.86941	ESTs	2.09	
101333	L47738	Hs.80313	p53 inducible protein	2.09	
100114	D00596	Hs.82962	thymidylate synthetase	2.09	
130536	T17045	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	2.09	
125772	R83903	Hs.78040	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.09	
132192	AA247569	Hs.4209	ESTs	2.09	
124697	R06273	Hs.186467	ESTs; Moderately similar to IIII ALU SUB	2.09	
127694	AI247780	Hs.117036	ESTs	2.08	
127895	AA772600	Hs.187998	ESTs; Weakly similar to ATP-binding cass	2.08	
121315	AA402883	Hs.82269	progesterone-associated endometrial prote	2.08	
			endometrial alpha-2-globulin; alpha ute	2.08	
112150	R46576	Hs.23239	ESTs	2.08	
105054	AA133584	Hs.26333	JM1 protein	2.08	
113151	T51620	Hs.9326	EST	2.08	
118783	N75285	Hs.50593	ESTs; Moderately similar to cytoplasmic	2.08	
126748	AA249580	Hs.239975	ESTs; Moderately similar to CDO [H.sapie	2.08	
135160	U77643	Hs.95655	secreted and transmembrane 1	2.08	
107518	X60152		zinc finger protein 2	2.08	
126055	N28990		yx39g04.r1 Soares melanocyte 2NbHM Homo	2.08	2.08
116982	H81933	Hs.40317	ESTs	2.08	
101756	M77235	Hs.169331	sodium channel; voltage-gated; type V; a	2.08	
116935	H75763	Hs.53468	ESTs	2.08	
118556	N68408	Hs.194637	Homo sapiens mRNA; cDNA DKFZp564D113 (fr	2.08	2.08
129812	L07807	Hs.166161	dynamin 1	2.08	
121946	AA429411	Hs.104888	ESTs	2.08	
133843	AA489045	Hs.76691	Homo sapiens clone 25100 mRNA sequence;	2.08	
122170	AA435744	Hs.163913	ESTs	2.08	
122399	AA446449	Hs.231112	EST	2.08	
105775	AA348274	Hs.6664	ESTs	2.08	
123943	AA621553	Hs.112998	ESTs	2.08	
105771	AA347967	Hs.256267	neuroblastoma RAS viral (v-ras) oncogene	2.08	
114454	AA021091	Hs.226208	ESTs	2.08	
125802	R78852	Hs.151099	ESTs	2.08	
131556	AA442853	Hs.2869	cyclin-dependent kinase 5; regulatory su	2.08	
118837	N79836	Hs.216338	ESTs	2.08	
107345	U26209	Hs.102307	solute carrier family 13 (sodium-depende	2.08	
131324	H58690	Hs.25625	ESTs	2.08	
105233	AA216759	Hs.191132	ESTs	2.07	
112886	T03864	Hs.7436	putative acyltransferase	2.07	
120252	AA169400	Hs.152701	DKFZP434F124 protein	2.07	
114867	AA235310	Hs.52899	ESTs; Moderately similar to IIII ALU SUB	2.07	
106715	AA464955	Hs.126062	ESTs; Weakly similar to EPIDERMAL GROWTH	2.07	2.07
125560	R51281	Hs.13692	ESTs; Highly similar to PROTEIN TSG24 [M	2.07	
112270	R53021	Hs.203358	ESTs	2.07	
134626	S82198	Hs.8709	caldecrin (serum calcium decreasing fact	2.07	

115723	AA417345	Hs.54846	ESTs	2.07	
123895	AA621192	Hs.112949	EST	2.07	
119906	W85818		ESTs; Moderately similar to IIII ALU SUB	2.07	
108559	AA085161		zn12c5.s1 Stratagene hNT neuron (#937233 IMAGE:54728 3' similar to TR:G1151228 G	2.07	
101246	L33799	Hs.202097	procollagen C-endopeptidase enhancer	2.07	
100663	HG2915-HT3059		Major Histocompatibility Complex, Class I, E (Gb:M20022)	2.07	
114178	Z39063	Hs.17930	Human DNA seq frm clone 1033B10 on chr 6p for GalT3 (beta3-Galactosyltransferase)	2.07	
125672	AA152281	Hs.78601	uroporphyrinogen decarboxylase	2.07	
118052	N53360	Hs.165133	ESTs	2.07	
102387	U41163	Hs.229731	solute carrier family 6 (neurotransmitte	2.07	
127305	AA535148	Hs.255277	ESTs	2.07	
101182	L19711	Hs.76111	dystroglycan 1 (dystrophin-associated gl	2.07	
131111	R33245	Hs.23076	ESTs; Weakly similar to putative [C.eleg	2.07	
112441	R63388	Hs.28412	ESTs	2.06	
117796	N48571	Hs.46689	EST	2.06	
116099	AA456309	Hs.58831	regulator of Fas-induced apoptosis	2.06	
125559	AA307550	Hs.119571	collagen; type III; alpha 1 (Ehlers-Danl	2.06	
135271	AA397763	Hs.97562	ESTs	2.06	
106083	AA418545	Hs.31659	thyroid hormone receptor-associated prot	2.06	
133419	U67369	Hs.73172	growth factor independent 1	2.06	
127816	AA743646	Hs.120604	ESTs	2.06	
127502	AA614422	Hs.183502	ESTs	2.06	
129371	M10321	Hs.110802	von Willebrand factor	2.06	
108417	AA075716		zn89e5.s1 Stratagene ovarian cancer (#93 CLUSTERIN PRECURSOR (HUMAN);, mRNA sequ	2.06	
102837	U94585	Hs.13495	regulim; apoptosis response zinc finger	2.06	
124226	H62396	Hs.190266	ESTs	2.06	
102254	U28131		Human HMGI-C chimerc transcript mRNA, p	2.06	
128472	X87212	Hs.10029	cathepsin C	2.06	
107545	Z82022	Hs.26433	dolichyl-phosphate (UDP-N-acetylglucosam	2.06	
135311	M36089	Hs.98493	X-ray repair complementing defective rep	2.06	
121727	AA420973	Hs.104234	ESTs	2.06	
131846	U02619	Hs.331	general transcription factor IIIC; polyp	2.06	
120415	AA235810	Hs.182522	ESTs	2.06	
110529	H57686	Hs.37486	ESTs	2.06	
104996	AA112307	Hs.105894	Homo sapiens mRNA; cDNA DKFZp434G231 (fr	2.06	
110351	H41222	Hs.196459	ESTs	2.06	
131261	AA223746	Hs.171776	inositol(myo)-1(or 4)-monophosphatase 1	2.06	
110585	H62223	Hs.133526	ESTs; Weakly similar to IIII ALU SUBFAMI	2.06	
129420	AA234259	Hs.99816	ESTs	2.06	
103796	AA112595	Hs.31146	Human DNA sequence from clone 1042K10 on lyase (EC 4.3.2.2; Adenylosuccinase; AS 3). Contains ESTs; STSs; GS	2.06	
119782	W72982	Hs.58262	ESTs	2.06	
108641	AA112059		ATP synthase; H+ transporting; mitochond	2.06	
134875	U66672	Hs.180513	ATP-binding cassette; sub-family A (ABC1	2.06	
106832	AA482015	Hs.30114	ESTs; Highly similar to C8 [H.sapiens]	2.06	
109403	AA224413	Hs.86937	ESTs	2.06	
115485	AA287667	Hs.188804	ESTs	2.06	
102923	X12517	Hs.1063	small nuclear ribonucleoprotein polypept	2.06	
123320	AA496792	Hs.139572	EST	2.05	
111901	R39066	Hs.17638	ESTs	2.05	
106558	AA455111	Hs.182447	heterogeneous nuclear ribonucleoprotein	2.05	
126885	AA293052	Hs.10101	ESTs; Weakly similar to coded for by C.	2.05	
113429	T85190	Hs.179808	ESTs	2.05	
102270	U30255	Hs.75888	phosphogluconate dehydrogenase	2.05	
103204	X72475	Hs.192989	H.sapiens mRNA for rearranged Ig kappa I	2.05	
106666	AA461072	Hs.37916	ESTs	2.05	
100947	HG907-HT907		Mg44	2.05	
102578	U60666	Hs.57693	testis specific leucine rich repeat prot	2.05	
105827	AA398255	Hs.31520	ESTs	2.05	
122324	AA442830	Hs.98921	EST	2.05	
101025	J04823	Hs.81097	cytochrome c oxidase subunit VIII	2.05	
115861	AA431768	Hs.90259	ESTs; Weakly similar to alpha 1 [H.sapie	2.05	
108081	AA045306	Hs.42996	ESTs	2.05	
133994	X74929	Hs.242463	keratin 8	2.05	
119131	R46700	Hs.129692	ESTs; Moderately similar to IIII ALU SUB	2.05	
129793	AA300151	Hs.126857	ESTs	2.05	
101653	M60284	Hs.161305	tachykinin receptor 2	2.05	
120300	AA191648	Hs.131476	ESTs	2.05	
106519	AA453415	Hs.8763	Hu DNA sequence from clone 889N15 on chr Thymocyte Marker CTX; the possibly alte	2.05	
114291	Z40690	Hs.123666	Homo sapiens mRNA full length insert cDN	2.05	
105747	AA293719	Hs.30251	ESTs; Weakly similar to GLUCOSE-6-PHOSPH	2.04	

125325	AA332944	Hs.8402	adenylate cyclase 3	2.04	
119978	W88623	Hs.59190	EST	2.04	
102449	U48231	Hs.46348	bradykinin receptor B1	2.04	
101454	M21812	Hs.50889	myosin light chain 2	2.04	
116086	AA455904	Hs.86023	ESTs	2.04	
102297	U32674	Hs.198252	G protein-coupled receptor 9	2.04	
130889	D57622	Hs.20985	sin3-associated polypeptide; 30kD	2.04	
100196	D21853	Hs.79768	KIAA0111 gene product	2.04	
120967	AA398111	Hs.97503	ESTs	2.04	
105735	AA293096	Hs.32417	ESTs	2.04	
135031	R41604	Hs.9344	ESTs; Weakly similar to III ALU SUBFAMI	2.04	
104882	AA052954	Hs.29546	ESTs	2.04	
132619	AA404565	Hs.53447	ESTs; Moderately similar to kinesin ligh	2.04	
127993	AA847856	Hs.124565	ESTs	2.04	
116441	AA620299	Hs.91696	ESTs	2.04	
102272	U30610	Hs.41682	killer cell lectin-like receptor subfami	2.04	
119566	W38209		Accession not listed in Genbank	2.04	
116622	D81171	Hs.45208	ESTs; Weakly similar to collagen type VI	2.04	
127182	AA248620	Hs.166011	catenin (cadherin-associated protein); d	2.04	
116870	H67146	Hs.38564	ESTs	2.04	
115448	AA284845	Hs.165051	ESTs	2.04	
127231	AA434584		zw52c03.r1 Soares_total_fetus_Nb2HF8_9w	2.04	
103457	X99728		H.sapiens NDUFV3 gene, exon 3	2.04	
134737	U00802	Hs.89434	drebrin 1	2.04	
117046	H89505		yu81f4.s1 Soares fetal liver spleen 1NFL	2.04	
			to contains Alu repetitive element, mR	2.04	
124579	N68345	Hs.127179	ESTs; Weakly similar to TERATOCARCINOMA-	2.04	2.04
112132	R45970	Hs.236349	EST	2.04	
132281	AA133300	Hs.43803	leukocyte-associated Ig-like receptor 2	2.03	
103668	Z83741	Hs.248174	H2A histone family; member M	2.03	
113501	T89107	Hs.13262	ESTs	2.03	
125021	T70060	Hs.163918	ESTs	2.03	
115754	AA420998	Hs.178095	ESTs	2.03	
123405	AA521370	Hs.191708	ESTs	2.03	
102054	U07695	Hs.155227	EphB4	2.03	
115627	AA401910	Hs.119175	ESTs; Weakly similar to ZINC FINGER PROT	2.03	
129252	AA234663	Hs.109773	ESTs	2.03	
103417	X96849		H.sapiens 5' mRNA of PECAM-1 molecule	2.03	
133721	U11863	Hs.75741	amiloride binding protein 1 (amine oxida	2.03	
114176	Z39059	Hs.27267	ESTs; Weakly similar to tetraspan TM4SF	2.03	
123966	C14068	Hs.21806	ESTs; Moderately similar to similar to N	2.03	
134236	D45371	Hs.80485	adipose most abundant gene transcript 1	2.03	
116381	AA598614	Hs.65394	ESTs	2.03	
103711	AA046737	Hs.102792	ESTs	2.03	
109316	AA206914	Hs.86322	EST	2.03	
123793	AA620343	Hs.112858	ESTs	2.03	
128462	M69238	Hs.166172	aryl hydrocarbon receptor nuclear transl	2.03	
117690	N40467	Hs.93834	ESTs	2.03	
113301	T67452	Hs.13104	EST	2.03	
134563	AA173430	Hs.85335	Homo sapiens mRNA; cDNA DKFZp564D1462 (f	2.03	2.03
108316	AA070160		zm69f4.s1 Stratagene neuroepithelium (#9	2.03	
135239	AA454599	Hs.19399	Homo sapiens chromosome 19; fosmid 39554	2.03	
120342	AA207105	Hs.45068	Homo sapiens mRNA; cDNA DKFZp4341143 (fr	2.02	2.02
103493	Y08976	Hs.234759	H.sapiens mRNA for FEV protein	2.02	
114204	Z39259	Hs.26096	ESTs	2.02	
125425	H62307	Hs.18575	ESTs; Weakly similar to KIAA0246 [H.sapi	2.02	
133027	AA402624	Hs.63236	synuclein; gamma (breast cancer-specific	2.02	
131323	H54036	Hs.25619	death-associated protein kinase 3	2.02	
121515	AA412133	Hs.104696	ESTs	2.02	
129780	AA291526	Hs.124699	ESTs	2.02	
131292	AF005039	Hs.200600	secretory carrier membrane protein 3	2.02	
132973	AA035446	Hs.214361	ESTs	2.02	
103727	AA059415	Hs.6289	growth factor receptor-bound protein 2	2.02	
113174	T54659	Hs.9779	ESTs	2.02	
120964	AA398085	Hs.142390	ESTs	2.02	
134303	AA457242	Hs.8141	etoposide-induced mRNA	2.02	
128118	T81623	Hs.21765	hypothetical protein of unknown functio	2.02	
121087	AA398751	Hs.97304	ESTs	2.02	
102806	U90306		Human iroquois-class homeodomain protein	2.02	
103195	X70940	Hs.2642	eukaryotic translation elongation factor	2.02	
126767	C17148		C17148 Clontech human aorta polyA+ mRNA	2.02	
105179	AA189083	Hs.21974	ESTs; Moderately similar to mBOCT [M.mus	2.02	
116797	H40486		yn87a08.s1 Soares adult brain N2b5HB55Y	2.02	
			3' similar to contains Alu repetitive e	2.02	
133268	AA099404	Hs.69307	ESTs	2.02	
123951	AA621721	Hs.231130	EST	2.02	

115463	AA286819	Hs.69485	ESTs; Weakly similar to similar to other	2.02	
110603	H65776	Hs.222403	ESTs	2.02	
101234	L29277	Hs.142258	signal transducer and activator of trans	2.02	
121208	AA400470	Hs.97805	ESTs	2.02	
122598	AA453465	Hs.99329	ESTs	2.02	
110668	H84882	Hs.33791	ESTs; Weakly similar to K:Cl cotransport	2.02	
117137	H96670	Hs.42221	ESTs	2.02	
119389	T88826	Hs.90973	ESTs	2.01	
102940	X13956	Hs.24998	Human 12S RNA induced by poly(ri); poly(2.01	
100748	HG3517-HT3711		Alpha-1-Antitrypsin, 5' End	2.01	
103012	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-bi	2.01	
132755	AA609201	Hs.182635	ESTs	2.01	
130842	H39589	Hs.20159	ESTs; Highly similar to CGI-92 protein [2.01	
133599	M64788	Hs.75151	RAP1; GTPase activating protein 1	2.01	
117250	N21081	Hs.15299	HMBA-inducible	2.01	
115124	AA256666	Hs.39156	ESTs	2.01	
128155	AA926843	Hs.143302	ESTs	2.01	
130574	AA379087	Hs.16178	apoptosis antagonizing transcription fac	2.01	
132601	R78838	Hs.54943	fracture callus 1 (rat) homolog	2.01	
117428	N27366	Hs.43933	EST	2.01	
121108	AA399053	Hs.97529	EST	2.01	
130518	X69550	Hs.159161	Rho GDP dissociation inhibitor (GDI) alp	2.01	
110606	H66049	Hs.19085	ESTs; Weakly similar to putative p150 [H	2.01	
120606	AA282956		z15h4.s1 NCI_CGAP_GCB1 Homo sapiens cDN		
			SW:CADR_MOUSE P3938 RETINAL-CADHERIN PR	2.01	
130070	T47969	Hs.194660	ceroid-lipofuscinosis; neuronal 3; juven	2.01	
130331	Z80783	Hs.239884	H2B histone family; member L	2.01	
109599	F02602	Hs.6749	ESTs	2.01	
131749	W78211	Hs.31547	ESTs; Highly similar to NADH:ubiquinone	2.01	
129463	AA376905	Hs.111742	ESTs; Weakly similar to IIII ALU SUBFAMI	2.01	
114880	AA235698	Hs.65862	ESTs	2.01	
114745	AA135523	Hs.139064	EST	2.01	
115637	AA402727	Hs.76925	ESTs; Highly similar to R31167_2; partia	2.01	
109043	AA159605	Hs.72580	ESTs	2.01	
128901	Z41411	Hs.107040	ESTs	2.01	
124427	N36812	Hs.178663	ESTs	2	
100673	HG3033-HT3194		Spliceosomal Protein Sap 62	2	
108436	AA078801		zm94a9.s1 Stratagene colon HT29 (#937221	2	
123764	AA610019	Hs.112654	ESTs	2	
129343	N70791	Hs.180060	ESTs	2	
122794	AA460254	Hs.105043	EST	2	
128688	AA161469	Hs.103755	receptor-interacting serine-threonine ki	2	
115592	AA399543	Hs.48026	ESTs	2	
111693	R22007	Hs.23321	EST	2	
113353	T79186	Hs.14468	ESTs	2	

Table 18: B survivor vs Mets – Up in Mets

Pkey: Unique Eos probeset identifier number ExAccn: Exemplar Accession number, Genbank accession number UnigeneID: Unigene number Unigene Title: Unigene gene title					
Pkey	Ex Accn	UniG ID	Complete Title	Ratio BS/Met	
106024	AA412059	Hs.111742	ESTs; Weakly similar to IIII ALU SUBFAM1	0.17	
110930	N48603	Hs.14947	ESTs	0.18	
105772	AA347973	Hs.221132	ESTs	0.2	
133271	Z48633	Hs.6940	H.sapiens mRNA for retrotransposon	0.2	
107109	AA609943	Hs.32793	ESTs	0.24	
109593	F02506	Hs.159591	thyroid hormone receptor interactor 8	0.24	
123016	AA480103	Hs.111730	ESTs; Weakly similar to alternatively sp	0.25	
100739	HG3484-HT3678		Protein Kinase (Gb:M59287)	0.25	
130252	U92014	Hs.153527	Human clone 121711 defective mariner tra	0.26	
105149	AA169253	Hs.8958	ESTs	0.26	
115412	AA283804	Hs.193552	ESTs	0.27	
105952	AA405263	Hs.181400	ESTs	0.28	
106596	AA456981	Hs.35349	ESTs	0.28	
120249	AA167567	Hs.133325	ESTs	0.28	
111676	R19414	Hs.166459	ESTs	0.29	
111161	N66767	Hs.124145	ESTs	0.29	
109364	AA215379	Hs.50418	ESTs	0.29	
132316	U28831		Human protein immuno-reactive with anti-	0.3	
104030	AA363131	Hs.222992	ESTs; Weakly similar to TRANSFORMATION-S	0.3	0.3
109825	F13663	Hs.16798	ESTs	0.3	
111110	N63165	Hs.23618	ESTs	0.31	
135315	W90583	Hs.9853	ESTs	0.32	
104792	AA029288	Hs.29147	ESTs; Highly similar to ZINC FINGER PROT	0.33	
123562	AA608893	Hs.190065	ESTs	0.33	
116079	AA455286	Hs.54982	ESTs; Weakly similar to IIII ALU SUBFAM1	0.33	
110671	H87770	Hs.153800	ESTs	0.33	
108819	AA130986	Hs.193253	ESTs	0.34	
115558	AA393806	Hs.1010	regulator of mitotic spindle assembly 1	0.34	
104781	AA026617	Hs.21610	ESTs; Highly similar to BAI1-associated	0.34	
111236	N69324	Hs.12526	Homo sapiens clone 23903 mRNA sequence	0.34	
113341	T77866	Hs.189703	ESTs	0.35	
125371	AI084676	Hs.133266	ESTs; Moderately similar to Sqv-7-like p	0.35	
115890	AA435853	Hs.44114	ESTs; Weakly similar to CGI-73 protein [0.35	
113571	T91116	Hs.15713	ESTs	0.35	
121683	AA417911	Hs.175663	ESTs	0.35	
105489	AA256157	Hs.24115	ESTs	0.35	
116320	AA490866	Hs.39429	ESTs	0.36	
111917	R39882	Hs.21397	ESTs	0.36	
127568	T53722		ya91c06.r3 Stratagene placenta (#937225)	0.36	
123541	AA608794	Hs.112592	ESTs	0.36	
123131	AA487207	Hs.193272	ESTs	0.36	
125069	T86914	Hs.194485	ESTs	0.36	
114757	AA136725	Hs.161990	ESTs	0.37	
132778	AA446695	Hs.5671	Homo sapiens clone 23926 mRNA sequence	0.37	
123132	AA487233	Hs.106711	eukaryotic translation initiation factor	0.37	
134029	AA378597	Hs.143601	ESTs; Moderately similar to 67A9.b [D.me	0.37	
126956	AI434405	Hs.171957	triple functional domain (PTPRF interact	0.38	
106869	AA487563	Hs.188813	ESTs	0.38	
107818	AA020957	Hs.167948	ESTs	0.38	
129974	K00629	Hs.199300	Human kpnI repeat mma (cdna clone pcd-k	0.38	
129477	D49728	Hs.1119	nuclear receptor subfamily 4; group A; m	0.38	
119369	T79020	Hs.245915	ESTs; Weakly similar to kinase-related p	0.39	
114021	W91995	Hs.16145	ESTs	0.39	
122024	AA431296	Hs.139433	EST	0.39	
130014	N50959	Hs.143102	amine oxidase; copper containing 2 (ret)	0.39	
110163	H19326	Hs.22073	ESTs; Highly similar to J KAPPA-RECOMBIN	0.39	
104641	AA004652	Hs.18564	ESTs	0.39	
124777	R41933	Hs.140237	ESTs	0.39	
125382	AA713494	Hs.194660	ceroid-lipofuscinosis; neuronal 3; juven	0.4	
120406	AA234999	Hs.111279	ESTs; Weakly similar to unnamed protein	0.4	
132734	R23653	Hs.164250	ESTs	0.4	
117001	H84719	Hs.40721	EST	0.4	
120905	AA371602	Hs.182930	ESTs; Highly similar to PHOSPHATIDYLINOS	0.4	
125488	AA355158	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	0.4	0.4

121989	AA430044	Hs.193784	Homo sapiens mRNA; cDNA DKFZp586K1922 (f	0.4
127921	AA806616	Hs.209523	ESTs	0.4
119830	W74700	Hs.53478	ESTs	0.41
106292	AA435571	Hs.148560	ESTs	0.41
102762	U82303	Hs.123080	Homo sapiens unknown protein mRNA; parti	0.41
113518	T89731		ye11f06.s1 Stratagene lung (#937210) H s to contains Alu repetitive element;cont	0.41
100635	HG2724-HT2820		Oncogene Tls/Chop, Fusion Activated	0.41
113319	T70356	Hs.193141	ESTs; Weakly similar to coding sequence	0.41
121319	AA402935	Hs.194242	ESTs; Weakly similar to IIII ALU CLASS B	0.42
111818	R34382	Hs.24779	ESTs	0.42
104883	AA052959	Hs.177409	ESTs; Highly similar to dJ1119D9.2 [H.sa	0.42
129258	W95592	Hs.251946	ESTs; Moderately similar to POLYADENYLAT	0.42
130576	T86475	Hs.16193	Homo sapiens mRNA; cDNA DKFZp586B211 (fr	0.43
106354	AA443271	Hs.26764	KIAA0546 protein	0.43
108841	AA132524	Hs.70614	ESTs	0.43
113922	W80741	Hs.37890	ESTs	0.43
120997	AA398285	Hs.97598	EST	0.43
108158	AA054597	Hs.221935	ESTs	0.43
124516	N58185	Hs.131830	ESTs	0.43
114477	AA032013	Hs.144260	EST	0.43
104290	C16652	Hs.107205	Homo sapiens mRNA; cDNA DKFZp434L2221 (f	0.43
126700	AI318412	Hs.108258	actin binding protein; macrophin (microf	0.44
110887	N38770	Hs.4283	ESTs	0.44
116141	AA460420	Hs.44949	ESTs	0.44
110689	H93046	Hs.15571	ESTs	0.44
115314	AA280583	Hs.256501	ESTs	0.44
110904	N39453	Hs.27371	Homo sapiens mRNA; cDNA DKFZp566J123 (fr	0.44
109482	AA233375	Hs.78085	ESTs	0.44
102284	U31449	Hs.11881	transmembrane 4 superfamily member 4	0.44
118654	N70582	Hs.49892	ESTs	0.44
115334	AA281244	Hs.65300	ESTs	0.44
113149	T51588		ESTs; Moderately similar to IIII ALU SUB	0.44
113721	T97931	Hs.18190	EST	0.44
111299	N73808	Hs.24936	ESTs	0.44
103778	AA094107	Hs.7187	ESTs; Weakly similar to similar to glyco	0.44
113204	T57865	Hs.10310	EST	0.44
100315	D50857	Hs.82295	dedicator of cyto-kinesis 1	0.44
115254	AA279024	Hs.194437	ESTs	0.44
125500	H46104	Hs.244624	ESTs	0.44
117387	N26011	Hs.53810	ESTs	0.45
135113	W42450	Hs.206833	ESTs	0.45
124517	N58204	Hs.199945	ESTs	0.45
120379	AA227849	Hs.238380	Human endogenous retroviral protease mRN	0.45
119205	R91954	Hs.153699	ESTs	0.45
128266	T70341	Hs.131897	ESTs	0.45
104106	AA422123	Hs.42457	ESTs	0.45
115864	AA432080	Hs.81200	ESTs	0.45
113771	W02695	Hs.18714	ESTs	0.45
126515	AI124649	Hs.252708	Homo sapiens mRNA; cDNA DKFZp586O031 (fr	0.45
127823	AA524806	Hs.78869	transcription elongation factor A (SII);	0.45
116665	F04405	Hs.223654	EST	0.45
106355	AA443272	Hs.27836	ESTs	0.45
132693	AA621429	Hs.55075	KIAA0410 gene product	0.45
107388	W01587	Hs.173319	ESTs	0.45
110688	H93021	Hs.182937	peptidylprolyl isomerase A (cyclophilin	0.46
116893	H69569	Hs.191316	EST	0.46
105375	AA236542	Hs.9512	ESTs; Moderately similar to IIII ALU SUB	0.46
115601	AA400277	Hs.48849	ESTs	0.46
106896	AA489707	Hs.29896	ESTs; Weakly similar to proline-rich pro	0.46
111770	R27975	Hs.187469	ESTs	0.46
115663	AA405838	Hs.40507	ESTs	0.46
131404	AA504744	Hs.26461	ESTs; Weakly similar to gc-rich sequence	0.46
108622	AA101828	Hs.189956	ESTs	0.46
128286	AI025771	Hs.144090	ESTs	0.46
105760	AA338960	Hs.28170	ESTs	0.46
100020			AFFX control: BioB-3	0.46
105209	AA205072	Hs.227743	KIAA0980 protein	0.47
111975	R41724	Hs.149566	ESTs	0.47
114688	AA121403	Hs.144331	ESTs	0.47
116994	H83918	Hs.40528	ESTs	0.47
118401	N64762	Hs.49053	EST	0.47
110997	N52540	Hs.74316	desmoplakin (DPI; DPII)	0.47
123791	AA620331	Hs.245351	EST	0.47
109858	H02266	Hs.167451	ESTs	0.47
115470	AA287122	Hs.48391	ESTs	0.47

130606	AA402109	Hs.16593	ESTs	0.47
116067	AA454827	Hs.124823	ESTs	0.47
125881	AA775807	Hs.150741	2',3'-cyclic nucleotide 3' phosphodiester	0.47
124028	F04112	Hs.177178	ESTs	0.47
108995	AA155574	Hs.172702	ESTs	0.47
125102	T95105	Hs.173772	ESTs	0.47
110421	H48462	Hs.36093	ESTs; Weakly similar to reverse transcri	0.47
105658	AA282914	Hs.10176	ESTs	0.47
129046	AA195678	Hs.108258	actin binding protein; macrophin (microf	0.47
113639	T95128	Hs.17529	ESTs	0.48
132575	AA045365	Hs.5188	ESTs; Weakly similar to 60S RIBOSOMAL PRO	0.48
132592	AA129390	Hs.5285	ESTs	0.48
107619	AA004955	Hs.60015	ESTs	0.48
118664	N70907	Hs.230619	EST	0.48
127612	AA917801	Hs.116076	ESTs	0.48
112319	R55615	Hs.26432	ESTs; Weakly similar to finger protein H	0.48
113635	T95087	Hs.15543	ESTs	0.48
119344	T62969	Hs.193348	ESTs	0.48
121080	AA398720	Hs.177953	ESTs	0.48
133686	X83378	Hs.211614	chloride channel 6	0.48
130395	R54534	Hs.87889	helicase-mol	0.49
127530	AA563806	Hs.145728	ESTs	0.49
132971	AA033951	Hs.61700	ESTs	0.49
127132	AA721156	Hs.190440	ESTs	0.49
129980	T72661	Hs.13969	ESTs	0.49
105323	AA234112	Hs.29075	ESTs	0.49
114439	AA018937	Hs.128629	ESTs	0.49
107632	AA007242	Hs.60179	EST	0.49
130952	AB002296	Hs.21560	Human mRNA for KIAA0298 gene; complete c	0.49
127595	AA927308	Hs.130464	ESTs	0.49
124276	H83465	Hs.221934	ESTs	0.49
125935	H30721	Hs.30172	ESTs	0.49
131275	U45974	Hs.25156	Human phosphatidylinositol (4;5) bisphos	0.49
131196	C20633	Hs.24129	ESTs	0.49
125505	AI127843	Hs.155071	ESTs	0.5
113327	T71776	Hs.12097	ESTs	0.5
104709	AA017146	Hs.34579	ESTs; Moderately similar to IIII ALU SUB	0.5
115772	AA423972	Hs.8154	ESTs	0.5
118296	N63150	Hs.48723	ESTs	0.5
131453	C20596	Hs.26985	KIAA0457 protein	0.5
104734	AA019528	Hs.32677	ESTs	0.5
119358	T70550	Hs.193651	ESTs; Weakly similar to alternatively sp	0.5

Table 19: B survivor vs Mets – Up in B survivor

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

Pkey	Ex Accn	UniG_ID	Complete Title	Ratio BS/Met
333601			CH22_FGENES.213_4	5.5
325300			CH.11_hs gi 5866908	4.67
333642			CH22_FGENES.231_2	4.64
333591			CH22_FGENES.208_4	4.46
332859			CH22_FGENES.27_2	4.39
304013	AW518573	Hs.156110	Immunoglobulin kappa variable 1D-8	4.23
333791			CH22_FGENES.274_10	4.18
327641			CH.04_hs gi 5867890	4.03
321172	H49160	Hs.133472	ESTs	3.9
334125			CH22_FGENES.334_4	3.88
333646			CH22_FGENES.234_2	3.88
326554			CH.19_hs gi 5867308	3.84
333650			CH22_FGENES.238_3	3.82
333647			CH22_FGENES.235_2	3.79
333626			CH22_FGENES.224_2	3.68
314671	AW236550	Hs.131914	ESTs	3.68
310847	AI420523	Hs.161282	ESTs	3.67
333657			CH22_FGENES.241_2	3.65
338522			CH22_EM:AC005500.GENSCAN.395-36	3.64
329464			CH.Y_hs gi 6456788	3.6
328868			CH.07_hs gi 6381930	3.6
333637			CH22_FGENES.229_2	3.59
329737			CH.14_p2 gi 6065779	3.5
317828	AI791749	Hs.128896	ESTs	3.44
330520	M96995	Hs.6289	growth factor receptor-bound protein 2	3.44
339271			CH22_BA354112.GENSCAN.11-2	3.44
314927	AI735482	Hs.159580	ESTs	3.42
334782			CH22_FGENES.432_7	3.42
313138	AW138842	Hs.196669	ESTs	3.4
332650	H51596	Hs.5541	ATPase; Ca++ transporting; ubiquitous	3.38
338648			CH22_EM:AC005500.GENSCAN.460-6	3.38
325677			CH.14_hs gi 5867017	3.34
312639	H50648	Hs.213221	ESTs; Weakly similar to IIII ALU SUBFAM I	3.33
326545			CH.19_hs gi 5867307	3.32
318364	R44616	Hs.138280	ESTs; Moderately similar to IIII ALU SUB	3.3
308385	AI625428		EST singleton (not in UniGene) with exon	3.26
328569			CH.07_hs gi 6004480	3.26
328582			CH.07_hs gi 6006033	3.24
310975	AI492857	Hs.170940	ESTs	3.24
336883			CH22_FGENES.322-2	3.21
324425	AW236939	Hs.172154	ESTs	3.2
337870			CH22_EM:AC005500.GENSCAN.48-3	3.19
306624	AI001043		EST singleton (not in UniGene) with exon	3.17
319091	Z45264		EST cluster (not in UniGene)	3.16
335247			CH22_FGENES.516_8	3.12
324945	AA088768		EST cluster (not in UniGene)	3.1
319468	R06504		EST cluster (not in UniGene)	3.09
301635	AI590720	Hs.192662	ESTs; Weakly similar to ZINC FINGER PROT	3.08
321215	AW378128	Hs.120243	ESTs; Weakly similar to CGI-56 protein [3.04
328507			CH.07_hs gi 5868473	3.03
330266			CH.05_p2 gi 6671885	3.02
326249			CH.17_hs gi 5867263	3.01
325649			CH.14_hs gi 6588011	2.99
304575	AA496437		EST singleton (not in UniGene) with exon	2.98
304559	AA488050		EST singleton (not in UniGene) with exon	2.97
338412			CH22_EM:AC005500.GENSCAN.341-25	2.96
308707	AI769997		EST singleton (not in UniGene) with exon	2.95
313027	N34307	Hs.184003	ESTs; Weakly similar to IIII ALU SUBFAM I	2.95
306590	AI000246		EST singleton (not in UniGene) with exon	2.95
306183	AA922622		EST singleton (not in UniGene) with exon	2.94
308611	AI735372	Hs.203820	EST; Moderately similar to TRANSLATIONAL	2.94
332454	T63265	Hs.11186	ESTs; Weakly similar to transformation-r	2.94

330081			CH.17_p2 gi 6721261	2.94
317671	AW138139	Hs.244598	ESTs	2.93
338705			CH22_EM:AC005500.GENSCAN.480-4	2.93
333737			CH22_FGENES.261_1	2.9
337756			CH22_EM:AC000097.GENSCAN.109-3	2.9
333572			CH22_FGENES.189_1	2.89
335349			CH22_FGENES.539_2	2.89
328835			CH.07_hs gi 5868339	2.89
319886	AA984628		EST cluster (not in UniGene)	2.88
311247	AI655313	Hs.197692	ESTs	2.87
303887	R72672	Hs.193484	ESTs; Weakly similar to Similarity with	2.86
337564			CH22_C65E1.GENSCAN.1-7	2.85
333225			CH22_FGENES.107_3	2.84
314938	AA515635		EST cluster (not in UniGene)	2.83
305803	AA846052		EST singleton (not in UniGene) with exon	2.83
305264	AA679505		EST singleton (not in UniGene) with exon	2.83
332646	AA386264	Hs.5337	isocitrate dehydrogenase 2 (NADP+); mito	2.81
338508			CH22_EM:AC005500.GENSCAN.391-1	2.81
308097	AI475411		EST singleton (not in UniGene) with exon	2.81
301130	AW194167	Hs.149418	ESTs; Weakly similar to salivary proline	2.8
325571			CH.12_hs gi 6552439	2.8
307054	AI148181	Hs.176835	EST	2.8
337456			CH22_FGENES.777-2	2.79
317870	AI797066	Hs.201995	ESTs	2.79
303171	AA065003	Hs.64179	hypothetical protein	2.78
333717			CH22_FGENES.253_3	2.76
303778	AW505368		EST cluster (not in UniGene) with exon h	2.76
304918	AA602697		EST singleton (not in UniGene) with exon	2.76
319373	R00371		EST cluster (not in UniGene)	2.75
336072			CH22_FGENES.685_4	2.74
306023	AA897764		EST singleton (not in UniGene) with exon	2.74
336127			CH22_FGENES.701_15	2.74
337355			CH22_FGENES.728-1	2.73
337885			CH22_EM:AC005500.GENSCAN.54-3	2.73
308506	AI686791	Hs.119598	ribosomal protein L3	2.73
300629	AA152119	Hs.155101	ATP synthase; H+ transporting; mitochond	2.73
333043			CH22_FGENES.70_4	2.72
327736			CH.05_hs gi 5867940	2.72
333007			CH22_FGENES.60_4	2.72
321966	AL122111		EST cluster (not in UniGene)	2.72
323179	AW452576	Hs.156875	ESTs	2.72
332459	AA609625	Hs.112933	Homo sapiens Tax interaction protein 40	2.71
326224			CH.17_hs gi 5867230	2.71
329114			CH.X_hs gi 5868650	2.7
333577			CH22_FGENES.196_2	2.69
300413	AW090347	Hs.243443	ESTs	2.67
304055	R07994		EST singleton (not in UniGene) with exon	2.67
301013	AI935304	Hs.125262	DKFZP586G1624 protein	2.67
337848			CH22_EM:AC005500.GENSCAN.33-1	2.66
327946			CH.06_hs gi 5868206	2.66
306300	AA937573		EST singleton (not in UniGene) with exon	2.66
331071	R01646	Hs.200538	ESTs	2.65
304841	AA587541		EST singleton (not in UniGene) with exon	2.65
301321	AI860987	Hs.189097	ESTs	2.65
311280	AI767957	Hs.197737	ESTs; Weakly similar to Y38A8.1 gene pro	2.65
338843			CH22_DJ246D7.GENSCAN.8-1	2.64
335720			CH22_FGENES.599_23	2.64
333670			CH22_FGENES.245_4	2.64
313588	AI803591	Hs.209667	ESTs	2.64
335750			CH22_FGENES.602_4	2.63
333240			CH22_FGENES.111_4	2.63
332721	R70212	Hs.79630	CD79A antigen (immunoglobulin-associated	2.62
338747			CH22_EM:AC005500.GENSCAN.511-1	2.62
303582	AA377444		EST cluster (not in UniGene) with exon h	2.62
336898			CH22_FGENES.330-1	2.62
325835			CH.16_hs gi 6552452	2.62
301660	F13112		EST cluster (not in UniGene) with exon h	2.61
335968			CH22_FGENES.652_1	2.61
336705			CH22_FGENES.63-2	2.6
309815	AW292760		EST singleton (not in UniGene) with exon	2.6
339220			CH22_FF113D11.GENSCAN.6-15	2.6
308582	AI709056		EST singleton (not in UniGene) with exon	2.6
334260			CH22_FGENES.367_8	2.6
309963	AW449073		EST singleton (not in UniGene) with exon	2.6
300178	AI282665	Hs.166969	ESTs	2.59
335690			CH22_FGENES.596_5	2.59

308127	AI492187	EST singleton (not in UniGene) with exon	2.59	
337835		CH22_EM:AC005500.GENSCAN.22-4	2.58	
333251		CH22_FGENES.116_3	2.58	
330319		CH.08_p2 gi 5932415	2.58	
314490	AI758114	Hs.197032 ESTs	2.57	
305934	AA878815	Hs.75442 albumin	2.57	
329665		CH.14_p2 gi 6272129	2.57	
328558		CH.07_hs gi 5868489	2.57	
336094		CH22_FGENES.691_3	2.57	
307899	AI380270	EST singleton (not in UniGene) with exon	2.57	
339312		CH22_BA354112.GENSCAN.22-10	2.57	
336442		CH22_FGENES.827_8	2.57	
317894	R60848	EST cluster (not in UniGene)	2.56	
330435	HG2689-HT2785	Mucin 5b, Tracheobronchial (Gb:X74955)	2.56	
327304		CH.01_hs gi 5867494	2.56	
308859	AI830787	EST singleton (not in UniGene) with exon	2.55	
302224	AI951549	Hs.161166 KIAA1094 protein	2.55	
304324	AA137045	EST singleton (not in UniGene) with exon	2.54	
338090		CH22_EM:AC005500.GENSCAN.176-3	2.53	
334797		CH22_FGENES.434_5	2.52	
303535	AL043430	EST cluster (not in UniGene) with exon h	2.52	
339037		CH22_DA59H18.GENSCAN.26-5	2.52	
327846		CH.05_hs gi 6531962	2.52	
325271		CH.11_hs gi 5866901	2.52	
312385	R42885	Hs.215555 ESTs	2.51	
302816	AI733918	Hs.204112 ESTs; Weakly similar to alternatively sp	2.51	
316941	AW449871	Hs.124591 ESTs	2.5	
300184	AI285912	Hs.254515 ESTs	2.5	
333762		CH22_FGENES.270_2	2.5	
317028	AA962623	Hs.189144 ESTs; Weakly similar to RENAL SODIUM-DEP	2.5	
326266		CH.17_hs gi 5867264	2.49	
326005		CH.16_hs gi 5867112	2.49	
301971	AJ003125	Hs.120330 a disintegrin-like and metalloprotease (2.48	
326539		CH.19_hs gi 5867307	2.48	
338896		CH22_DJ32110.GENSCAN.9-4	2.48	
306773	AI040750	EST singleton (not in UniGene) with exon	2.47	
336279		CH22_FGENES.763_3	2.47	
321017	AL050345	Hs.227637 hypothetical protein	2.47	
306090	AA908609	EST singleton (not in UniGene) with exon	2.47	
333216		CH22_FGENES.104_8	2.46	
338593		CH22_EM:AC005500.GENSCAN.435-2	2.46	
333587		CH22_FGENES.205_2	2.46	
300396	AW295466	Hs.232051 ESTs	2.45	
304693	AA554263	EST singleton (not in UniGene) with exon	2.45	
338934		CH22_DJ32110.GENSCAN.18-2	2.45	
325751		CH.14_hs gi 6682474	2.45	
334137		CH22_FGENES.337_1	2.45	
333581		CH22_FGENES.200_1	2.45	
302083	AI422807	Hs.134012 C1q-related factor	2.44	
307318	AI208577	EST singleton (not in UniGene) with exon	2.44	
302181	AW374284	Hs.157732 Homo sapiens chromosome 19; cosmid R2689	2.44	
337425		CH22_FGENES.761-1	2.44	
336227		CH22_FGENES.730_2	2.44	
314657	AI015953	Hs.125265 ESTs	2.44	
338529		CH22_EM:AC005500.GENSCAN.398-10	2.44	
333680		CH22_FGENES.247_7	2.43	
324834	AJ003258	Hs.250891 ESTs	2.43	
305093	AA642917	EST singleton (not in UniGene) with exon	2.43	
335787		CH22_FGENES.611_3	2.43	
311704	AI655206	Hs.121512 ESTs; Moderately similar to kinesin like	2.43	
329382		CH.X_hs gi 5868868	2.42	
334785		CH22_FGENES.432_10	2.42	
330130		CH.21_p2 gi 6002196	2.42	
327206		CH.01_hs gi 5867447	2.41	
319235	F11330	Hs.177633 ESTs	2.41	
334691		CH22_FGENES.420_4	2.4	
327610		CH.04_hs gi 5867868	2.4	
327646		CH.04_hs gi 5867894	2.4	
337093		CH22_FGENES.465-18	2.4	
335081		CH22_FGENES.488_4	2.4	
333576		CH22_FGENES.193_2	2.4	
337604		CH22_C20H12.GENSCAN.16-5	2.4	
329879		CH.15_p2 gi 6466518	2.4	
328444		CH.07_hs gi 5868420	2.39	
335700		CH22_FGENES.598_1	2.39	
331255	Z41009	Hs.21446 ESTs; Weakly similar to HYPOTHETICAL PRO	2.39	

327927		CH.06_hs gi 5868173	2.39
334354		CH22_FGENES.377_1	2.39
308517	AI689279	EST singleton (not in UniGene) with exon	2.39
303669	AW499648 Hs.233750	copline V	2.39
333648		CH22_FGENES.237_2	2.38
318318	AI653893 Hs.174463	ESTs; Weakly similar to alpha3b subunit	2.38
338336		CH22_EM:AC005500.GENSCAN.310-8	2.38
304125	H40976	EST singleton (not in UniGene) with exon	2.38
304983	AA617786	EST singleton (not in UniGene) with exon	2.38
334935		CH22_FGENES.464_3	2.38
314326	AW170057 Hs.133179	ESTs	2.38
330406	D49490 Hs.76901	for protein disulfide isomerase-related	2.38
307646	AI302236	EST singleton (not in UniGene) with exon	2.38
338911		CH22_DJ32110.GENSCAN.11-3	2.38
319952	T79532 Hs.225725	ESTs; Moderately similar to CGI-101 prot	2.37
336878		CH22_FGENES.318-5	2.37
338140		CH22_EM:AC005500.GENSCAN.203-6	2.37
300564	AI383878 Hs.225588	ESTs	2.37
304635	AA523976	EST singleton (not in UniGene) with exon	2.37
334091		CH22_FGENES.327_47	2.37
336328		CH22_FGENES.812_7	2.37
325310		CH.11_hs gi 5866864	2.37
338043		CH22_EM:AC005500.GENSCAN.153-2	2.37
307090	AI161024	EST singleton (not in UniGene) with exon	2.37
335768		CH22_FGENES.607_2	2.37
334969		CH22_FGENES.466_2	2.37
333640		CH22_FGENES.230_2	2.36
330002		CH.16_p2 gi 6623963	2.36
338829		CH22_DJ246D7.GENSCAN.5-12	2.36
323808	AW250114	EST cluster (not in UniGene)	2.36
327755		CH.05_hs gi 5867955	2.35
306426	AA975039	EST singleton (not in UniGene) with exon	2.35
336481		CH22_FGENES.830_1	2.35
335163		CH22_FGENES.502_7	2.35
322012	AL137357	EST cluster (not in UniGene)	2.35
337345		CH22_FGENES.723-1	2.35
334625		CH22_FGENES.414_3	2.35
320957	AI878933	EST cluster (not in UniGene)	2.35
334915		CH22_FGENES.457_4	2.35
336295		CH22_FGENES.787_1	2.35
321556	N46402 Hs.14570	ESTs	2.35
338491		CH22_EM:AC005500.GENSCAN.385-2	2.35
335517		CH22_FGENES.571_34	2.34
330639	X90872 Hs.75854	SULT1C sulfotransferase	2.34
310383	AI263102 Hs.145596	ESTs	2.34
331526	N49967 Hs.46624	ESTs	2.34
334396		CH22_FGENES.381_2	2.34
332993		CH22_FGENES.57_2	2.34
327487		CH.02_hs gi 5867785	2.34
335920		CH22_FGENES.636_16	2.33
336463		CH22_FGENES.829_22	2.33
319000	Z44318	EST cluster (not in UniGene)	2.33
332992		CH22_FGENES.57_1	2.33
332920		CH22_FGENES.37_6	2.33
337590		CH22_C20H12.GENSCAN.6-5	2.33
327059		CH.21_hs gi 6531965	2.33
334399		CH22_FGENES.382_5	2.33
300982	AA837754	EST cluster (not in UniGene) with exon h	2.32
327430		CH.02_hs gi 5867754	2.32
326808		CH.20_hs gi 6682504	2.32
309324	AW015373	EST singleton (not in UniGene) with exon	2.32
329779		CH.14_p2 gi 6002090	2.32
330492	M25809 Hs.64173	ATPase; H+ transporting; lysosomal (vacu	2.31
330080		CH.19_p2 gi 6015314	2.31
334342		CH22_FGENES.375_20	2.31
336306		CH22_FGENES.793_5	2.31
336400		CH22_FGENES.823_15	2.31
323735	AA323714	EST cluster (not in UniGene)	2.31
334496		CH22_FGENES.397_12	2.31
336075		CH22_FGENES.687_1	2.31
335566		CH22_FGENES.580_1	2.31
337657		CH22_EM:AC000097.GENSCAN.32-9	2.31
327816		CH.05_hs gi 5867968	2.3
308465	AI672480	EST singleton (not in UniGene) with exon	2.3
330112		CH.19_p2 gi 6015238	2.3
304465	AA421948	EST singleton (not in UniGene) with exon	2.3

308449	AI660854		EST singleton (not in UniGene) with exon	2.3	
328171			CH.06_hs gij5868071	2.3	
328271			CH.06_hs gij5552415	2.3	
328803			CH.07_hs gij5004475	2.3	
330063			CH.19_p2 gij5165044	2.29	
312281	H11643		EST cluster (not in UniGene)	2.29	
328974			CH.09_hs gij5868520	2.29	
333859			CH22_FGENES.290_18	2.29	
326253			CH.17_hs gij5867263	2.29	
325703			CH.14_hs gij5867028	2.29	
338925			CH22_DJ32110.GENSCAN.14-3	2.29	
328552			CH.07_hs gij5868489	2.29	
337244			CH22_FGENES.646-8	2.29	
314770	AI732722	Hs.187694	ESTs	2.29	
324560	AW502208		EST cluster (not in UniGene)	2.29	
310603	AW376860	Hs.156398	ESTs	2.29	
337363			CH22_FGENES.733-2	2.29	
308015	AI440174	Hs.228907	EST; Weakly similar to GUANINE NUCLEOTID	2.28	2.28
309206	AI961962		EST singleton (not in UniGene) with exon	2.28	
337455			CH22_FGENES.777-1	2.28	
327605			CH.03_hs gij5004463	2.28	
301611	W22172	Hs.59038	ESTs	2.28	
317222	AI206964	Hs.130051	ESTs	2.28	
338278			CH22_EM:AC005500.GENSCAN.290-3	2.28	
337291			CH22_FGENES.673-2	2.27	
337913			CH22_EM:AC005500.GENSCAN.59-10	2.27	
306406	AA971973		EST singleton (not in UniGene) with exon	2.27	
332947			CH22_FGENES.47_10	2.27	
321763	W01148		EST cluster (not in UniGene)	2.27	
304424	AA293494		EST singleton (not in UniGene) with exon	2.27	
303782	T64737		EST cluster (not in UniGene) with exon h	2.27	
326943			CH.21_hs gij5004446	2.27	
324977	R14439	Hs.209194	ESTs	2.27	
325480			CH.12_hs gij5866957	2.27	
327743			CH.05_hs gij5867944	2.27	
333221			CH22_FGENES.105_1	2.26	
336498			CH22_FGENES.833_3	2.26	
321583	H84421		EST cluster (not in UniGene)	2.26	
334191			CH22_FGENES.352_6	2.26	
327089			CH.21_hs gij5531965	2.26	
310001	F18939	Hs.153827	ESTs	2.26	
304056	R08577		EST singleton (not in UniGene) with exon	2.25	
324700	AW504745	Hs.103913	ESTs; Moderately similar to !!!!! ALU SUB	2.25	
330637	X86371	Hs.95659	lethal giant larvae (Drosophila) homolog	2.25	
307642	AI302103		EST singleton (not in UniGene) with exon	2.25	
336985			CH22_FGENES.402-6	2.25	
334425			CH22_FGENES.384_13	2.25	
321216	AI078042	Hs.126691	ESTs	2.25	
315785	AW205946	Hs.150319	ESTs	2.25	
305809	AA853998	Hs.124580	EST	2.25	
331334	AA284858	Hs.89134	ESTs	2.25	
317131	AI991125	Hs.189109	ESTs	2.25	
334216			CH22_FGENES.358_1	2.24	
330330			CH.08_p2 gij5670267	2.24	
326923			CH.21_hs gij5456782	2.24	
333774			CH22_FGENES.272_5	2.24	
324311	AA443061	Hs.202520	ESTs	2.24	
338551			CH22_EM:AC005500.GENSCAN.413-2	2.24	
306716	AI024916	Hs.251354	ESTs	2.24	
337689			CH22_EM:AC000097.GENSCAN.77-5	2.24	
300079	AI192520	Hs.147178	EST	2.23	
334617			CH22_FGENES.411_16	2.23	
336890			CH22_FGENES.326-10	2.23	
334495			CH22_FGENES.397_10	2.23	
327301			CH.01_hs gij5867493	2.23	
337856			CH22_EM:AC005500.GENSCAN.41-3	2.23	
307072	AI150424	Hs.146817	EST	2.23	
330515	M85247		H.sapiens dopamine D1A receptor gene, co	2.22	
325943			CH.16_hs gij5867138	2.22	
338947			CH22_DJ32110.GENSCAN.21-4	2.22	
317465	AW197361	Hs.131360	ESTs	2.22	
332458	M33493	Hs.184504	tryptase; alpha	2.22	
333195			CH22_FGENES.98_17	2.22	
304837	AA587139		EST singleton (not in UniGene) with exon	2.22	
307602	AI288843	Hs.231239	EST	2.22	
337078			CH22_FGENES.457-1	2.22	

335862			CH22_FGENES.629_7	2.22	
301979	L28168	Hs.121495	potassium voltage-gated channel; Isk-rel	2.22	
335668			CH22_FGENES.590_19	2.22	
305068	AA639618		EST singleton (not in UniGene) with exon	2.21	
329034			CH.X_hs gjl5868561	2.21	
318403	AI131241	Hs.143234	ESTs	2.21	
328058			CH.06_hs gjl5902482	2.21	
335513			CH22_FGENES.571_28	2.21	
330803	AA004699	Hs.150580	putative translation initiation factor	2.21	
331427	H54764	Hs.237339	EST	2.21	
338973			CH22_DJ32110.GENSCAN.27-6	2.2	
336723			CH22_FGENES.85-3	2.2	
327290			CH.01_hs gjl5867483	2.2	
337240			CH22_FGENES.644-1	2.2	
306201	AA926818		EST singleton (not in UniGene) with exon	2.2	
303659	AA868464	Hs.126263	ESTs; Highly similar to FIBRILLARIN [H.s	2.2	
334517			CH22_FGENES.399_7	2.2	
334189			CH22_FGENES.352_4	2.2	
335199			CH22_FGENES.508_8	2.2	
333705			CH22_FGENES.250_19	2.2	
305794	AA845324		EST singleton (not in UniGene) with exon	2.2	
303273	AA316069		EST cluster (not in UniGene) with exon h	2.2	
313384	W85694	Hs.118335	ESTs	2.2	
329158			CH.X_hs gjl5868687	2.2	
337551			CH22_FGENES.847-8	2.2	
328792			CH.07_hs gjl5868309	2.2	
303737	AW502711		EST cluster (not in UniGene) with exon h	2.19	
324529	AW502466		EST cluster (not in UniGene)	2.19	
323103	Z45529	Hs.92030	ESTs	2.19	
333773			CH22_FGENES.272_4	2.19	
337906			CH22_EM:AC005500.GENSCAN.56-19	2.19	
327129			CH.21_hs gjl6531976	2.19	
305710	AA826544		EST singleton (not in UniGene) with exon	2.19	
335595			CH22_FGENES.581_34	2.19	
323646	AA310926	Hs.154412	ESTs	2.19	
328368			CH.07_hs gjl5868388	2.19	
325802			CH.14_hs gjl6552451	2.19	
337167			CH22_FGENES.562-27	2.19	
305059	AA635756		EST singleton (not in UniGene) with exon	2.18	
321445	AW245524	Hs.121590	ESTs; Weakly similar to ZINC FINGER PROT	2.18	
332790			CH22_FGENES.2_4	2.18	
336750			CH22_FGENES.128-4	2.18	
310999	AI520706	Hs.171012	ESTs	2.18	
329798			CH.14_p2 gjl6523160	2.18	
327012			CH.21_hs gjl5867664	2.18	
304599	AA506638		EST singleton (not in UniGene) with exon	2.18	
335351			CH22_FGENES.539_4	2.18	
310661	AI354717	Hs.223908	ESTs	2.18	
332791			CH22_FGENES.3_1	2.17	
333022			CH22_FGENES.65_1	2.17	
310502	AI458973	Hs.170422	ESTs	2.17	
324963	AA853440		EST cluster (not in UniGene)	2.17	
325275			CH.11_hs gjl5866902	2.17	
328338			CH.07_hs gjl5868377	2.17	
333063			CH22_FGENES.75_6	2.17	
308895	AI858423		EST singleton (not in UniGene) with exon	2.17	
338685			CH22_EM:AC005500.GENSCAN.472-4	2.16	
325655			CH.14_hs gjl5867007	2.16	
332420	H49570	Hs.108074	ESTs; Weakly similar to CEREBELLIN 1 PRE	2.16	
337216			CH22_FGENES.613-10	2.16	
335660			CH22_FGENES.590_11	2.16	
337145			CH22_FGENES.542-2	2.16	
335753			CH22_FGENES.604_2	2.16	
301766	R02224		EST cluster (not in UniGene) with exon h	2.16	
303442	AI953998	Hs.152510	ESTs; Weakly similar to L-SERINE DEHYDRA	2.16	2.16
311009	AI949701	Hs.210589	ESTs	2.16	
307093	AI167606		EST singleton (not in UniGene) with exon	2.16	
300262	AI874402	Hs.170810	ESTs	2.16	
337989			CH22_EM:AC005500.GENSCAN.112-7	2.16	
326263			CH.17_hs gjl5867264	2.16	
319402	W21298		EST cluster (not in UniGene)	2.16	
321010	Y17456	Hs.227150	Homo sapiens LSFR2 gene; last exon	2.16	
301706	AI929150	Hs.241496	ESTs	2.16	
307412	AI241753	Hs.241507	ribosomal protein S6	2.16	
335662			CH22_FGENES.590_13	2.15	
332480	AA092932	Hs.12570	tubulin-specific chaperone d	2.15	

329273			CH.X_hs gi 5868762	2.15	
339383			CH22_BA232E17.GENSCAN.3-20	2.15	
332795			CH22_FGENES.5_1	2.15	
335227			CH22_FGENES.513_13	2.15	
326925			CH.21_hs gi 6456782	2.15	
332403	AA424199	Hs.106529	ESTs; Highly similar to CGI-65 protein [2.15	
317786	AI859605	Hs.155686	ESTs	2.15	
326582			CH.19_hs gi 5867318	2.15	
336494			CH22_FGENES.832_11	2.15	
329656			CH.14_p2 gi 6448516	2.15	
307581	AI284415		EST singleton (not in UniGene) with exon	2.15	
335670			CH22_FGENES.591_2	2.14	
332452	AA040369	Hs.11170	SYT interacting protein	2.14	
309387	AW079943	Hs.156110	Immunoglobulin kappa variable 1D-8	2.14	
308427	AI652677	Hs.195055	EST	2.14	
322027	NM_004551		EST cluster (not in UniGene)	2.14	
301693	Z45023		EST cluster (not in UniGene) with exon h	2.14	
334308			CH22_FGENES.373_11	2.14	
301131	AW134518	Hs.131807	ESTs	2.13	
338495			CH22_EM:AC005500.GENSCAN.387-1	2.13	
329600			CH.10_p2 gi 3962481	2.13	
307980	AI431696		EST singleton (not in UniGene) with exon	2.13	
337260			CH22_FGENES.652-15	2.13	
304655	AA527887		EST singleton (not in UniGene) with exon	2.13	
303141	AF195951		EST cluster (not in UniGene) with exon h	2.13	
327957			CH.06_hs gi 5868210	2.13	
334317			CH22_FGENES.374_1	2.13	
302870	AF011407		EST cluster (not in UniGene) with exon h	2.13	
333806			CH22_FGENES.278_2	2.13	
329947			CH.16_p2 gi 5540101	2.13	
309602	AW182523		EST singleton (not in UniGene) with exon	2.13	
322790	AI700273	Hs.122162	ESTs; Weakly similar to KIAA0557 protein	2.13	
337706			CH22_EM:AC000097.GENSCAN.87-11	2.13	
306894	AI092731		EST singleton (not in UniGene) with exon	2.13	
325530			CH.12_hs gi 6525289	2.12	
321087	AL110227	Hs.241533	Homo sapiens mRNA; cDNA DKFZp434J194 (fr	2.12	
309853	AW298169	Hs.57553	tousled-like kinase 2	2.12	
326822			CH.20_hs gi 6117831	2.12	
328776			CH.07_hs gi 5868309	2.12	
335112			CH22_FGENES.494_20	2.12	
334564			CH22_FGENES.405_4	2.12	
333455			CH22_FGENES.157_4	2.12	
317395	R55044	Hs.124130	ESTs	2.12	
334221			CH22_FGENES.360_1	2.12	
331374	AA442134	Hs.70573	ESTs; Weakly similar to HINT PROTEIN [H.	2.12	
304473	AA428343	Hs.140	immunoglobulin gamma 3 (Gm marker)	2.12	
328907			CH.08_hs gi 5868493	2.12	
319448	R05539	Hs.108738	ESTs	2.12	
333676			CH22_FGENES.247_3	2.12	
324767	AA630931	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	2.12	
318585	Z43405		EST cluster (not in UniGene)	2.12	
331732	AA251192	Hs.177708	ESTs	2.12	
329553			CH.10_p2 gi 3962492	2.12	
336910			CH22_FGENES.343-6	2.12	
326959			CH.21_hs gi 6469836	2.12	
305417	AA725228		EST singleton (not in UniGene) with exon	2.11	
301573	AI150328	Hs.226402	ESTs; Weakly similar to mitochondrial ci	2.11	
326935			CH.21_hs gi 6004446	2.11	
335176			CH22_FGENES.504_6	2.11	
337210			CH22_FGENES.603-5	2.11	
311284	AW027025	Hs.239262	ESTs	2.11	
330240			CH.05_p2 gi 6671858	2.11	
327463			CH.02_hs gi 6004455	2.11	
332938			CH22_FGENES.41_3	2.11	
332785			CH22_FGENES.1_1	2.11	
301035	AI358105	Hs.123164	ESTs	2.1	
305712	AA826701		EST singleton (not in UniGene) with exon	2.1	
318651	AW003150	Hs.240165	ESTs	2.1	
302753	M74299		EST cluster (not in UniGene) with exon h	2.1	
334635			CH22_FGENES.417_2	2.1	
319447	AA456745		EST cluster (not in UniGene)	2.1	
301204	AW008544	Hs.239994	ESTs	2.1	
333950			CH22_FGENES.303_6	2.1	
325947			CH.16_hs gi 5867138	2.1	
337683			CH22_EM:AC000097.GENSCAN.76-1	2.1	
328962			CH.08_hs gi 6456775	2.1	

336655			CH22_FGENES.34-3	2.1
336596			CH22_FGENES.163_2	2.1
330486	M13755	Hs.833	Interferon-stimulated protein; 15 kDa	2.1
314356	AA531607	Hs.125143	ESTs	2.09
314976	AA524725	Hs.162108	ESTs	2.09
336650			CH22_FGENES.29-6	2.09
339026			CH22_DA59H18.GENSCAN.22-6	2.09
302395	AW297357	Hs.114606	ESTs	2.09
323280	AI910263		EST cluster (not in UniGene)	2.09
338857			CH22_DJ32I10.GENSCAN.1-1	2.09
335374			CH22_FGENES.543_12	2.09
308766	AI808510		EST singleton (not in UniGene) with exon	2.09
331027	N48584	Hs.6168	KIAA0703 gene product	2.09
337853			CH22_EM:AC005500.GENSCAN.37-1	2.09
302498	NM_002991		EST cluster (not in UniGene) with exon h	2.09
312607	AI337440	Hs.169375	ESTs	2.09
314309	Z44049	Hs.184352	ESTs; Weakly similar to cDNA EST EMBL:D3	2.09
311695	AI142078	Hs.135562	ESTs	2.09
333280			CH22_FGENES.126_2	2.09
333518			CH22_FGENES.173_3	2.09
337199			CH22_FGENES.583-11	2.09
337819			CH22_EM:AC005500.GENSCAN.13-9	2.08
300546	AA214450	Hs.250913	ESTs	2.08
322577	AA354452	Hs.59075	ESTs; Weakly similar to WD40 protein Cia	2.08
336028			CH22_FGENES.672_1	2.08
300238	AI394673	Hs.254030	ESTs	2.08
307429	AI243573		EST singleton (not in UniGene) with exon	2.08
326444			CH.19_hs gil5867385	2.08
310641	AI345597	Hs.254727	ESTs	2.08
337633			CH22_C20H12.GENSCAN.32-1	2.08
336008			CH22_FGENES.668_6	2.08
339030			CH22_DA59H18.GENSCAN.24-1	2.08
333952			CH22_FGENES.303_8	2.08
329149			CH.X_hs gil5868685	2.08
335192			CH22_FGENES.507_7	2.08
308225	AI557713	Hs.177592	ribosomal protein; large; P1	2.08
330519	M94172	Hs.69949	calcium channel; voltage-dependent; L ty	2.08
331809	AA402482	Hs.97312	ESTs	2.07
324837	AJ003669	Hs.246171	ESTs	2.07
332608	D00749	Hs.36972	CD7 antigen (p41)	2.07
327291			CH.01_hs gil5867483	2.07
315936	AW069807	Hs.247094	ESTs; Moderately similar to IIII ALU SUB	2.07
317917	AI143593	Hs.129419	ESTs	2.07
328674			CH.07_hs gil5868254	2.07
338654			CH22_EM:AC005500.GENSCAN.460-55	2.07
320828	AJ012590	Hs.194728	hexose-6-phosphate dehydrogenase (glucos	2.07
337896			CH22_EM:AC005500.GENSCAN.56-3	2.07
335310			CH22_FGENES.532_3	2.07
300076	AW074835	Hs.145223	ESTs	2.07
303588	AL046182		EST cluster (not in UniGene) with exon h	2.07
328848			CH.07_hs gil6381921	2.07
318723	C18060		EST cluster (not in UniGene)	2.07
335352			CH22_FGENES.539_5	2.07
339316			CH22_BA354I12.GENSCAN.22-15	2.06
335873			CH22_FGENES.631_1	2.06
335261			CH22_FGENES.520_2	2.06
322032	AL079807		EST cluster (not in UniGene)	2.06
308771	AI809301		EST singleton (not in UniGene) with exon	2.06
310024	AI252661	Hs.145224	ESTs	2.06
320555	R36212	Hs.235534	ESTs	2.06
319314	T74062		EST cluster (not in UniGene)	2.06
334642			CH22_FGENES.417_9	2.06
335767			CH22_FGENES.607_1	2.06
336159			CH22_FGENES.707_3	2.06
336358			CH22_FGENES.818_1	2.06
334687			CH22_FGENES.419_12	2.06
339389			CH22_BA232E17.GENSCAN.4-7	2.06
335898			CH22_FGENES.635_6	2.06
328847			CH.07_hs gil6381920	2.06
313431	W91884		EST cluster (not in UniGene)	2.06
313270	AI374993	Hs.159611	ESTs	2.06
339211			CH22_FF113D11.GENSCAN.6-6	2.06
333860			CH22_FGENES.290_19	2.06
308952	AI868157	Hs.224226	EST	2.06
305471	AA743947		EST singleton (not in UniGene) with exon	2.06
300619	AA991438	Hs.233293	ESTs	2.06

302962	AI693349	Hs.228981	EST	2.06	
332446	AA112799	Hs.238756	ESTs; Weakly similar to unknown [H.saple	2.06	
334972			CH22_FGENES.468_2	2.05	
330196			CH.05_p2 gij5165140	2.05	
304754	AA579795		EST singleton (not in UniGene) with exon	2.05	
309726	AW248521	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	2.05	
333939			CH22_FGENES.301_5	2.05	
304836	AA587008		EST singleton (not in UniGene) with exon	2.05	
302087	AA324163		EST cluster (not in UniGene) with exon h	2.05	
308424	AI650714		EST singleton (not in UniGene) with exon	2.05	
304347	AA176914		EST singleton (not in UniGene) with exon	2.05	
333141			CH22_FGENES.85_1	2.05	
310573	AW292180	Hs.156142	ESTs	2.05	
337565			CH22_C65E1.GENSCAN.1-11	2.05	
304295	AA084082		EST singleton (not in UniGene) with exon	2.05	
326624			CH.20_hs gij5867553	2.05	
326443			CH.19_hs gij5867385	2.04	
339012			CH22_DA59H18.GENSCAN.19-2	2.04	
337384			CH22_FGENES.745-1	2.04	
332326	T79623	Hs.111787	ESTs	2.04	
303706	AW501525		EST cluster (not in UniGene) with exon h	2.04	
336046			CH22_FGENES.679_8	2.04	
301770	R05887		EST cluster (not in UniGene) with exon h	2.04	
326726			CH.20_hs gij5867597	2.04	
330485	M11186	Hs.113216	oxytocin; prepro- (neurophysin I)	2.04	
332956			CH22_FGENES.48_13	2.04	
300021	M97935		AFFX control: STAT1	2.04	
306872	AI086920		EST singleton (not in UniGene) with exon	2.03	
302744	L03151		EST cluster (not in UniGene) with exon h	2.03	
338507			CH22_EM:AC005500.GENSCAN.390-11	2.03	
334020			CH22_FGENES.317_1	2.03	
333870			CH22_FGENES.291_3	2.03	
330552	U40223	Hs.248157	pyrimidinergic receptor P2Y; G-protein c	2.03	
335486			CH22_FGENES.570_18	2.03	
339374			CH22_BA232E17.GENSCAN.2-5	2.03	
328384			CH.07_hs gij5868392	2.03	
334690			CH22_FGENES.420_3	2.03	
310318	AI733942	Hs.145338	ESTs	2.03	
325893			CH.16_hs gij5867088	2.03	
331373	AA435513	Hs.178170	ESTs; Weakly similar to DUAL SPECIFICITY	2.03	
329784			CH.14_p2 gij5912597	2.03	
335087			CH22_FGENES.488_11	2.03	
310582	AI336563	Hs.254585	ESTs	2.03	
332611	R06751	Hs.1600	chaperonin containing TCP1; subunit 5 (e	2.03	
339258			CH22_BA354I12.GENSCAN.8-3	2.03	
336851			CH22_FGENES.274-1	2.03	
305596	AA780664	Hs.8734	ESTs; Moderately similar to IIII ALU CLA	2.03	
330364			CH.X_p2 gij3126882	2.03	
302940	AL137619		EST cluster (not in UniGene) with exon h	2.03	
317349	AA923657	Hs.126359	ESTs; Weakly similar to IIII ALU SUBFAM	2.03	
309869	AW300314		EST singleton (not in UniGene) with exon	2.03	
333422			CH22_FGENES.147_2	2.03	
325233			CH.10_hs gij6381943	2.03	
330586	U77968	Hs.79564	neuronal PAS domain protein 1	2.03	
336725			CH22_FGENES.88-1	2.02	
334157			CH22_FGENES.340_7	2.02	
303357	AW006352	Hs.159643	ESTs; Weakly similar to MLD [H.saplens]	2.02	
328533			CH.07_hs gij5868482	2.02	
309210	AI962817		EST singleton (not in UniGene) with exon	2.02	
327412			CH.02_hs gij5867750	2.02	
333172			CH22_FGENES.94_7	2.02	
334869			CH22_FGENES.447_3	2.02	
301047	AA971465	Hs.116136	ESTs	2.02	
329394			CH.X_hs gij6478817	2.02	
301736	F12128		EST cluster (not in UniGene) with exon h	2.02	
335591			CH22_FGENES.581_30	2.02	
338234			CH22_EM:AC005500.GENSCAN.260-7	2.02	
334433			CH22_FGENES.385_8	2.02	
334904			CH22_FGENES.452_18	2.02	
318443	AI939323	Hs.157714	ESTs; Weakly similar to NEUR ACETYLCHOLI	2.02	2.02
300151	AI243445	Hs.189654	ESTs	2.01	
310348	AI478563	Hs.145519	ESTs	2.01	
310898	AI439868	Hs.165742	ESTs	2.01	
332860			CH22_FGENES.27_3	2.01	
301699	AI879117		EST cluster (not in UniGene) with exon h	2.01	
332554	W96450	Hs.23111	phenylalanine-tRNA synthetase-like	2.01	

327994		CH.06_hs gl 5868218	2.01	
315613	AW137420	Hs.192311 ESTs	2.01	
335356		CH22_FGENES.541_3	2.01	
334028		CH22_FGENES.318_7	2.01	
335277		CH22_FGENES.523_3	2.01	
308657	AI749855	Hs.236497 EST; Weakly similar to GLANDULAR KALLIKR	2.01	2.01
305913	AA876109	EST singleton (not in UniGene) with exon	2.01	
323681	AW247730	Hs.102548 glucocorticoid receptor DNA binding fact	2.01	
333533		CH22_FGENES.175_20	2.01	
328753		CH.07_hs gl 5868298	2.01	
302397	L01694	Hs.211523 guanine nucleotide binding protein (G pr	2.01	
304643	AA526588	EST singleton (not in UniGene) with exon	2.01	
333065		CH22_FGENES.75_8	2.01	
316192	AA904441	Hs.221286 ESTs	2	
302533	L36149	Hs.248116 chemokine (C motif) XC receptor 1	2	
312988	AA813689	Hs.123436 ESTs	2	
333612		CH22_FGENES.217_7	2	
333615		CH22_FGENES.217_10	2	
316085	AI027959	Hs.132300 ESTs	2	
337936		CH22_EM:AC005500.GENSCAN.85-7	2	
330972	H18467	Hs.118983 ESTs; Weakly similar to diaphanous 1 [H.	2	

Table 20: B survivor vs Mets – Up in Mets

Pkey: Unique Eos probeset identifier number ExAccn: Exemplar Accession number, Genbank accession number UnigeneID: Unigene number Unigene Title: Unigene gene title				
Pkey	Ex Accn	UniG_ID	Complete Title	Ratio BS/Met
316625	AA780307	Hs.122156	ESTs	0.28
316076	AW297895	Hs.116424	ESTs	0.3
315943	AA699756	Hs.117335	ESTs	0.38
317198	AI810384	Hs.128025	ESTs	0.38
320082	AA487678	Hs.189738	ESTs	0.39
313510	AI147291	Hs.154006	ESTs	0.39
323683	AI380045	Hs.225033	ESTs	0.39
318558	AW402677	Hs.90372	ESTs	0.4
310264	AI915771	Hs.148867	ESTs	0.4
314945	AW276866	Hs.192715	ESTs	0.41
313403	W86995	Hs.113157	ESTs	0.42
321505	H73183	Hs.129885	ESTs	0.43
312171	AW444619	Hs.138211	ESTs	0.43
324585	AI823969	Hs.132678	ESTs	0.44
316695	AA809844		EST cluster (not in UniGene)	0.44
319818	AA825819	Hs.136952	ESTs	0.44
337522			CH22_FGENES.819-1	0.45
324714	AA574312	Hs.245737	ESTs	0.45
315060	AA551104	Hs.189048	ESTs	0.46
300548	AI026836	Hs.114689	ESTs	0.47
304483	AA431441		EST singleton (not in UniGene) with exon	0.47
313096	AI422367	Hs.163533	ESTs	0.47
306501	AA987294		EST singleton (not in UniGene) with exon	0.47
329086			CH.X_hs g 5868604	0.47
320176	AA167566	Hs.133325	ESTs	0.47
320418	AI674461	Hs.199638	ESTs	0.47
302982	W92391	Hs.198222	ESTs; Weakly similar to C2H2-type zinc f	0.48
315609	AW207535	Hs.224012	ESTs	0.48
317056	AA904908	Hs.250643	ESTs	0.48
314361	AL038765	Hs.161304	ESTs	0.49
315169	AI371390	Hs.158667	ESTs	0.49
323743	AA324992	Hs.257168	ESTs	0.49
313903	AW167439	Hs.190651	ESTs	0.49
315061	AA551196	Hs.188952	ESTs	0.49
300969	AI140799	Hs.76230	ribosomal protein S10	0.5
331950	AA454595	Hs.99369	ESTs	0.5
315076	AI623817	Hs.168457	ESTs	0.5
300975	AI283548	Hs.149668	ESTs	0.5

TABLE 1-20A

Table 1-20A, shows the accession numbers for those pkeys lacking unigeneID's for Tables 1-20. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT Number Accession

108446	112224_1	AA085383 AA126091 AA074174 AA075373 AA079120 AA070831 AA075978 AA075372 AA128503
108474	116896_1	AA115179 AA079667 AA115897 AA079771
100635	10605_34	BE259039 W29128 AW410299 X72990 BE246492 NM_005243 X66899 AI909006 AW248151 AL031186 AA012966 BE273549 BE311429 BE253102 Y07848 BE538102 BE256863 BE261240 BE312156 BE618412 BE257322 BE620446 AW806629 AA376777 AA325384 BE256808 BE251039 BE257878 BE275352 AA357169 AW403562 AA204995 AA093259 W95953 BE256279 BE336683 BE252465 BE251266 AA380754 BE294942 AA380941 AA380999 BE297164 BE249995 BE294719 BE295372 AI270673 BE305132 BE563752 BE295357 AI525421 BE263980 AA057505 AA020915 BE266318 BE206948 AI474020 BE296420 BE297374 BE408545 BE019366 BE407372 BE266180 BE279437 R58233 T19567 BE300738 AW381179 AA357571 AW361285 AA436908 AA301019 AA301022 N20202 BE408777 BE548638 BE167415 AA071260 BE088429 BE280092 W23117 T19568 R51681 AW402216 W22784 BE185607 AI457224 BE544120 AL134874 S72620 AA375079 D51319 AW818280 BE514686 AW853024 BE563744 AA300469 T07592 BE622190 BE272834 W21781 BE315450 BE542367 BE393120 AA988441 H55137 BE562296 BE622502 BE395960 AA329733 AA332348 AI768317 AA456866 AI497832 AW878437 AA857042 U18018 BE621418 AI818790 AI949507 BE397693 AI885545 AI858854 AI355147 BE169028 S62138 AW732191 AA856891 BE266060 X71427 BE268557 AF095890 AW001288 AI799634 AI623498 AA071346 BE547662 BE261446 AI564543 BE559759 U35622 BE314249 BE264915 AI638591 AI538385 AW090025 BE384754 AI888689 AW778800 AI925273 AA075797 AW949130 AV660275 AW438697 AI587137 AI524121 AA806249 AW628247 AA808241 AI244388 AI761125 AW117672 AA911782 AI129250 AA654447 H55291 BE258050 BE206162 W95867 AA857187 AI871378 AI660103 AW103827 AI220929 AW149949 BE465561 AI302857 AW168841 D82190 AW249814 AI623432 AI687358 AW951077 R51592 W60458 AI092863 AW474693 D12765 AI911646 D82208 D82187 AW074031 AI358527 AW338497 AA970893 AW072573 AA205364 AI858886 AA012830 AW148763 AI863056 AA548656 BE250325 AI016994 AI864005 BE046122 AI497746 C75340 R58896 D82141 AW168240 C19048 AI741090 D29465 AI222365 AA948288 AI583522 AW572212 AI091290 AA582727 AA579897 AA570629 W60883 AW516989 AL038160 AA577334 AI865872 AA994043 AA922583 AA464778 AA209178 AI829479 AI370235 BE246529 AA384177 AA456255 AI699730 W60654 AL035744 AA862042 R32756 AI886886 AA993087 AI289479 AA627840 AA464184 AI619503 R32755 AW075358 AI432315 AA457024 AA020865 R92132 AA454629 AA746059 AA454643 AA456240 AA826984 BE163738 AI806470 AI991074 AI802560 AA587095 AA558714 AA968521 N87780 AI538246 N71794 AV661738 AI368903 AA362570 AI989445 AI674962 S75762 BE245204 AA975296 D20123 AW005704 AA693328 AA582270 AI918474 AW205707 AI696299 AA220990 AA101538 T29030 H27201 AW262526 AI610530 AA126840 AA126790 X92120 AW367868 BE299644 BE299451 AA476561 BE300044 AA134363 BE295222 AA307504 N42337 AA319098 N39502 AW964461 N57241 BE299049 N86332 R51156 AA085859 T75212 AA133939 AA147129 AA156161 BE543953 BE538848 AA133676 BE299745 AA135050 AA218535 AW406401 AW411287 BE410528 C01410 NM_004083 BE314959 AA836413 AA085862 AW024370 AA471059 AW467508 AA001025 AI828231 AA633221 T95517 AA147038 AA476447 AW027012 AW078627 BE513200 AI192297 AA886279 AW081806 AA316185 AA010506 AI269929 W93139 AI682935 AA609555 AA378028 AI093877 AA999997 AA730698 AI143923 AW575315 AA890550 AA494353 AW576601 AI796336 AA826130 AA609207 AI539618 AI088539 AI089090 AA825505 AA632978 AA015892 AW204713 AA156495 AA824613 AA133630 N29826 AA527476 AI633352 T27908 AA134364 AA133940 AW043601 H37775 AA772375 AA057871 AA047888 AA054225 H86568 AA001511 H25718 AW189507 AA165589 AA054433 H85549 AA165486 AA058972 AA454911 AA464064 AA493802 AA428253 R85508 AW302469 AI611812 BE162582 F11073 T95518 N26811 AI783929 H40669 AW611745 AI658803 R51042 R45276 AA528386 AA782875 AW880218 AL138391 AA314536 AW949338 AA149466 AA149552 AI346513 AA216776 BE349131 AW007654 AI141803 AA622688 AI185131 AW057635 AA101539 AA627986 H27202 AI536847 W93084 AI973148 AI246788 AW572108 AI469414 AA454835 AA612707 AA430746 AI084991 AA010400 AA856636 AA463928 AI248310 R07170 AA834033 D12244 AI655670 AA054350 AA639480 AI702067 AI475389
100643	3931_1	NM_005032 M34427 AA332167 AW409711 AL119718 BE297581 BE299855 AA082284 AA226855 AA149568 AW391953 M22299 BE163594 AW847881 AW366993 BE142871 AW847885 AW604137 AW847753 AW847886 AW376442 U48350 AW607478 AA373011 AA334080 BE294177 AL121355 AA302236 BE540666 BE170588 AA346884 BE541512 AA226818 AA082001 AA366490 AW604122 AA205784 AW607791 BE168496 AA058497 T64373 BE165633 AW802804 AW847878 AA187408 AA088397 AI751745 AA344103 AA034463 AI906008 AA363580 AA379193 AI332642 AI143569 W52748 W52754 AA385532 AA085967 F05943 AA363422 AA133444 AA133477 AA029541 N48387 N83348 AA376066 AA147671 W70187 AA316255 BE174987 AA452776 AA089605 AL047776 BE162673 H39532 BE168406 AA357654 AA328728 AW813442 D57844 AW839748 AW839663 D57357 AA334536 AW268674 AW950788 AW409888 AI160544 D57821 AW664382 D25884 AI755101 AW130365 AI609094 AI984064 AI806523 AA492516 AI755258 BE157210 AA374884 AI983923 AI831088 AA706501 AI754957

AI688651 AI088623 AI336114 N38752 T56004 AA845200 AA858377 BE157397 AW069347 AA045366 AW316918 AW130372
 AI355398 BE157396 AI751746 AI375820 AA129935 W60002 N24781 AI805924 W60009 AA044283 AA121161 AI539277
 AA301885 AW019944 AA133445 AA101108 AA033559 W70060 AA617751 AI986261 AI023234 D82235 AA085846 AW754181
 D82093 D82100 AA147653 AA600256 D57884 AI753982 AI568050 AI146490 AW302280 AI433051 AA329188 AW572150
 AW166345 AI337981 AA778973 N67577 AA227207 AA838281 C06190 AL046997 AI217662 AI752979 AW627538 AI127171
 AI440461 T64184 AA845190 AA227111 AA877394 R60962 AA505646 AA770545 AI696264 AA953747 AA904094 AA058318
 D57026 T17158 AA578545 AW085082 BE148939 AW815069 BE152843 BE149068 BE149036 AW815073 AW753691 BE149040
 AW815065 BE152842 BE149072 AW753692 AW815055 BE152837 BE152849 BE152840 AW815070 BE152829 BE152846
 BE148972 BE149042 BE149074 AW753668 BE152832 BE152841 BE149082 BE149050 AA347261 BE152852 BE152847
 R65797 F02189 AA483448 AI954410 AA865375 BE152838 BE152838 BE152839 T17300 BE152844 BE152833 BE152834
 AA029542 AI567601 AI362353 BE162140 AI381384 BE152851 D57038 D57043 AI418363 AA133478 BE149051 BE149083
 BE152850 BE149052 BE149084 AA886686 BE149064 BE149032 AA044093 AA129934 AA303976 BE157211 AA187291
 BE152830 AA046552 BE149047 BE149079 BE149033 BE149065 BE149044 BE149076 BE149053 BE149085 BE149034
 BE149066 BE149048 BE149080 BE149038 BE149070 BE149045 BE149077
 100670 22023_1 AA332178 BE259177 BE545625 T09105 S62076 M16424 NM_000520 BE244309 F13516 BE251567 BE514981 AL119537
 AA336739 BE261801 AA278642 N32708 T77034 W24621 W42478 AW630382 AW856214 AA134234 M13520 BE379212
 AA287459 BE019379 BE297192 BE162970 AW405668 AW403322 BE272280 BE208703 BE304428 BE162807 BE162828
 BE162887 BE078944 BE163025 BE162878 BE162909 BE162898 BE162791 BE162880 BE073563 BE163086 BE162896
 BE162770 BE073565 BE162906 BE162913 BE162947 BE162803 BE262199 BE162811 BE080697 BE315095 AW206024
 AI291054 BE087364 AL046839 AA304422 AA847660 AA669876 BE392765 AI567798 AW026644 AW151258 AA996314
 AI828660 AI571158 T61941 AW103503 AW172698 AI923115 AI823709 T62167 AW771381 AW151782 AI799284 AW242271
 AA128031 BE261306 BE312241 AI674880 BE261057 AA630684 AA831305 AI139546 AW082447 AA916854 AA916855 T05970
 AA599395 AA921680 AI244674 AI041920 AA424998 AI362999 W42543 T51260 AI362486 AI699366 AI827925 AI027381
 AI027370 AI209049 AA782220 AI334014 AI279051 AI217711 AI674210 AI193370 AI701683 T23782 AI927545 AI784291
 AA128007 AI370630 AI972736 AA853763 N92379 AI916746 AA639633 AA907603 AI479452 AW950971 T28985 AI685825
 AA563654 AA745291 AW089417 F10858 AI354227 R38108 AI668647 AA994088 AI740910 AW880973 AI739410 AI480346
 N78987 AI473892 BE162903 BE254430 BE260426 AA650012 AW006426
 100673 21517_2 AW403342 AW248986 BE561709 AA357312 BE311834 BE389496 BE294887 AW732696 BE047868 AI702383 BE019155
 AI702367 BE408966 BE280458 BE313759 BE513492 BE535404 BE280258 AC005263 NM_007165 L21990 AW732711
 AI564920 AW249094 BE265365 AW607186 AW607346 BE005217 H27211 U46230 BE260066 BE207043 BE546782 AW248659
 AA085228 AA085161
 108559 41469_9 AA082885 AA114265 AA085398 AA113184
 108569 118606_1 AA932794 BE540417 AW409802 AW410765 BE296651 BE294197 BE164813 AW381886 AW381806 AL048654 AW403058
 100700 17137_1 BE207228 AA464654 AW966967 AA326831 BE407277 BE408669 AA476527 AA115576 AA359697 AA476357 AA449939
 BE263719 AL045304 W21442 R28919 BE395990 AA252273 AI346812 BE538487 AA507160 W93950 N42025 AI088439
 AL134931 AA031524 AI887287 AW470017 AA476423 AA464553 AW410766 AI569421 AA577476 AI248935 AI912371
 AW615674 AA824237 AA807746 AA827377 AA890268 AA476309 AI086424 AW409698 AA031553 AW451901 AI520934
 AW050554 R49825 N30302 AA532541 W94004 N93402 AA115549 AA331202 L25665 NM_005275 AA436745 AI122671 R49779
 R18508
 100734 35197_1 AI807481 AI500404 AI092260 BE348962 AI143675 AA772399 AA772398 AI368565 AI379172 AI083781 AI871363 AA843793
 NM_000141 M87770 X52832 M55614 Z71929 W05259 AA548551 AI498743 BE081295 BE162251 F05643 AI127918 H83199
 W07463 BE551725 R28404 AW206461 AW590506 AI885536 N69800 R93496 R25381 AA443093 AI143063 AI284647 AI703144
 AA309032 AA309031 AW949426 AW949428 AI638387 AI638356 R77173 R38513 T89263 F01900 H87979 R70205 AA664355
 AA235910 AA033657 AI436212 N50463 AI433805 AI081876 AI421090 AW020818 AI559529 AI887420 BE154202 AA889062
 AA723410 BE537575 AA236812 AI218552 AI264866 AI290617 AA424365 AA424505 AW073347 AA032183 AI142488 N55322
 AI884363 AI336070 N67307 AA608928 T94993 AW514184 AA724695 N66630 AI379638 AI274671 AW628470 AA235346
 AA687581 AI073906 AI263602 AI869111 AI805693 AI423808 AI076491 AI374640 H82967 AA776567 AA256191 T29856
 AA953586 AI140801 AI805484 AA984329 R93497 AI017114 AI263355 N81103 AW418776 D57474 AI918460 AA256152
 AI683268 AI042628 AW196650 C00195 AI918567 T28903 N95383 R13671 T94939 AI275235 AA235751 T84335
 100739 2738_3 M59287 L29222 AI251890 BE244986 AI708332
 117040 46956_1 AW970600 AA503323 H89218 AF086031 H89112
 100748 41861_1 X06096 X05826
 100760 1334_7 AW794626 M27126 M27014
 100779 458_127 BE561958 BE561728 BE397612 BE514391 BE269037 BE514207 BE562381 BE514256 BE514403 BE514250 BE397832
 BE269598 BE559865 BE396881 BE560031 BE514199 BE560037 BE560454
 100787 458_127 BE561958 BE561728 BE397612 BE514391 BE269037 BE514207 BE562381 BE514256 BE514403 BE514250 BE397832
 BE269598 BE559865 BE396881 BE560031 BE514199 BE560037 BE560454
 130872 21268_1 U61084 NM_004900 U61083 AI761325 AI826909 H79385 T81886 AI222763 N68038 AI281048 H79274 AA603662 AA721720
 T71211 C00488 AA994672 AW136970 AW368715 AA380767 AL022318
 AA112059
 108641 853_-13 U79251 AA843851 R38201 R66461 R44908 AA683289 H17477 R37364 R52832 AW298336 AA351391 NM_002545 L34774
 100818 19604_3 AA296886 AW967001 T28889 R13451 T77331 AL119196 AL118830 H08459 AW892812 AW905838 H17585 R52878
 130930 2773_1 NM_005658 U19261 BE622108 AA313592 AW950162 H25107 R71725 R50630 AI524201 AI476301 AW014547 AW195770
 AI378122 AI554908 AI927196 AI913959 AW044513 R50534 AI379950 AI311593 BE043305 R82981 AA769375 R77429
 AW196220 AI269033 AA883433 R71691 F11489 AW771234 AA402642 AA399408 AW771244 AI400707 R55446
 124394 5590_5 AI950447 AW027427 AI640151 AI139433 AI400708 AW779975 AI739122 AI384000 AW079410 AI473425 AA150109 AI766579
 AI351784 AI209046 AI474732 N29724 AI382653
 100882 458_127 BE561958 BE561728 BE397612 BE514391 BE269037 BE514207 BE562381 BE514256 BE514403 BE514250 BE397832
 BE269598 BE559865 BE396881 BE560031 BE514199 BE560037 BE560454
 100885 12707_3 X07881 NM_006249 X07637 AA376715 AA376677 X07715 X07704 S80916
 100896 205_6 M91803 X65362
 100898 8542_1 BE387614 R51501 AA199714 AW674779 F08178 BE269071 AA376313 H08264 AA380420 H18785 AL042151 BE277758
 BE267438 NM_005850 L35013 BE540833 BE390902 BE391494 BE277459 BE385592 BE390612 BE384263 BE387779
 BE388647 BE537373 BE547158 AW409585 AW374033 AW602185 AA355725 AW577548 AW935015 AW935160 W40232
 AW938647 AW374332 AA434040 BE293488 AL138361 BE560260 AI745075 AA317980 AW949382 AI834311 AI653582
 AI831042 AI361878 AA618606 AA729052 AI424969 AA199715 AW769374 AI828422 AW044307 AI862816 AI203583 AW084461

AW514655 AA831883 AA290672 AA831286 AA578510 AW089965 AW150746 AA292743 H22232 AI469275 AW439312
AA292744 AW471443 AI473989 AA593336 AA464070 AI678937 AW069451 AA970763 AA610480 AA593328 AA464009
AA768985 AI298928 AA436600 AA464718 AA699361 D61482 D55935 AI369591 AA470695 AI809135 AA640627 AI568446
R51502 W45467 AI655316 AA463934 AW168609 AW518663 BE045525 Z41251 AI868091 AA908160 AI026697 AI886259
AI612932 AA215437 AI956014 BE541087 BE255652 BE265878 BE394102 W27502
AA121820
108706 13255_3 AA121959 AA121960
108710 133560_1 AA335738 AI817426 AA099503 AA643106 AA650582 AW188499 AA155785 AW024305 AA992590 AW793619 AA121250
108712 14671_1 H93101 AA994582 AW007456 AW799974 AA535738 AI460362 AI571942 AW517220 BE044613 AI830018 H50382 AW391334
AA741035 AI697291 W37616 AA866185 AW264926 H52854 AW796893 AI660673 AA464961 AI808376 H13850 H81969
W92615 H41636 H73900 H66731 AA281556 AA026801 AA479538 AA588901 AA446262 R86974 H84761 R62958 H70493
AI991716 AI833075 AW800109 R54692 W94542 R78651 AI694890 AW845181 W31325 AA224371 AA359813 AW178868
H53738 F22305 AI874075 AI567440 AA853303 H25886 AA550734 AI874064 AW148463 AI586928 T28979 AW950966 AI828723
AI918890 F16942 AA223763 AA622370 AA630985 AA402644 N70971 AI147210 AW410026 AA485517 AI129376 AW337522
AW136362 AI123362 AI281243 AW339600 AI478990 AI339256 AW768289 AI660065 AI309560 AI141111 AI280844 AI338227
AI310719 AA733112 AA903203 AI073351 AI348225 AA974151 AI141386 AI311925 AI042124 AI193176 AI186999 AI735528
AI335702 BE550806 W47157 W70086 W44788 AI218741 AI074049 AI168088 AW050904 AI083978 AI131084 AW328532
AI969255 AA069140 AA328735 F20431 AI625929 AA621514 AA384576 H98823 AI371848 AI360520 AW079514 AW845177
AA948626 N52236 AA464158 H43126 AA465035 AA464221 AA365164 AI539264 AW250430 N27769 AA157036 AI124029
AI635488 AA374090 AA515126 AA614763 AI872210 AI160916 AI002016 AA813669 AA190550 AI262671 AI460058 AI690719
AA805473 AA523207 AA477649 H13898 AI056086 H42356 R32267 R99431 AA481898 AI130779 AA769777 AA910293
AI284079 AA936692 AA903953 AA947753 AI568924 AA902966 AA807082 AA489337 N58247 AA872223 AA485362 AA024906
AI092224 AA443621 AA603059 N58248 AA927262 AA329524 AA026369 N73450 AI244031 AI192676 N25190 W32248 W32324
AI284307 AA074470 N33116 AA947399 H52855 T52343 AA643260 AA573752 AI031889 AA877690 AA531409 X13710
AI500538 R32315 BE168562 AA401993 AA883251 W37615 AA305694 W78964 AA024905 H53678 W47278 AA224423
AA371881 AA335679 AA336008 T52416 H69646 AA300266 AA325728 N73204 N77626 R54691 W24032 AA868340 BE407766
H81968 W46665 AA883934 AA187290 AW571425 AI280505 AI079662 AI470373 AA991617 AA173165 AI244032 AA922440
AA856918 W80458 AA121251 AI160062 H50349 T67744 W46574 AA969287 W01485 BE615302 BE388184 AA314246 H85693
W31948 AV650437 AW160467 W44891 AA723773 AA328531 AA313224 AA299527 R86894 AA312505 H21582 AA157493
H78480 N36060 N77627 BE218674 W02853 AW954844 AA429974 BE382847 AI541225 H93229 BE281553 AA147790
AA327374 AW839840 AA969229 R99337 BE278812 AI190450 AA479549 AA156012 R78705 AA224081 N44944 D56066
AA969012 AW178878 AW105500 N52391 AA622301 AA858204 AI290372 AI205676 H51289 AA548013 BE544240 AA280160
BE170901 AI192429 R77056 AA310925 AI219128 AA121993 AA070432 R63012
AA128946
108785 4962_6 H08948 AA353935 R14985 U17977 H15387 F05567 R88476 AW968314 R89646 R87941 AA258917 AW895155 AW947450
102156 33676_1 AA223175 AA223559 W92508 W02327 AA322882 AW960879 H39040 H39039 R90891 AA580343 BE155037 BE154984 N40110
AL137683 BE265131 R17329 AL096733 M79202 AA625234 AA427472 AW361296 AA658045 AA322177 R54596 AA171880
AL042331 U18920 AA298036 AW051888 AI378803 AW601640 AI885103 AA297019 AI192706 AW055183 BE312004 H42382
AA534726 AA205943 AA204817 AA298966 AW015511 AA223176 H08864 AW028026 R45676 AI023345 AW263046 AI161297
AI168747 AW024885 AI832106 R88436 R86849 W92509 AA857908 N26989 AI589169 AI570370 AA223525 AA171552
AA405862 AW001095 AI864651 H39060 AA776342 AI682761 AA768233 R86855 AI367878 R42675 AA832040 R89042
AI984848 AI524629 AI289021 AW014020 AI241757 AI421241 AA430654 AI360728 AW299692 AA258155 AA782959 AI684411
AA531501 H41286 AI125231 H15388 M62002 R88819 AI203108 Z38537 AI432593 AA887767 AW023638 H39016 AI424700
102186 33745_1 U20285 AW674959 W69617 NM_004127 AU076538 BE245805 AW250694 AW248164 BE294678 AA298083 BE266030
BE262348 AL038115 BE253256 AA330082 AW401492 BE070159 BE619216 AW379955 AW379968 BE266381 AL046753
AW379969 Z45804 H12155 BE543514 Z44978 AA026010 AA776140 AA337940 AA315980 AA308668 BE156554 R33383
BE271569 BE378456 AA972517 AW748739 R73336 AA302223 AA279618 BE561802 AI693878 BE560858 BE513865 BE267975
R36064 AI056387 AI961737 AW167515 AA280965 AI479985 AI859762 AA309009 AA573934 AI669053 BE046497 H14545
BE222639 AI910094 AA484398 AA521025 AA807224 AW247126 AW732050 AA377850 AW951499 R73316 AI458542 AI564292
AA974663 AI951858 AA595162 AI685726 AA604679 AI813703 AI091930 AI567797 AI521316 AI377236 AA583446 W79901
AI743281 AA913078 AI139695 AA994505 AI202810 AA662524 AI810703 AA988395 AI272746 AA569807 AI299166 AI799551
AI492268 AI131335 AA969251 AI240890 AA580208 AI928074 AA716051 AA657992 AA988396 AA994504 AI952561 AW188344
AW246831 AI471309 AA757891 AA931856 AI272794 AA766100 F24931 F24930 AA749404 AA708597 AA732155 AI796670
AI825867 BE245682 AI638230 AA434157 AW249881 AA481945 AI090239 AA923622 R72864 F25087 AW674940 AI808546
AI470209 AI285895 AW189219 AW474426 AI818261 AW300960 AW513345 AW073126 AI868353 AA862926 AW592528
AA502647 AW591711 AI354982 R49145 AI360724 AI458656 AW304052 Z41443 AI864783 AW651615 AI270639 AW316592
R43741 AA482068 R72852 AW190442 AW651631 AW470902 AA911918 AW779251 R72820 AA279995 AI394715 AW105688
AI097434 AA670473 F08806 AA035597 AW008688 AI689117 AI911859 BE387696 AW166880 AA847278 W78016 AI886548
N35512 T86152
125077 1814028_1 T88822 T80794
124440 22853_1 AA532519 AA770627 BE326342 AW073299 AW205539 Z83851 AA725380 AI457288 AA976882 BE220181 AA988940 AI914073
N46435
100941 3303_2 U15422 NM_005425 X63758 X63759 Z46940 L03378 AI220577 AA634325 AI381479 AA994994 AA994988 AA416961
117286 558874_1 AI188710 AI032142 AW078833 N30308 AW675632 AI219028 AI341201 N22181 H95390
117291 1047256_1 N81189 AW172914 N22182 N22289
132316 10556_2 U28831 AA088359 N56023 AA069486 AL038872 AI683185 AA632516 AI281643 AA447146 AI699884 AI281642 AA832250
AI909017 AA781851 BE090060 AA058888 AI440090 AA040563 AA069449 AI702237 AA045495 AA088258 AA229820 AI925213
AA928183 N90591 AW794070 AI884470 AA219147 AI632560 AA553416 T10311
102295 26281_1 AB007881 U32581 AW131202 AW995994 W31964 N24261 AI033045 H98694 AW364848 AI222031 AA907216 AI215730
AA776981 AW473826 W31373
132380 166896_2 AW373665 AW373648 AW373647 AW393531 AA284401 AA253299 BE168092 AA196249 AA810695 AA278353 AI806177
BE552269 AW001862 AA749299 AA253300 W37080 AA805586 H72533 AI698623 AA292703 AA748852 H75291 H68018
AA883728 N48304 N49030 BE168089
102337 553_1 AI814663 AA806761 AA765241 AA019317 AA092255 AA035405 T85079 AA890151 AI373959 T85080 BE153728 AA740848
BE080682 AL048137 AW182316 AI699468 AW274481 AW407538 AA306562 AW950024 AW949943 AL045703 AW843196
W25132 BE612794 AA304266 AW958054 H25673 AV646563 AV646573 BE172990 AW593488 AA385181 AA164998 AI246476

AA345406 AI277554 AA134749 AA856624 BE613247 AA299003 AL048138 AA028121 T92510 AI923835 AW020440 AI401594
 AI889401 N93290 AA044247 AA028100 AI582845 AA811151 AI741811 AI925878 AA448277 AA172221 AI214783 BE220793
 AA022746 AI082882 AA022849 AI928385 AA573472 AI420686 AW072902 AI799493 AI873506 AI468977 AI192079 AI468976
 AA044272 AW015701 AW316979 AA933042 AA609017 AI318393 AI424571 AI934945 AA172023 AW050917 AA846180
 AA134748 AI003947 AI766769 AW006697 AA653517 AW575680 AI474214 AA401478 U36922 AA927064 AA868000 D62654
 T91745 AW500202 AA194764 AA746346 AA130464 AW117498 AA054526 N26432 H02534 H04964 AW303367 BE300931
 AI218049 AI208073 AW182749 AA983630 AI147585 AA194765 AA054534 AA922720 AI436585 AI346535 AA134269 AA280923
 AA897422 AA019559 AW274010 AA035406 AA917879 H99327 W32908 AI216046 AW496823 AA019414 H82288 W35284
 AI936621 AI767113 AA866177 AW367874 H82398 AF032885 AW300151 AW467069 AA809346 AI188507 AI494178 AA872752
 AI631631 U02310 NM_002015 AA815006 AI382453 AW197658 AI761654 AI804396 AI382221 AI813640 AI439635 AI523901
 AW517242 AI221705 AW298104 AW204560 AW573095 AW028783 AW014650 AI766744 AI808294 AI698758 AI041809
 AI766667 AI479103 AA872797 AA769305 AA765080 AA334166 AI472322
 AI541246 AW055046 BE312897 NM_008623 AF006043 AL038012 BE256739 BE272577 AA143633 AA143643 BE464595
 AI312112 H01791 R26319 BE170902 AW131612 F29120 AA455866 AI540181 AI885777 F36716 AI149501 AI246028 AI373003
 AL046700 AA455869 W69120 AA146617 AI188256 AI937281 AI806751 AI087240 AI123219 AI589686 AI332501 W69087
 AI494321 AA725793 AI222350 AA625736 AA644568 AI472282 AI370905 AA934652 AA913035 AI128576 AW341709 AI269125
 AA975139 AI620890 AI969828 AI356660 W95879 F32252 AI218442 AI928601 AI474470 AI245409 AI601111 AA928594
 AI809316 F19498 AI373442 AI218893 AA573914 AA906869 AI833041 AA993899 AW250763 AA887142 AA884655 R26108
 AI919414 H01042 AA534622 AA723368 AW005753 AI871394 AA661885 BE171317 BE271194 AW249310 T83902 BE246962
 BE279817 BE562094 BE513363 AL045369 BE561008 BE267526 BE544065 BE559579 BE561747 T35796 BE250596 BE268704
 T31298 BE536521 BE561183 BE269560 BE269944 BE514005 BE561068 BE268145 BE267559 BE559744 BE560930 BE278335
 BE513832 BE561017 BE396371 BE562260 BE281009 BE281327 AW410446 BE259628 BE547443 BE311971 T83809
 AW249441 BE270204 BE295488 R90868 BE269359 BE397222 BE396694 AW248394 BE397708 BE268174 AW247676
 AW248404 AA093721 BE397622 AA093706 T09027 BE408338 BE261454 BE260628 BE295110 AF171237 BE295135
 BE407534 BE536635 BE264727 BE296052 BE270265 BE546712 BE298269 BE547732 BE548734 BE253463 BE312238
 BE261042 BE545186 BE313055 BE542602 BE538530 BE535215 BE208107 BE513616 BE295982 BE561273 BE560057
 BE562005 BE280371 AW247443 BE259311 AA126209 AA171445 AW674121 AA134790 BE018733 AA233357 AA121604
 AA114201 BE265626 BE260086 BE313195 BE313434 BE261587 AA223432 AL039212 BE260762 AL046154 BE549057
 AA316523 BE259727 BE260759 BE208754 BE019077 AA206899 T33021 BE255340 AA182643 BE258057 BE258040 BE254759
 BE544454 AF171236 AA224410 T08700 AL037155 BE279638 W78185 BE545040 BE261376 BE261692 BE259694 AA313254
 H09056 AA357719 BE619163 BE018472 BE277966 BE278390 AA353616 AA378769 AA356685 BE564039 BE300236
 BE250358 BE543245 AF171235 BE384461 BE408141 AA137039 AI355285 BE535442 AA356783 AW675020 AI810351 W17380
 BE074695 AI978750 AA316052 BE278523 BE619725 BE270953 AW026987 R89415 BE271359 BE515234 AW008497
 AW386938 AI038839 AI862998 AI719458 AA113414 AI859984 AI870773 AA129452 BE047253 AW673881 AA827034 BE302302
 AI572915 AW264575 BE294567 AA805899 AI625116 AA310115 AI460065 AA169760 AA955009 BE302084 AA629846
 AA640597 W63787 AI805738 W94207 AA114165 AI240462 BE349066 AA668794 AA134085 AW050730 AA134084 BE540728
 AA910015 AW248892 AW247299 AA564678 AI139117 T16008 AI754100 AI091987 AA856537 BE205770 AI199445 AA603509
 AW771741 AI126994 AI000820 AI023844 AW250047 AI873263 T35536 AA126049 AI668802 T35470 AA224348 BE247113
 AI367665 AA223233 AA206815 AI284773 AA093396 AA113268 T03547 AA234268 AA101404 AA991274 AI275931 AA918855
 AA236365 AA226966 AI685723 AI284774 AW248023 AI754314 H09057 AA844271 AI272992 AA315077 AA205718 D57244
 AA742550 AA219567 AI927435 AI042620 AW247957 T35545 T15567 R90845 AA719914 AI085499 AI970845
 AF151074 AF070529 AI969222 AW874125 AI198308 AW470316 AI079388 AW134783 AW206208 AI093223 AI924789 N26130
 AI934430 AI857979 AA928091 NM_016496 AI074817 AA663800 AW300768 AW264438 AI884506 AI025192 N27628 AI199456
 BE044999 AI277491 BE044964 AA095316 AI076515 AA836677 AI942491 T80147 AI417945 AI668895
 U48936 L36592 X87160 NM_001039 AL036606 AL036420 U35630 AW298574
 R07785 T85948 T86972
 M86849 AA315280 NM_004004 AA315269 BE142653 AA461400 AW802042 BE152893 AW383155 AA490688 AW117930
 AW384563 AW384544 AW384566 AW378307 AW378323 AW839085 AA257102 AW378317 AW276060 AW271245 AW378298
 AW384497 AI598114 AW264544 AI018136 AW021810 AA961504 AW086214 AW771489 AW192483 AI290266 AW192488
 AW384490 AW007451 AW890895 AA554460 AA613715 AW020066 AI783695 AI589498 AI917637 AW264471 AW384491
 AI816732 AW368530 AW368521 AW368463 AA461087 AI341438 AI970613 AI040737 AI418400 AA947181 AA962716 AI280695
 AW769275 AW023591 AI160977 AA055400 N71882 AA490466 AW243772 AW316636 AI076554 AW511702 N69323 H88912
 AA257017 AI952506 H88913 AI912481 AA600714 BE465701 N64149 C00523 N64240 AA677120
 H72971
 AA827860 AA253460 AW971543
 M61982 AA491766
 AU077018 X67683
 U89337 AF019413 Y17868 AL044866 M25813 AL042665 N77388 R00971 BE392997 W52502 AW797536 X71937 BE394176
 T29553 AA114976 AA114835 AW316671 AI799888 BE044614 W51953 AI498690 AW580466 AI972232 T58430 AW137401
 T58462 AI870560 AI696138 F33285 U52696 Y13782 AW292936 AW375206 AW751873 AW352417 AW375162 AW375201
 AW375188 AW375198 AW375178 AI024335 AW375169 X71927 U52701
 H65527 N28990 AA359399 N24306 H65329 AA056928 AW504127 AA486661 AA040017 AA634817 AA595340 T93478
 AW015508 C02093 BE513950 AW410741 AW193200 AA813934 AW439574 AI077876 AI954356 AW629350 AI612865
 AW675663 AA226255 AI816714 AA010653 AA973778 AW276616 AI277607 AI218492 AW275190 AA911289 AI302550 N53061
 AI244408 AA709434 AA876151 AI206461 AI354477 AA954030 AI241127 AI187313 AW440434 AW074284 AI265804 AA872499
 AI202853 AA906037 AI241581 AA134769 AW074122 AI004585 BE300852 AA873196 AI813620 AW504945 BE619639
 AA037624 AA641954 AA037625 AW814771 AA134768 N73248 R02524 AA226533 AA216115 R29049
 AA221032 AK001651 AW732625 BE140495 AI366484 BE297579 AL039675 AL042801 AI678076 AL042802 BE208853
 AI961484 AW190561 AW027201 AA864499 AI344032 AI432437 AI934618 AA572961 AI499074 AW769938 AA917094 AI955647
 AI342638 AW974120 AI761488 AI289643 AI564533 AW272378 AI796156 AI867205 AA884306 AI766584 AA456581 AW769937
 AA713594 AI383037 F24965 AL137599 BE259667 BE313085 BE383358 AA322347 H67555 AA298993 AA304712 AA377693
 BE327057 AL041340 BE273248
 AW162087 AA224538 AA471218 AA088655 AA375275 BE440052 AF090891 AA324435 AF063549 AI110675 AA322223
 AW953306 AA233590 AW949864 AW949859 AA383721 AA081878 U33821 NM_006024 AA350900 AA081588 AI148087
 AF268075 AA088185 AI142478 AA081824 AI887930 AA070570 BE185248 AI459825 BE257794 AA420459 AA420859
 AA777997 AA081219 AW815721 AW854758 AA157932 BE018208 AW378974 AL041212 AI247564 AW581897 AI002897

BE543242 AI811690 AW852076 AW852270 AA360969 AA094943 AA090680 AW601554 AA099673 AA662226 AA356814
AA330174 AA187544 C02751 AA315460 BE168358 AW080447 AI813764 AI624222 AW156901 AI954032 AW473780 AI861975
AA173643 AW511541 AI951492 BE301686 AA669760 BE182212 AA081009 T69431 AI186207 AA604124 AA707346 AA173953
AI016700 AI125916 AA358962 AI673719 T90593 T90497 T10776 AW513002 AW304292 AA724885 AW474759 AI811621
AW068925 AA666305 AI580161 AI128023 AW471151 AA534849 AA666358 AI078833 AI139223 AI244874 AI381658 AW263441
AI432440 AW802882 N66401 AA224251 AI167469 AI141060 AA099214 AI537130 AL120428 AA948655 D53110 AA076099
AA938617 AA826543 AI357914 AA565098 AA807994 AI288812 AA632832 AA157933 AA639802 AA634268 AA282337
AA551431 AA557374 AA256923 AA872943 AA009665 H89626 AA810386 T92925 T36145 AA632190 AA130436 AI686635
AA130437 AW392904 AW392839 AW392848 AW392836 AA729737 AA070450 AW392890 W04825 AA771848 AA084634
AA481985 AI263840 AI801006 AA235380 AI954229 AI559330 AI208724 AA887638 T25894 AA041269 W44443 AI581770
W46171 AA878485 W46535 AA197336 AA894945 AA394224 AI766834 AI582590 AI033007 AA481889 AW190598 AW392855
R27279 AA398137 AI248407 AI241386 AI991753 AI826585 AA865699 AI096806 AI833030 AA041279 AW888745 AI703279
N70572 AI912553 BE549931 AI240422 AW376187 AW591692 AA975905 AW614967 AA009666 W44332 AA664659 T06561
BE468150 AI650695 AA587920 AI473310 AI032991 AA256499 AW104241 BE163782 AI984973 BE163613 AI263906 AA628191
AA282072 BE163769 BE163775 AI492939 AI473315 D56907 AA587930 H89480 AI362373 AA598483 D56595 AI167590 C16223
AI935415 D62555 D62884 D63130 AI760286 AI650286 AW173598 AI499145 AI122566 AW903408 AI810569 AA854936
BE049510 D62065 D61900 D62101 R27475 AI469835 AI669086 N80399 N48922 N48746 AA481381 R22858 H13912 AC004549
AW602500 AW768788
102571 31561_1 U60115 NM_001449 U29538 F01103 U60118 AW612050 F33160 F37125 AI138362 AA853999 AI700031 AA868700 AA411791
AA782026 AA861693 AA430022 F29006 AI026854 AA236496 AA100266 R60856 AW606023 AW380619 BE150801 AW391508
AI682304 AA947687 AI284419 AA782989 F00277 AI202147 F01221 BE161576 AW385226 AW361913 R30713 AW607124
AA505577 W96539 T74511 AA211624 Z41920 AA263163 AA216297 BE164746 H56334 W03218 H61947 AA101716 AA134667
Z19275 N55888 AA702365 T30562 F00587 AW967294 R58121 W47367 AW608017 N45005 N42952 N69255 AA179110
AA196349 AW376390 Z19411 H56335 AA197096 AA651681 AA873207 H61734 BE140426 AA047105 R64437 W45585
AA149058 AW984577 AA192500 AW984588 AW984523 AA037874 W93436 AA195586 Z19330 AA523870 T92443 AA149059
BE166015 AI033716 AA725097 AA456394 AA180784 W02792 AI921585 AA211488 AA192626 AW364704 AI819174 AA193240
AA130173 AI337854 AA181265 W45548 AA779753 AA211417 AI197031 AA037875 AW469501 AA037241 AW024276 F32512
AI084805 BE169896 AA192242 R60857 AI089511 F31828 N20892 AI335027 F32813 F22400 F27858 F31766 F33413 AA192610
W96433 AI394501 AI150206 AI827777 AW130567 AI932997 T17424 AI288559 R52402 AI806130 AA126040 AA669576 F25175
AI148159 AI041869 AA860296 F25152 AI948570 AA479422 F21920 AA778131 AI276508 AI948577 AA114870 F32631
AW028047 F35241 AI373951 AA114869 AW138423 AI889537 F24663 F27705 F37165 AI392774 F29432 AI090589 AA450321
F24561 W93346 F29070 F25579 F31362 F33440 F22652 F31494 BE169905 AI818513 AI680754 F36378 N38871 F22082
F31950 AA665830 AI765076 AA868225 F22733 F35957 F33418 F34871 AA085944 AA035499 F28471 AI653552 BE047474
AI362282 AI131185 AI763052 AI028105 AA211569 AW241290 AI086746 F33041 AI767780 AI080600 AA101717 AA086422
F32855 AA047242 F33893 F29113 F21510 F21509 AA039540 F26344 F29047 AI937919 W19338 N40995 F31929 AI084510
AA026507 AA086200 AA207130 AI399877 F21370 AA733197 AA086205 AW340573 F33682 H05220 F25782 F25048 AI127208
F29940 W47368 Z19261 N29900 F25141 F32890 R63826 F35206 F30119 AA706742 F35143 F25142 F33599 AI659403 F25821
AA216171 AA991774 F22761 F34089 AW082748 AI093709 F29359 W46627 F26632 F30291 F36082 F20945 F30582 F22531
F24027 F33960 AW028172 F24674 F36597 F21959 AA729612 F34366 AA732967 AI582660 F29363 F22167 AI086792
AI804183 F33102 AW075510 AI367611 AI784054 AI453418 F34901 AI161157 F26622 AA651987 F35237 AA013303 F32632
AA664876 F21736 AA928616 F21384 F25357 F23467 F31185 AI537850 AI868952 F31707 AW089232 AI363826 AI702766
AA136298 AI767887 AW089312 AA578225 AA130181 F19251 AA581649 AA449418 F21171 AA455925 AA450322 AA196199
AW007853 F26059 AW085130 AI202616 AI674315 F20318 AA747182 Z38215 AW075230 AI159764 AA134668 F00420 F33094
AA455054 AA729265 F04647 AA746994 AI658702 AA478718 AA578161 AI080025 AI352604 AA989440 H30904 Z28506
F22649 F34880 D45580 C20561 T32638 AA020946 AI439878 AA746991 AA194883 AI219226 Z45773 AA089657 AA180825
W25548 R58180 W46675 N38870 AA137104 AA026506 AW984583 AW984539 AA020945 AA035101 AA039539 F30993
H14793 AA211688 T91484 F34313 AW815933 F29167 F31099 F31949
101923 30543_1 X99133 X83006 W38398 AA401137 AA298242 AA366738 AA308126 AW583781 AA298668 AW845024 BE140204 AW845005
U47734 AA837575 NM_005564 AA329732 AA421943 BE171567 S75256 AI750047 AI762213 AA100735 AW612993 AI474120
AW062884 AI940001 AW062852 AW062899 BE182639 AW778875 AA528093 AW517424 AI939989 AA076188 BE182636
AA169569 AA167439 AI283967 AA167783 AA076140 AI749649 AA166792 AI708618 AA400973 AA514773 AA514789
AA164458 AA167440 AA074845 AA421944 AA514874 AA079557 AA102361 AA587027 AA642930 AA878029 AA164459
AW176400 AW475086 AA857522 AA148193 AA838234 AA593897 AI284506 AW193324 AA148194 AW583341 AI669077
AW264913 AA074902 AI680515 AA169874 AA169614 AA079651 AW591737 AW190644 AA076565 AA662747 AA075896
AA535642 N27757 AI306666 AA074727 N79823 AA524360 AI826800 AA173827 BE140374 BE004062 AW265060 BE184103
AI199258 AA857853 AA299459 AA837890 AI626104 AA503624 BE183618 BE183717 AA573267 AI833071 AW270590
AA506601 BE004010 AA837854 AI675895 AI810491 AI184883 AW664712 AA076046 AA515574 AW352267 AI797418
AA172395 AI749194 AI559933 AA502597 AA321220 AI866124 AI695633 AA494293 AW085635 AA165649 AA165663
126117 1610460_1 W01520 H78617
126122 82445_1 H80181 AA005287
126136 285360_1 H85525 H83353 AA418447
126168 20960_4 L44530 AA322034 T79009
126196 21198_2 AA084092 AA084394
102675 5145_4 U72512 T98357 R31335 F18090
118387 65081_5 N64579
126256 10840_1 AK001774 R02029 Z21327 R02030 Z21124
126291 86990_1 AA017609 N42090 AA984485 BE177239 AI912269
104008 27385_1 AW134482 N93060 AI694673 AW241458 AI161320 AI582177 AI623166 AI492337 AA724337 AA749177 AA741055 AA283954
W38395 W24693 AB033047 AA159179 AA588310 AA654615 AA630891 AA639240 AL121157 N79820 AA653941 AA279925
AA132883 AA253947 BE502673 AI191149 AF208847 NM_016620 AA132773 AA532724 AA933782 AW997589 AA749442
AA356531 AK001587 AW500170 AA369990 AW582815 AW582838 AA451773 AA233995 AA427982 AA334630 AA282933
BE349308 AA300682 AI384093 AW364014 R31977 R69849 AW364012 AW364015 AW364019 N76465 R80458 AI267509
AI760785 AW628405 AI224905 N59362 AI351352 AA513728 AA729606 R80659 AA573139 AW614666 AA310325 AW471080
AI091339 AA830587 AI051323 N67319 AA621436 AA449856 AA648966 AA954973 N51766 AI952427 AA829053 AI468601
AA649186 AW592210 AA449968 AA465374 AI474865 AI185456 R31932 AA621108 AA975015 AL121156 AW962752 R69850

103417 15279_1 L34657 M28526 NM_000442 M37780 AW407571 AA488822 AF281299 AF281296 AF281297 AF281295 AF281301 AF281298
AF281287 AF281294 AF281293 AF281289 AF281288 AF281290 AF281291 AF281292 AF281300 BE140137 AA082477
AA182953 AI902545 BE185251 D58483 T73117 AW902845 AA303912 AW403488 AA039356 AW401604 S66450 AW371090
AA477959 T97049 AA486710 AW607916 R76264 AA303959 AA385484 AA181062 AI218959 AI384084 AW387030 BE044508
AI942423 AI910438 W04423 AI148494 D58775 C18167 C18011 R68293 AW340705 AI587613 AW772278 AI942486 AA304612
AW276352 N41586 AI248619 AA151818 AW593959 AW137371 AI470913 AI916891 AA181063 AW261863 AI271376 AW007613
AA359765 AW874428 AI033514 AA181110 AA181092 H57149 AW514341 AI971318 R95876 AA713790 W93076 AI936184
AW665574 R82381 R82269 R53795 R26391 AA989385 AI076568 R68262 AA716613 AA933639 AA678079 AI686366
AW294984 N30812 AA486245 AA693877 T95097 T72992 AW193473 AA001726 AI808737 AI247488 N53545 R08174 AA305676
N76004 AA761616 R78126 AA564715 AI031710 AI913454 AI475239 AI081733 AW264881 AW518741 AI783794 AA449390
C15249 AI922914 AI498549 AI808250 AA486711 AA002005 AA035777 AA151817 AI834300 AI168387 T96940 AI675272
AA056355 AA299130 AI127297 T95197 AI818125 X96849 AA486244 W93075 H57223 AA302220 R22071 R33251 AA301548
R95875 AA372192 AW838188 H01353 R78125 R22459

103425 30014_1 AB016092 AB016089 AW161159 AW160794 AW163150 AA776677 AW168207 AW161625 AW157477 AW157176 AI739521
AI906428 AW073890 AW467016 AI745171 AA738238 AW090343 BE245923 AW002703 AW293743 AA249074 AW328076
AW328075 AF161338 AI991472 AW515714 AI655953 AW393827 AI653282 AI652717 AW393832 BE550526 AI654896 AI203310
AW590658 BE550597 AW390889 AW390900 N93494 AI654677 AW573041 AB016087 AI874387 Z28839 AW806640 BE168075
Z25196 AA743746 AI906104 AW402640 AA833814 W03404 AW881095 AI863478 BE019680 BE163120 AW939109 AW939159
AB016090 AW939112 AW939162 AW939157 AW939107 AA229457 AB002322 BE081002 AW895217 AW367778 AW502353
AW502650 AW372535 AW372524 AW372551 AW372527 AW372544 AW893113 BE147617 AA347209 AA772783 AW892035
H38889 T19958 T19957 BE171421 AI902871 M78867 BE167584 AI902950 AW862975 AB016091 BE168093 BE087521
AW603182 AW499660 AW499661 AW503473 AI902486 AW752292 BE174018 AW752296 AL041888 AW363953 AW605221
AW605216 BE142816 AI435786 AA683040 AI907872 AW369725 AA380303 AA836230 AW419434 AW501816 AW502342
AW502333 AW499671 AW502991 AW501843 BE168376 AW501486 BE245921 AW372603 AW372604 AW372601 AW372608
AW372609 AW372612 AW372607 AW753096 AI902532 AI902594 AI902533 BE062377 AW811106 X97301 AA315458
AL041463 AA287787 BE544417 BE311801 AW797378 AI940181 AA326261 AA326712 AW964943 AW751304 AW751303
AI940199 AI940192 AI940189 AW751305 AI940167 AW176500 AI940202 AI940190 AI940201 AI940196 AI940203 AI940210
AI940193 AI940177 AI940179 AI940204 AI940171 AW382746 AW382738 AW751312 AI940753 AW062939 AW803210
BE175400 BE175388 BE094921 F28478 BE066456 AW372263 BE066575 BE066320 AW372262 BE066580 BE066455
AW576937 AW392415 BE183395 AA381175 BE388469 BE066460 BE066315 AA377951 AA171585 AW605004 AW605007
AW934766 AW934869 AW580606 AW605280 AW834728 R83817 AL121069 R20109 AA291361 AA524293 AW374653 H30144
H44678 W24212 W06948 BE247374 BE180909 AA778442 AL041464 AA172255 AI962941 H26136 AA995288 AI921770
AL040081 AI913019 AI829562 AI339531 AA837865 AI375317 AI762975 AW338852 AA938195 AI982701 AA682389 AW001982
AW591316 AW173712 AW005552 AA039605 AW002560 AI559320 AW272286 AA045667 AI799670 AI803146 AI374801
AI811885 BE326490 AW276312 BE049418 AI986113 AA286830 AI634266 AI198953 AI202521 AI380918 AA999947 AI492102
R83376 AI337411 AI962358 AI635535 AW241544 AW003959 AI144276 AW576619 AI926506 AI889528 H43845 AW050926
AI380249 R43161 AA581617 AI983302 BE465975 AI345956 AI341453 H26401 AW189035 BE350636 AI582500 AW316665
AI439844 AI804761 AI470679 T32375 AI570375 AI273528 AW796804 AA658160 AA652859 AA503941 AA573555 AI358272
AA573547 Z24817 AW576624 AA428059 AW023495 AI033000 N49249 AI969076 AA205445 AI636203 T30328 AI394724
AA403302 AI968272 AI492974 AI582619 AI470826 AA894924 AI912962 AA569977 AI675362 AI473131 BE046814 AW300260
T31879 AW168376 AI659621 AI810463 F35064 AI271700 AI699563 AA776537 T36184 AA565451 AI678338 AW438921 R16094
N91497 AV662182 AI432919 AA910303 N91964 F18684 AA381902 AW364462 AI276689 AB015644 AW247214 BE047724
AA347210 BE391395 H81815 N67777 BE208123 AW939117 AW939167 AW939108 AW939172 AW939123 AW939158
AW605520 AW605509 AW605515 AW939122 AW939171 AA229095 AA229096 AA229232 BE382710 AI902544 M78278
AW799890 AW889685 AW863018

103436 42952_1 X98206 AA693431 AA244304

102806 8441_2 AI246240 AF124733 NM_016358 U90306 BE407995 BE281254 AI566193 AI652266 AI671516 AI950190

103491 36109_1 AF264750 AA904457 AW884708 BE183627 Y08478 AW962945 AA305849 Y08479 BE255205 BE258400 Y08468 AB040939
T05961 AW807004 AW062952 AA135076 AW997220 AA090128 AW137099 AI640514 AW592676 H01987 AA134913 AA599219
AA913906 AW573059 AA904722 AA904721 AA368411 W04955 H82698 AA077280 AW014128 AI191700 AI298476 AI540051
H82435 AA774512 N53899 Y08482 AA332025 AW965281 AA331817 AW803125 AW992770 AA329962 AV659521 R78277
R75636 AI681382 AL079859 AV659778 AA314956 AA127627 AA116095 AA121529 AI693624 BE612540 R21914 AA135986
AI697706 AA234595 AI189138 AW055042 AI144389 AI263904 AI400175 AI275540 AW997221 AI742458 AI079937 AI138511
AW196435 AW291117 N68458 H73663 AA116096 AA236552 AI983684 H73722 AA282356 AA932090 AA811462 AA737189
AI636190 AW873132 AI468635 H01064 H13088 R22563 BE539692 AI581680 Y08470 AW836778 BE080692 AI091839
AI572125 BE006050 BE006047 AW836837 AW501631 R09599 AW973566 AW263143 H61053 AA553507 AI214982 H02081
AW997046 AW505183 BE143139 Y08836 Y08477 H73356 Y08465 H73223 N91302 AA641936 Y08464 Y08466 Y08483 Y08481
AA506064 AW807922

126363 185896_1 N94706 AW302202 N54724 W01777 AI949662 AA917338 N50068 AI857652 BE550711 AI340079 N63025 AA971513 AI467976
AI694919 BE328279 AW206626 AI310369 AI307346 AA425773 AI862813 AA628674 AW475016 H10786 AI932791 AA244420
AI567886 AA621126 AA244453 AA369087 AI678489

127008 175968_1 AA223753 AA223879

127027 41793_1 AL390088 BE207034 Z42964 BE242833 AW583731 BE616399 BE621126 BE272661 BE561537 AW328160 BE513636
AW732368 AA367575 AA317809 AA325684 AL043346 AW997819 BE207681 AA442690 N33908 AA329967 AV661996
AA364929 AA132857 R41876 W30718 AA340232 AA923628 BE618790 BE383719 BE384891 AW973886 AI680631 AL042633
AL044048 T64995 AI814372 AA046927 AA707444 AI351042 AW157778 AW303835 AA559116 AW157476 AW440951 AI146410
AI570583 AW473765 AA931145 AI654587 AI089717 AA132763 AI199778 AI144493 AW473769 AW087749 BE166742 AI089476
AW083264 BE206437 BE222620 AW615413 AI356436 H98622 AI674887 AW583314 AI081960 AA133159 AI932568 AA641830
AW245125 AA543056 AI289158 AI538987 N67489 AW836308 AI042462 AA639343 AA706144 AA653493 AI363727 AA724790
AA596032 BE277184 AI126007 AI241020 AW627956 AW440961 N30667 AI806651 AA583594 AA732028 AA731516 AI439229
AW995619 AA133204 AW248060 AI914553 AI689519 AI521043 AI566390 AI245111 AA594407 AI797417 AA131580 AA035240
T33853 AI362604 AA535337 AI273040 R68453 AA043655 AI587360 AW572022 AA935227 AI697259 AA749181 BE263051
R68454 BE560435 BE277826 Z49985 U30174 D61707 BE390825 BE618267 U30173 D61706 Z49984 BE268853 N99057
AI874052 AA568135 R68452 H21498 AA043654 AA046984 AA362959 AA035318 R17261 AA131629 BE166750 BE298260
N25142

127036 1150_2 AI468598 AA232868 AL043752 AW881016 AW881015 AW881214 AW880761 AW881018 AA255767

103513	42559_1	Y10209 AW341910
127041	1534405_1	Z43067 F12549 F06090 R11929 T74454 R12925
126406	95703_1	N76683 AA034096 AA034082
127064	1690305_1	T84214 Z43709 R05654
133660	27207_1	H14843 C14857 F06523 AA322683 AW964649 H83334 AW894647 AW894608 AW578353 BE007437 AW894648 AW894609 AW896993 AW897085 AW581270 R36029 AL117536 AW896412 AW993019 AW859782 AW859772 AW376619 BE082963 AW376687 H24066 AW847946 AA091541 D51576 D52043 D52146 D51628 D52155 D51675 D51777 D52101 D51602 D51843 D51878 D51751 D51820 AA319632 AA351569 AW630840 BE073033 D51985 AW838560 AW838633 AW838631 AW838554 AW838557 AW838559 AW608175 AW608194 AW838558 AW838562 AW838564 AW838571 AW608170 AI926544 AW608177 AA296774 AW838624 AA318941 AA319199 AW960724 BE073078 AA773508 AI925495 AI889128 AI633207 BE221497 AI126062 AI344458 AW608176 AW838627 AW194765 AW838630 H24379 T23982 R62391 BE620113 W02397 R87373 AA364488 AW963466 AI696793 AA012998 N72571 C18550 AI298061 AI084648 D51984 C14379 D52154 T03606 AI499301 AA017178 AA017170 BE077301 AI889566 AI002790 AI205010 AW104793 AA298374 AI049720 D51575 D52042 D51627 AI281148 AW104111 AI142928 D51601 D51842 D51819 D53690 AI242974 AL049247 AL036365 AL036366 D45664 X13451
102934	16110_-11	T78141 T75126 AW953462 AW956923 T08967
126479	1297811_1	AW969436 AK000755 AA176076 BE258269
125877	18687_2	H16443 T66760 H11411 Z70220 F12208 T66258 AW950931 AA350846 H06005 F12617 N51174 T74154 R87613 T33928
103650	43833_1	Z45881 AW961235 T31307 AW891440 H24171 R18227 R19098 W26891
127191	206872_1	AA625286 AA297581 AA303053 AA303052
103682	41323_1	AF275815 AA018302 AA000993 AA021290 H86017 R69197 AA056286 R88858 AI570404 H43774 AA059385 AA010839 AA056237 AI436578 AI769179 AA019840 H86715 H84086 AA000994 H85881 AI762043 AI079265 AI738426 AI654986 AI738440 AW197623 AA021232 AW161646
126568	163056_1	AW749469 W68106 BE162986 AA190515
125925	1502610_1	BE550996 H28737
125952	87085_1	AA017723 H40709
125953	1582862_1	H41682 H40829
104328	243947_1	R11272 D81932
104340	46289_10	AA426189 F15201
127231	221630_1	AA317400 AA434584
126619	186375_1	AA247746 Z28861 Z18915
126621	164483_1	F01180 F22065 F21334 AA192638 Z28873 F31558 F33176 F30552 F35761 F18952
119404	115373_1	AA302840 T93016 T92950 AA077551
127331	379388_1	F20186 AA622352
127347	133106_1	AI922293 AI123420 AA833906 AI417534 AA402715 AW275969 AA470879 AA402585 AA425800 W74482 AA410632 AW051466 AW057511 AA443121 AA121406 F09029 F37501 AI909933 AI909928 AI909925 AI909932 AI909931 AI909926 W79080 AW958666 AA312211 AA428350 AA410631 BE382380 BE394251 AA122083 F11368 F05224
127357	288073_1	AA424107 AA452788
127359	16354_-4	H72971
127378	299674_1	AA446387 AA452696
126730	297653_1	AA442429 T19477
126759	109907_1	AA063089 AA679118 AA063642
126762	110350_1	AA064613 AA064671
126767	327401_1	AW968865 AA491199 C17148
112309	1576900_1	R55021 H26613
128099	501940_1	AA905327 AI148973
127452	327502_1	AA504447 AA491317
126808	121207_1	AA662559 AA086320
126844	133298_1	AW881997 AA121637 AA299325
103985	19574_1	AB032251 AW852071 AA279887 AW852124 AW129468 AI583544 AA704421 AW999851 BE081960 AW390494 AW582002 AI862331 AA700432 AI186130 AI720707 AA236286 AI336961 AW015054 N91172 AI698141 W32818 AW896124 AI701519 AW894048 H87416 AA234040 W17142 R84565 AI803033 AW867682 H27242 AA366224 AA357157 H86935 BE090270 AW753846 AW362772 BE464864 AA704907 AA704948 AA704938 H27235 AI033427 AW850923 AA480900 AW502989 AW851237 AW851374 BE252815 AA084307 AA313880 AW961200 AA480961 AF114105 AF114103 AA486042 AW375963 AW752365 AW375959 AI290321 AA488659 AI242380 M85386 AI825492 AW499531 AW502114 AW502349 AI825312 H45002 AA177096 AA248058 AA252844 BE327236 AW418631 W74679 AW582000 AW390459 AW609218 F05276 AA425478 R14173 AW609219 AW868913 AW868854 AW868905 AA333683 H02382 T35574 D12400 C14910 AW894285 AW903587 N64611 AW975302 AA541375 AI479002 AW006220 N51384 AI142472 AA659902 AA534253 D58103 H02279 W74710 H44955 AA425278 N59267 H28589 AA804452 AI191286 AW197903 AI864639 AI122991 AA469450 H28584 AA252812 AA467779 AW130113 AW872897 AA789290 AA935730 AA906959 AI990477 BE504778 D57881 AA721144 AI341486 AI638797 AA765502 Z18803
126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
127553	202308_2	AA505046 AW969109 AA505047
127568	479942_1	AW892676 AA853877 D44747
126977	171173_1	AA210697 AW962138 AA309665 AA210819
126982	171753_1	AA211419 AA211566
113195	178688_1	H83265 T63524 AA304359 AW960551 AI672874 AI749427 AA227777 AW027055 AA971834 T49644 T54122 AI983239 AI808233 T91264 T96544 AI350945 AI709114 R72382 T48788 R48726 AW385418 AI095484 T49645 AA928653 AA570082 AW007545 T57178 AA516413 AA913118 T57112 AA564433 AA774503 AA367671 T59757
128260	38164_1	AF119848 AI132994 AA505575 AI307657 AW205687 AW291922 AI347642 AI308117 AA398902 AA741579 AW269612 R72857 AW418818 T23611 AI016388 AA641630 AW009309 AI078310 AW263980 AI971867 Z32873 R00068 AW028860 R57097 AA402507 AW965254 AA114126 AA331445 AA333324
128279	1561282_1	H18818 H08885

113213 23798_1 NM_001395 Y08302 AI434619 AI470328 AI261807 AW024965 AI806537 AI830549 AI640337 AI219065 AW271700 AW028488
AI133339 AI859205 R51175 U87167 BE379324 BE392008 AA340819 AA343110 T57275 D59164 AW299312 AI434422
AI936390 AW024975 R40262 AW269126 R09430 T56590 AI367247 AI253132 BE464248 T58658 AW207785 T58607
120461 22556_18 AA810830 AA251301 AW962926 AW962922 AW962925 AA371510 AW817535 AW817579 AA251629 AW837817
127705 966283_2 AJ003322 AJ003324
127787 458957_1 AA809310 AW975709
112746 93768_1 AA541537 AW009489 AW950203 F25552 AA834645 N56270 AA029543 AI633587 F30948 C04983 AI628613 AA885458 T49449
F13651 AW004753 AA369573 AA356955 AA355112 T49448 AA918022 AI910358 H40428 AI292038 AI684655 AI244426
AA522725 AA352551 AA909796 AA494329 AA873880 AW957305 AW955082 AA552169 AA974888 AA977363 R93237
AI865725 AI201852 AI244721 H40429 AI204631 AA029544 AI015353 AI245274 AI191342 AA662656 AA829667 AW001837
AA626833 AA585220 AA522987 AI339186
128410 288073_1 AA424107 AA452788
128440 210591_1 AW090340 R52194 T87269 R17095 T91445 N76763 R82785 AW512315 AA534961 AW002002 H41133 AI985800 AI278720
AI762576 AI798477 AW081499 AA314880 AI918168 W92216 T91358 T79785 F04683 AI824664 T78491 AA302483 AW958008
T85160 T87183 R11236 R16208 F01406 AW150480 AW627337 T79354
127854 443883_1 AW976796 AA769520
120606 39874_1 AF169690 F08337 AA282956 AA282955
120734 208882_1 AA299948 AA299949
105897 8177_1 H03573 AA310766 AL133603 AI700910 H00505 R82804 H60605 T10498 BE176241 N99617 BE537165 AA443413 H02733
AI267539 AA094718 AI299771 N50199 R64087 AA709363 R26971 AI962859 H03899 H03888 R63010 AI346026 AA328951
AI025251 H89260 AI472009 AW029442 AA211594 AI310418 AI913561 AW515607 AW593597 AI926843 AW073920 AW002745
R62957 AI439422 AA401091 H58246 R82805 AI174264 AI590100 AW510481 R26739 H02624
100097 17246_13 AF002224 AA017358 AL119785 AI379446 AI632616
106782 83684_1 AW054886 R48313 AI200750 AI358095 H28124 AW613845 AA010033 AW182407 AA010034 AI986052 AI032851 AI719051
AA478487 AW410484 R48418
114610 117244_1 AA525225 AA525299 AA081079
114636 109698_1 AA075488 AA129081 AA074851 AA082852 AA074732 AA084908 AA084751 AA076042 AA131172 AA085374 AA079519
AA074510 AA113824 AA102437 AA070833 AA070143 AA084693 AA084389 AA076373 AA075492 AA062834 AA084335
AA078829 AA079344 AA069916 AA079275 AA070914 AA654069 AA081976 AA080957 AA083115 AA070942 AA085296
107518 45315_1 X60152 AI871483 AI871473 AI871251 AI631860
107521 44111_1 X78262 AL037659
130420 23038_2 NM_003105 U60975 Y08110 AW501858 AA984813 AL042811 C14671 D59983 AW996611 AW502726 AW408730 AL120016
T07220 AA972515 BE169618 AA053753 N45548 AV655750 AA485180 AW080086 T51689 AA714788 AI089413 AA748187
AA744864 AA977151 AW167224 AA465100 AI692864 AI800689 AI419483 AI915371 AI264290 AI919227 AA687175 AI498499
AI089844 AA721674 AW291409 AI377801 AI049681 AA767458 AA053631 AW473092 AW079490 N48698 R38875 AW501274
AI817699 AA847277 AA761843 T07221 AA873077 AA568215 T51538 AI474852 AW505117 N50751
100403 19804_1 AA302974 AW952936 AA297841 T17453 AL040862 AL042305 R18514 Z45908 H09477 R51937 H02949 AW672666 AA339081
AW024007 AI910124 R41507 R02276 W72600 AW606045 T30584 AI968122 AA532894 AA047712 AA024602 AI814501
AI479333 H09478 AI801077 R63410 AI469769 R63363 AA731181 W67437 AA613000 AA125822 W60322 AI199934 AI032499
AI673744 AW675418 AA594241 AA047679 AI148807 AA948543 AI805752 AI362640 AA883795 AI873413 AW292015 BE503009
AA960821 AI302435 AA911051 AI192308 T31342 AW589705 T32492 AW384043 AI968407 BE501316 AA074832 AI611662
AI969799 AI216685 AL117466 NM_016733 D85527 AW992053 Z44073 BE078508 R70709 AL046533 AA402079 AA125952
AA337799 BE252284 BE253079 AA325230 C18518 W67436 T83901 AA353025 AA024601 BE068484 AA782927 AA401915
AA369003 R53606 W76565 AL040863 W60241 AI967950 AI424849 AI582302 AI769611 AI394573 AI949294 AI656190 AI885933
AA670336 BE465592 T17452 AI569505 AA075098 Z41532 T35104 AI699545 R02275 AA368470
100476 24092_2 NM_001907 X71877 X71874 BE140276 AA748397 AA213801 AA830996 AA765114 AW874469 AA811623 AA844904 AI371956
AW451919
108360 112653_1 AA129037 AA071539 AA071460 AA129036
108390 112416_1 AA121999 AA121985 AA071108 AA071116 AA071434 AA148869 AA075070 AA122000 AA121986 AA071117 AA071109
AA148655 AA075232
108392 113549_1 AA075124 AA075208
100534 20653_36 T85231 AW161503 AW401856 BE397508 BE387085 BE514425 BE387606 BE391894 BE562022 BE561561 BE537755
AA326129 BE397421 T49865 BE259375 BE562435 AA206146 BE272379 AA206012 BE252021 BE264415 BE559498 BE622499
BE560425 AF141349 AF070600 BE260687 BE267430 BE273769 BE409463 BE378506 BE410826 BE540360 BE514334
BE265991 BE259493 BE257982 BE541302 BE275305 BE249816 BE263407 AA306533 BE312339 BE537252 BE313173
N44590 BE397957 BE314066 AF070593 AF070561 BE395620 BE539980 BE278635 BE622457 BE561276 BE561240 BE539757
BE398025 BE539587 BE264804 BE312816 BE618175 BE312236 BE536880 BE275163 BE409064 BE268157 BE256878
BE396565 AA094095 BE512689 BE539943 BE613640 BE561500 BE314652 BE560895 BE270780 BE394023 BE314771
BE258043 BE545484 BE539560 AI524946 BE268922 BE313646 R21491 BE257007 J00314 T55776 BE514288 AA079759
V00599 AA090885 BE268939 AI424151 BE393150 BE513223 BE311978 AA427899 Z36874 BE267470 BE270600 BE270542
AA092574 BE513746 T56664 BE260686 BE561863 T80533 BE614348 AI003020 AA196886 BE395929 BE256732 T80512
BE561248 H10806 N23553 AA090625 BE378633 BE299481 BE251134 F03598 BE158989 BE271056 BE271117 H39974
BE537728 T95426 T93847 R15283 T82017 BE561756 BE254463 BE250916 AA522520 BE562294 BE561853 BE562013
BE410876 R17504 BE254605 BE254904 BE315454 BE408837 BE256847 BE259444 BE265709 BE395378 AW869359
BE019791 BE378840 BE270975 AW246214 AA352945 AA378509 BE275472 BE389534 AI609281 BE295688 AI972188
BE388702 AW351598 BE617054 AI922439 BE258416 AL119346 AW351963 AW351971 BE388178 AI624652 AA780798
BE268311 R35263 BE251613 AW366022 AW177828 AW057797 AW366021 AW177888 AW366065 BE140945 AA670139
AA773017 BE539636 BE139520 BE270946 AW058238 AA191567 BE312975 AW089641 BE398147 BE268285 AW272598
AL119339 AW079784 AI829482 AI982828 AI862019 AI816169 AI633046 N59068 AW731944 AA093100 H03237 AW575087
BE301207 AW780181 BE141633 AW664164 AA626909 AW516663 AW872823 AA551910 AW571502 AI954158 AA548713
AA599912 AA301057 AW574903 AA614152 AA613830 AW771103 AA706556 AI023390 AA551248 AA780901 AA633446
AW419192 AA404660 W58436 AA523401 AA578734 AW615710 T65580 T57191 AA486211 AA604684 BE208800 AA669875
AA622085 BE302083 BE263081 AA548072 AW156997 AI568868 AI627575 AA565217 AI870317 AI282474 AA704034 AI253598
BE328271 AA564664 AA161128 AA604105 AA609087 AW103504 AA605238 AA704108 AI221585 AW574515 AW117994
AA058521 AA604281 BE251293 BE017988 AI754462 AW245235 BE094031 AW862436 AW105529 BE544089 AW303918
AW130826 AI721132 AA433888 AL038189 AW474816 AW182745 AA551345 AI445794 AA398452 AI224993 AI689213

AW249709 H15542 AW196813 AA618551 AI445281 AI638121 AA807410 AA911530 AI334093 BE269844 AA847782 AW276513
 AW589524 T03418 AW170654 AW468976 AA570676 AA570715 H41474 AA010074 AA600283 AI755222 AI193239 AA774176
 AW770036 AI332603 AI129785 AI280055 AA666338 AW732127 AW028394 AA102641 AI920834 AA602712 H06697 AI095237
 AA401908 AW250765 AA631796 AA550854 BE260391 BE614352 AI690333 AA452272 AW575264 AA878265 AA190483
 AI832049 AA195830 BE439812 BE208085 AA826727 AI929438 H10785 AI520704 AI364235 AA605138 AA513116 AI250046
 BE263592 BE538689 AA171900 T03755 AW241170 AA565529 AA186883 AA872245 AI251930 BE538023 AA181759 AA187178
 H28109 AA115169 AA513309 BE545993 AA714730 AW897950 AA143782 T15562 T49475 AA196794 AA219637 AW574805
 R61459 BE294610 AA653641 AW246595 AA122178 AA079030 BE259347 AA125802 AA223509 AA071105 AA056515
 AA115965 H98828 AA975764 R44928 AA122173 AW499013 W68765 AI306457 H70716 AI866327 AA101102 AA523008
 AI567597 AA146744 R88666 AA197332 AI086825 AA197306 AA127186 AA648686 AI758939 H66791 AA158684 AI423641
 BE622207 H96899 AW748838 AI683391 T57141 AI360649 AA084328 AA205369 AA605035 AA730337 AA190782 AA622674
 H70715 AL035929 R53569 BE410471 AA826991 BE304945 T57181 AA190793 AI826886 R61544 AA357249 AA730680
 AA349636 AA598937 AW075466 W52142 AI270583 AA693372 D53633 T78875 AI874190 AI926336 AI744448 AA458786
 AW019919 AI903107 AA243188 AA127188 AA085973 R50969 AW674943 AW674933 N33158 T99016 AA386238 H05817
 AA227228 T93797 BE408530 AL035916 AA199872 AA196440 T61038 AI193541 T03458 H04813 T26581 AW074308 F28259
 AI420254 AW406597 AI752919 AA349540 AI961511 AI026726 T16511 T61589 AI872394 AW069694 AA350697 AI766468
 N84462 AA085828 AI049703 F09506 AW247712 T16319 T95336 AA427580 AA219549 N54075 BE383804 AI934238 T23636
 T23966 AI540707 AA852250 AA480844 F03543 AI682148 AW029145 AA350647 T57116 AA121780 AA362506 T89452 F03033
 BE544518 BE537982 AI400848 AW249805 R40175 BE547154 AW194658 BE304905 F03972 AI887116 AW662060 N64153
 AW090474 AA111861 BE544487 AW247971 AW189742 AA083676 AI689361 AI865447 AA205201 AA995389 T57070 AI749217
 AA620398 AI205275 BE278095 W25238 AW498851 AA361225 W24643 BE293452 T60878 BE378902 AW675067 AW419249
 BE546138 BE622685 H37989 BE298837 W02581 W03143 W03350 BE090146 D56472 AA477356 AA369046 BE617569
 AW405756 BE068241 H94917 R93689 BE536003 H78709 BE293724 BE207577 AA324949 AW406102 R66280 AW404427
 AW498515 AA283600 BE091536 N78168 N94034 H13896 H40383 AA426247 H38210 AW381001 AW381031 AW384779
 AI187246 AA356920 BE614174 AA361144 AA954817 AA373947 N51059 AA714393 AA361010 AA858368 AA128860 AA186577
 R97861 BE300605 BE617658 AW407835 AA007136 W04495 AA714521 W01702 AW675093 AI129627 W23528 BE622513
 D52760 AA580710 D54714 D54912 H39979 AI189140 AA604554 AA379346 AA379753 BE293739 AI247952 H19587 H23957
 H22624 AA022986 H80389 H80376 W32684 H74304 W73673 BE619989 H46803 AA326012 BE256750 BE293868 AI687073
 BE540791 AI554627 AI669399 AI052649 N74381 BE254994 W35343 R83888 AW405482 BE300603 AA190680 AW409945
 AI565178 Z25891 H95714 AI587135 AW881291 N74433 AW580801 AI126014 AW583313 AW385805 BE392285 AI002971
 R86251 AA928186 AW883103 AW577705 N47822 AW245647 AI186441 AA455487 AA876464 AA512933 R48210 AA167661
 AA715724 T56604 BE315352 R25751 BE163471 W77978 AA617822 AA618045 AW973348 AA641395 N32598 N58159
 AA604336 AA617894 AA748311 AA599921 AA617899 H94863 AA029390 AA706656 AA206124 AA778101 BE300604 T15728
 W57648 AW575696 AA029389 AA599861 AA640585 AA613863 AA526077 AA577614 AW575035 BE183827 AI709081
 BE183680 AA330412 AA580149 AW574766 AI609157 AA557458 AI801804 AW085646 AW339731 AA907669 AA489663
 AA486665 AW166938 AI500319 AA181843 AA605173 AA486566 W94458 AI623349 AA858195 AA558201 AI249662 AI092843
 AA905720 AI682690 AA773433 AA434385 AA022948 AI249681 AI619676 AI084530 AA554408 AI376770 W35304 AW574722
 AA279871 AA641309 W00970 AA564566 AA206053 AI682641 AI686270 AA216784 AI371057 BE208021 AI816060 AA977763
 AA988221 W56716 R66281 T60692 AI371108 AW316667 AW090548 AW263786 AI688536 BE300865 AW118162 AW089606
 AW157567 AW439435 AW673929 AW027607 AW474885 AI984259 AW571884 AI880916 AA758525 AA070410 AW190306
 AW246746 BE221650 AI630670 H28485 AW468627 AW651608 AA360204 AW513778 AI608753 BE302410 AI750057
 AW674261 AW510365 W94350 AA761293 AI869840 AA301790 AA933607 AA227144 AA716677 AA181762 R83889 AI079599
 AI000208 N99897 AA070466 AW245167 W68620 N83377 AI361698 AA464157 AA496711 AA205826 AI361699 H80288 R50934
 H98743 AA179708 D52483 AW249546 T49476 H80293 W73625 AA099853 H03238 AA179703 AI880803 AA653206 AA457733
 AA931701 AA190330 AA906004 H79483 AI084626 T57243 AA079760 T55734 AA507899 W73915 T74565 AA523607 N69544
 R97811 AA190385 R86252 AI359329 AA157496 AA070716 AW162385 AI929421 AW651618 AW087897 AW770466 AW073321
 AI813809 AA113799 AI342925 AI754395 W60153 AA665490 AA653483 AW087840 AW169380 AI754330 AA181774 AW243958
 R76858 AA936814 AA477111 H80279 AA496723 AA633000 AA243218 AW169688 H80274 R48211 AA743251 AI221630
 AW593584 H40328 W56761 H95640 R93010 AW250165 AA497004 AA279793 W20432 AA775006 AA401150 T34421 T29637
 AA678773 W23704 AA723093 AW073071 AI140379 AI188662 AA680074 AI081730 AW874489 AA226908 AI452689 AA531164
 AW498837 AA670295 AI061112 D20132 AI937246 AA580593 N70277 AW993170 AA205918 AA581651 AA129695 AA548261
 AW673898 AI000118 C13991 BE247777 AA653439 AI198072 R26594 AA282708 C14467 C14444 AI000629 C14510 AA775369
 AA885560 F30063 D51934 D51834 D51478 D51931 D52011 D51918 D52160 D52045 D51888 AW245330 D52030 AA936639
 D51494 D52144 D51448 D52138 D51730 AI419648 D52007 AW021403 AA935494 AA935487 AW770291 AI702431 AA687083
 AA362527 D51696 R29267 AA653197 AA888552 D54444 C15448 AA478045 AI589903 D55942 H40340 AI864969 AI341782
 AA353097 AW439647 AW305322 N54940 AA935976 AW248042 AI783806 BE349217 AA969923 AA383726 AA357323
 AA007135 AI915436 N71185 AI123662 AA328354 AA331419 N21981 T03306 D54551 AA983808 D54942 D55074 AA113880
 D52740 AW020376 AW020367 AA936029 AA555005 AA969180 AW812036 BE544746 N89212
 M55405 AW752552
 M55405 AW752552
 H08773 R37687
 Z99916 U71216 NM_004076 X15144 X15145 X15146 AA652300
 L14561 AW496834 AW059849 Z99413 T29666 R14900 R93603 R51525 S49852 U15687 U15686 AI033177 W94597 AI056839
 R02057 AA134349 F05667 H73767 BE326691 AI984023 AI695688 AI750184 AI434336 AW029158 AI440089 BE046108 R51526
 R53074 AA025218 AW083388 R93604 AA732638 H47642 AI859270 R41222 AA593057 AA760815 H43399 N29456 AI337321
 H98205 AI752749 AA442913 AW961129 AL134557 AW439527 AI341304 AW190061 AW613371 AW439931 AA806627
 AA781883 W05800 AA731599 AI863791 AI370277 Z38623 AI470448 H15877 R53656 D82513 D82467 D82386 D82515 R15295
 AA096386 AW892808 AA300686 AW954282 AW959453 H29807 R25259 N46722 N46679 D60314 AA736829 Z99414 AI076802
 AW576457 H16400 AA933075 AI752748 N75064 AW873040 N39235 AI310710 BE328592 N39576 AI672714 AA747547
 AW769967 AI625462 AW169755 AW615361 R53545 AI758375 R46612 AW273091 AA736697 H29808 R42200 C14108
 AI783809 AI270395 AA952981 AA746745 R37023 C75654 Z39578 C75656 AW956278 AA338702 AA338701 AA279433 W58753
 AA041264 R02056 AW842224 AI215415 AW951238 AW022139 AA658234 AL119699 BE537020 AI795941 AA927068 AI765979
 AV655427 AA041498 AI436090 AI190267 AA397563 H43344 AI718564 AW192067 BE328781 AW768573 AI358433 AW631373
 AA262804 AW235152 AI570253 AA934641 AA776029 AW182028 AA279606 AV657690 AV657727 AV657350 N41480 AI926218
 T29285 BE143058 N72769 AA385114
 M60495 M60499 M60500 M24355 M62201 BE389102 M96943 L01090

100544 22955_11
 100545 22955_11
 124087 1561179_1
 100560 30266_1
 100571 7592_1

100572 13049_1

100582 26433_2 D13897 AI183955 NM_004160 D13899 L25648 AW136574 AI654355 AA913288
 108409 113869_1 AA075631 AA075578
 100627 tigr_HT2798 Z25424
 123526 genbank_AA608657 AA608657
 100663 tigr_HT3059 M20022 M32505 M32506 M32507 M32508 X64880 X87678 X87680
 100684 tigr_HT3283 S66933 U15688
 100687 tigr_HT3291 L18862
 100695 tigr_HT315 M31126 M38243 M74197 M94890 U04323 U08196 U08197
 116389 genbank_AA599011 AA599011
 100702 tigr_HT3413 L27065
 100756 tigr_HT3768 M88357
 100809 tigr_HT4261 L33990
 100810 tigr_HT4262 L33994
 100854 tigr_HT4464 U08607
 102185 entrez_U20230U20230
 125090 genbank_T91518 T91518
 100961 entrez_J00148 J00148
 102254 entrez_U28131U28131
 125145 NOT_FOUND_entrez_W38001 W38001
 125153 NOT_FOUND_entrez_W38294 W38294
 116797 genbank_H40486 H40486
 102354 entrez_U38268U38268
 102474 entrez_U49973U49973
 116902 genbank_H70739 H70739
 116905 genbank_H71420 H71420
 102643 entrez_U67849U67849
 125576 205199_1 R21635 R66208
 118579 genbank_N68905 N68905
 120256 genbank_AA169801 AA169801
 120274 genbank_AA177051 AA177051
 113149 genbank_T51588 T51588
 127759 808057_1 AI369384 AA719568
 113518 5697_40 AW367788 AI093217 AA533602 AI300430 AI860318 AI869201 AA933015 AA077695 AA649045 AI016319 AW084216 AI969650
 AW169170 AI440341 AI744376 AA905125 AA194528 AA971323 AW510721 AA194483 AA076744 AW182167 AI955513
 AA578875 T89731 T89829 AA828731
 113608 genbank_T93113 T93113
 101046 entrez_K01160K01160
 122731 genbank_AA457549 AA457549
 108316 genbank_AA070160 AA070160
 108328 genbank_AA070204 AA070204
 108394 482708_1 AA642953 AA075144 AA084113 AA070130
 108395 482708_1 AA642953 AA075144 AA084113 AA070130
 108417 483241_1 AA070853 AA075749 AA075716
 108436 genbank_AA078801 AA078801
 108491 genbank_AA082973 AA082973
 108499 genbank_AA083103 AA083103
 122922 genbank_AA476268 AA476268
 122938 genbank_AA477119 AA477119
 122948 genbank_AA477483 AA477483
 117046 genbank_H89505 H89505
 101427 entrez_M19508 M19508
 101559 entrez_M32053 M32053
 117437 genbank_N27645 N27645
 101798 entrez_M85220 M85220
 117590 genbank_N34904 N34904
 110349 genbank_H40988 H40988
 101909 entrez_S69265S69265
 103392 entrez_X94563X94563
 119053 genbank_R11501 R11501
 103457 entrez_X99728X99728
 119174 genbank_R71234 R71234
 119229 genbank_T03229 T03229
 103654 entrez_Z70759Z70759
 103679 entrez_Z86000Z86000
 119329 genbank_T51832 T51832
 119343 genbank_T62873 T62873
 119347 genbank_T64349 T64349
 119523 NOT_FOUND_entrez_W38041 W38041
 119526 NOT_FOUND_entrez_W38049 W38049
 119529 NOT_FOUND_entrez_W38053 W38053
 119564 NOT_FOUND_entrez_W38206 W38206
 119566 NOT_FOUND_entrez_W38209 W38209
 126908 533102_1 AA180024 AA169866
 119906 genbank_W85818 W85818
 123022 genbank_AA480909 AA480909
 114604 485245_1 AA075966 AA076128 AA128755 AA128339

114666 genbank_AA112274 AA112274
 100221 entrez_D28383D28383
 123143 genbank_AA487595 AA487595
 114718 480609_1 AA080912 AA075318 AA083403 AA078992 AA076594 AA062835 AA084926 AA081881 AA082953 AA113913 AA083821
 AA070343 AA134801 AA113892 AA075419 AA063293 AA071252 AA078900 AA113888 AA071406 AA075072 AA100879
 AA112153 AA062836 AA113865 AA074554 AA643251 AA084110 AA078783 AA084346 AA078993 AA079022 AA079776
 AA070181 AA085031 AA082954 AA082971 AA131328 AA063179 AA083366
 100478 tigr_HT1067 M22406
 100547 tigr_HT2219 M57417
 100563 tigr_HT2324 Z11585
 100564 tigr_HT2324 Z11585
 123473 genbank_AA599143 AA599143
 123490 genbank_AA599723 AA599723
 322024 43541_1 AA334384 AL137436 AA352089 AW341247 BE327629 AI669284 AI274156 AI123562
 322033 33332_1 AL137507 AW879790 AA349971 AI624899 AW294742 AW271762 T06484 AA788895 R35098
 314251 194954_1 BE011657 AA713589 AI440513 AA278620
 320825 29807_1 NM_004751 AF102542 AW360893 AF038650 BE304708 AW360892 AW360931 AW842622 AA307800 BE292814
 AW582119 AW582122 AW374998 AW374874 AI587061 AA583339 AW662377 AW192901 AW887756 AW887761 AI955582 AI150400 AA568218
 AA583146 AI832775 AA294858 AI445680
 320832 170589_1 AA214584 D56572 D57294 AA207006 AA210987 AA601292
 320882 41486_1 AK000655 AW024515 AI499162 AI673527 AA903900 AW084419 AI219549 D60890 AW243134 AI832098 AI811630 BE348831
 AI022831 AI475320
 322128 46785_2 R95860 AF085903 R95859 AI346033
 322135 46801_1 AF075082 H48639
 322141 46810_1 AF075092 H53478 H53853
 322152 78409_4 BE614761 AA263136 W00335 W00327
 321525 27440_1 AJ006077 AA377082 H78875 AA263148 AW958548 AA381830 AA381631 AW748909 H47990 AW402973 R31722 R82733
 AW195851 AI650977 AI635744 AW136376 AI913496 AI569147 AW263050 AW075972 AI538882 AI762430 AI924045 AW613027
 R74454 AI638560 AI476181 AA873030 AA936769 AI862049 AI955522 H00589 R31680 C20629 AI799176 AA835126 AA310578
 H13126 AI858430 AA377081 BE244193 AF288208 W26453 AV659072 AF288209 BE622910
 320913 24943_3 AA663733 D62598 D62472
 321583 87512_1 AA018518 AA059305
 320957 39063_1 AF151534 AI929478 W40378 H17557 AW163309 BE074271 AW854041 AW604408 AW853903 AA206576 AA133144
 AW854378 BE271915 F08002 AW293257 R58383 W95032 AI022248 H18001 R19681 F11341 AA778166 AI435068 AA702525
 AW176505 AA318946 AA705230 AW136167 AA704931 AW157512 W93328 AI694445 AW157539 AI301999 AA975516
 AA722698 AI569683 AI674496 H17453 AI910812 AI598186 D53709 N80796 AA285026 AA704939 AA159340 AA565703
 BE464932 AA477953 AA402072 AA476988 AI929436 AA133096 AI912377 H61238 AI457179 H18002 BE047110 H56139
 AA633441 AI500607 AA401959 H55753 AI767655 N93886 AA402908 H78194 D80936 R44236 H61239 BE551612 AI638233
 AI953226 AI744095 F09000 Z41080 AI700837 AW768854 AI872712 AA283182 BE383452
 320994 9353_4 BE618027 H22381 AA326465 AA326466 AW962215 BE207339
 322209 46967_1 H89360 AF086037 H89546
 322224 47029_1 AF086064 AA013034 N50099 AW903279
 315021 344728_1 AA533447 AF158241 AI240598
 322264 47231_1 AF086242 W67679
 322265 47233_1 AF086244 W68829 AI539008 W68737 AI685168 AI351133 AI633948
 321632 286374_1 AW812795 AA419617 H87827 AW299775 AW382168 AW382133 BE171659 AW392392 BE171641 AA541393
 314429 238740_1 BE146577 AA339680 AA972551 BE146576
 306624 25108_1 AA329384 S49006 AW405735 AW404287 AW405848 AW405979 BE538908 H70947 AI814190 AA381896 AW582731
 AW975580 T94914 AW474500 AW869616 AW974125 AW946246 H44560 AW802184 AI538108 AW609912 AW865715
 BE007659 AA443571 AW376161 AW797783 AA713566 AW577973 AA745472 AW270172 AA910107 AA713717 AW364122
 AA533898 AI523353 AA715899 H44507 AW947263 AW390753 T89943 R66359 H44320 T64100 AA715879 R54661 AW579645
 H68597 AI499528 AI699010 AW605041 AW605043 AA236700 AI290767 H27472 AW079688 T69967 T87728 AW869468
 AW873389 AI250670 AA617786 AI566627 AW627605 AW302334 AA617836 AW793186 H16015 R83107 T85409 AA643479
 AA582449 AW794654 AI819995 AW865810 AW380149 AW793863 AI281629 T64021 AA501599 R49882 AA565066 R69406
 N23918 T59642 R54662 AW973199 R53006 AA401087 AA496563 AW934874 BE171294 AW793133 AI581595 AW605835
 AW605040 AW605055 AW605033 AW605058 AA291844 AW382472 AW605005 AA421881 AA513106 AA744190 AW386065
 AW613785 AW605829 AA580905 AW605027 AW364134 AA464027 BE012096 BE008565 AA809035 AA809154 AA911395
 AA713636 AA745324 AA826230 AW368498 AV646747 T89967 H51164 AI540661 AA721571 C02031 AA523762 AA523746
 AI287256 AW841164 AA962139 AW797014 AA515246 AW364140 H45842 T94267 T72111 R49771 T70151 H42664 R83656
 R83590 AW380297 AW380263 X95750 T57717 AW391436 AA293355 AW380185 X95749 X95748 X95747 AW796510
 AA318628 AI001043 AA744404 AA745567 AA650437 AA715526 AW392762 AA516228
 306644 34348_2 BE263222 BE312445 AI002913
 306669 7570_1 AI340462 AI583268 AA079086 AI950777 AI301866 AI925108 AW876954 AW877000 AA525418 AA888549 AI934220 AW380220
 AA804858 AI927576 T61151 AW384053 BE391691 AA533856 AA248400 T48202 N57156 R68346 R26020 AL050332 W30806
 H61369 AA092592 AA230324 BE271217 AW372903 T48772 AA358002 AA094302 AA559856 AW373308 AW373315 AW373297
 AW373311 AW373314 AW373309 AW877055 AW770140 AW379805 AI581609 AW364144 AA078921 AA715432 AA654210
 AI004899 AA602209 W47464 AA506588 R26822 AU076528 AI535743 AI535704 AI535681
 322302 47349_1 W76021 AF088052 W72465
 322309 47372_1 W76622 AF086372 W72660
 322337 47496_1 AA249804 AF086490 W93549
 322340 47509_1 AF088076 W95222 W92523
 322362 36526_1 AF039697 AI860821 AW406650 AW515052 R49969 AA834501 AI951401 AA761660
 321708 64670_1 AA126365 AA055269 AI768638 N46910 BE047017 AA488423 AW021548 AW612323 AW007669 AI333685 AI633142 AI638022
 AI765587 AI151494 AA443764 AI373599 AI140433 AW295946 AA088183 AI811417 AI277748 AL079978 AI341834 AI144434

AA055164 AI765262 AI140147 AI160673 AI686050 AA130038 AI699503 AI580411 AI276910 AW296875 AI927239 AW470427
 AI174424 AI675518 N20396 AI308224 BE221055 AI926097 H89681 H90776 AW023381 AA126261 AA025391 AA347308
 AA476817 N25488 AA442811 AW297971 AA025454 D81551 D81214 D61126 C15599 AA130037 AA088653 AV654662
 321763 166644_1 AA195602 W01148 N40632
 313913 653504_2 AW391342 AI813778 AW190911 AI963486 BE049275 AI922735 AI935914 AI263291 AI679178 AW192178 AW338885
 AW473496
 306710 52443_1 BE564350 AI024221
 313960 130872_1 AA113301 AA130859 AI805438 AA846950 AA130915 AW862833
 306773 563488_1 AI040750 BE062532
 323014 140817_1 AA305198 AW962351 AA134366 AA259244
 315276 383168_1 AA860090 AI961138 AW592114 AW087700 AI798907 AW340674
 321847 45225_1 T08401 Z83934 T16897
 308069 33294_5 AI470895 BE386951 BE391680 BE277351 BE385202 BE300283 BE299619 BE254885 BE391698 T17015 AL048342 BE387417
 BE315548 AA345769 AA374932 AA304724 BE277135 T31443 BE387617 AW582877 T33057 AA054826 AA305115 BE378981
 BE615689 W07028 BE537075 BE615271 BE252353 BE563255 BE391752 BE545875 AW580149 AA747256 AW276731 N85015
 AA299609 AA365061 AA302265 AW951660 BE538115 AW404883 AW583622 AA374519 AA225917 AA037286 W24285
 BE255801 BE254061 BE278256 AA377959 AA319628 AA316739 AA378914 W24421 AA658882 N87533 AA526881 AA376559
 AA378175 AA300193 AA330503 W69498 C03856 N85298 AW957966 C02647 H19560 BE616753 BE263169 AW250280
 AW162197 AW163162 AA301672 AW249055 BE616277 AA225272 AI557298 AW276939 AA327042 N83648 AW404841
 AI903202 AA314875 AI546852 BE616559 BE262330 AA385891 BE182717 AI557551 AA082310 AA354394 AI541339 AA327616
 AA344981 D53311 AA363102 AA171801 AA089673 AW162085 AA379891 BE277324 AA157651 AA304574 W52799 AA186652
 AW328567 AA187480 BE386732 AA369717 AI815603 AA303651 AW160407 AA056711 AA082790 AA329861 T39426
 AA650419 AI268280 AA471236 AA308712 AW733012 BE256165 AA745013 W06997 W21418 AA531583 AA308694 AI133371
 AA324238 W24570 N88175 W45648 AL022721 AA378455 AA378168 BE393810 AA317384 W21121 AA371342 N31367
 AA359623 NM_007104 U12404 BE388017 AA374579 AA380618 AA334401 AI557552 AA337150 AW732322 AA327632
 BE263809 AA657772 D30933 AW663232 AA315817 AA314480 AA370766 AA317760 AA315084 BE383638 AW327814
 BE302619 W21304 BE390854 AA373219 R94330 H84395 AA377636 BE252526 AW732866 AA299524 AW328563 AW674382
 W38535 W06840 AA332645 AA355580 BE258503 BE256923 BE271400 AA380757 AA385628 BE256989 AA332349 AA314985
 AA186515 AA305031 AA357482 AA316998 AA379264 BE390621 BE255056 AI207414 BE252354 BE254152 BE254578
 BE252547 BE266591 BE257651 BE294792 BE277990 BE391235 C15642 BE391151 AA301280 AA384750 BE273056
 BE312333 BE296962 AA314715 BE256346 BE313459 BE269894 AA310988 BE300029 AA157523 BE250757 AA545754
 AA083546 AA315252 AA224003 AV655919 AA315169 AA310685 AA301191 W19623 BE392967 AA303515 AA379649
 AW327286 BE560669 AW580113 AA352149 AA360956 AA316107 BE563100 N31353 AW675322 AA379584 BE019308
 AW583963 W37951 BE295910 BE251482 BE385588 BE270412 BE378750 BE396426 BE295210 AA336973 BE314395
 AA354788 BE295227 D55985 BE615081 BE260566 AA320506 BE278254 AA285366 AA303825 BE275375 BE313367
 BE260703 BE279256 BE382903 BE315113 BE313341 BE260804 BE620531 BE615973 BE266048 AA093478 BE616196
 AA360276 BE253746 AA314344 AA315622 BE386557 BE313445 BE253355 BE561084 BE296088 BE531299 BE255860
 BE408279 BE273842 BE378885 BE255055 BE271521 BE563765 BE252792 BE391016 BE258218 BE273725 BE273968
 BE272901 BE313660 BE304527 BE257956 BE254227 BE275320 BE253909 BE407614 BE614755 BE378776 BE613909
 BE407708 BE395973 BE513022 BE157875 BE615399 BE252775 BE279463 BE257109 BE271307 BE256275 BE276484
 BE257302 BE384605 BE258461 BE546662 BE409191 BE280351 BE252294 AA285364 BE378324 BE264740 BE292822
 BE620927 BE296544 BE271710 BE257492 BE252712 BE395931 BE266143 BE255921 BE255720 BE300136 BE531292
 BE391204 BE409180 AA320604 BE295038 BE390679 AF075335 BE315084 BE394350 W04926 AI110836 BE615235 BE295593
 BE275680 BE409184 BE253595 BE294473 BE253714 BE512867 BE295544 BE295554 AA296596 BE255510 BE378700
 BE513852 BE512932 BE257734 R31451 BE293044 AA379511 BE261311 BE397180 BE278214 BE407490 D56163 BE563686
 AA070681 BE255940 AA348975 BE253849 BE390468 BE396140 AA186986 W20120 BE389750 AA307189 BE378407
 AA125980 BE407415 BE276230 AA304996 BE389228 BE512779 BE617120 BE512670 BE272223 AW407102 AA370834
 H21183 W07800 BE562889 W05304 H02179 AA327191 H18595 H22622 BE257450 W46597 BE262207 AA002219 AW405652
 AA334037 BE294871 AW606479 AW384255 AA085885 AI903205 AW405432 BE298839 BE292956 BE262232 AA363253
 BE276322 AA300909 BE389123 AI909563 BE407174 AI535831 BE260382 BE382583 AA532637 AA380091 AI114568
 AA193129 AA192984 BE384600 BE407214 BE182724 BE539061 AW733001 AW406350 AA374881 BE384674 W87442
 BE276668 BE299430 BE274869 BE378528 BE396131 AW239494 AI630538 AA053478 BE280557 AA218746 AA299674
 AW406770 W07830 AA808817 AA146904 BE272999 AW408211 AW580062 AW606478 W07669 AW580120 AA379387
 AW580130 AA101207 BE394409 AA362957 AW392453 AA101121 W03827 AA166722 AI909564 R30769 AW580069 T58944
 BE261760 BE313004 BE312309 BE260766 BE314007 AA724391 BE538878 W04777 AA657588 BE259359 AA631041
 AA070065
 314661 296144_1 AA578229 AA436432 AA481375 AA481363
 307474 25106_2 AB037864 AI223793 AI916099 AI332699 AI264023 AW962587 AA412310 R37910 R37827 AI191724 N22920 AI916409
 AA932668 AA782068 AA865648 AW467014
 323115 155930_1 AI921875 AA170835 AA866613
 322505 38889_1 AF147315 AW173079 T53029
 323170 980026_1 U83527 AL120938 U83522
 322518 38914_1 AI133446 T50819 AF147343 T50665
 323183 3032_1 X73874 NM_002637 F00757 BE172051 BE081451 AW891243 W20171 BE619896 AA927528 AW374434 N90546 F01171
 AI681314 AI621208 AI366791 T27589 AW960206 AW393850 AW892627 AW892626 AW833974 AW833971 AA194696
 AW274557 AI813660
 323185 18915_3 R52177 AL121177 AW749837 AA354099 AA318422 AA318513 AA318429 AW961486 AW964802 AW961475 F12011 R12085
 R12113 R20096 AW836716 W87916 F12265 T64809 R96961 AA340929 R88075 F11199 H11127 W68153 BE465310 W67653
 AA777659 AA630420 AI423300 AI744317 AI681159 N81151 AI758899 AI991528 AI640256 AI361299 AA039678 R52083
 AI161215 AI240851 AA806482 AI159875 AW452889 AA987856 AI581408 AA746962 AI277132 AW802982 AI567611 AA761163
 AI277294 AW244127 H11684 AI381224 AI277139 AW952835 AI480237 AA188967 AA041517 AI798651 AA906163 AI081406
 AI032939 R41802 H95399 AW023038 AA890250 T65065 AA340673 F09658 AI248293 H11039 AA340628 AI955106 F11007
 AA028186 H98922 AA810707 AI769491 N21690 AI670911 AW005066 AI692255 AA028093 AA748907 AI919266 H11597
 H95373 R36867 R36878 AI222427 T23945
 315322 444861_1 AA770599 AI215099 AA992267
 321920 1023421_1 AW089866 N63915

321966 30334_1 AL122111 M79226 AI656413 BE502197 F32670
 321986 22722_2 AL133656 AW269409 AI138865 AA954306
 323243 140566_2 W47525 AA134047 BE391212 AA330333 AA376355 BE304871 BE167342 H87402 AA631722 W45724 AA715517 AI925438
 AI804849 AW241617 AW403807 AI653435 AA134048 AW747874 AI922327 AI814967 AI935895 AA228865 AW504076
 AA225008 AW673858 C03914
 316041 417912_1 AA719183 AA736442 AA709125
 322644 82848_1 AW841642 AW747992 AW748000 AA007413 AA568664 AA779192 AW188983 AI471878
 322649 24892_1 F01266 NM_016549 AF239742 BE219554 AA902371 AI298989 AA533735 AA599216 AW025283 AI336116 N75315 AA621418
 AI671706 AI373650 NM_014556 AF216184 AI269271 AA780274 AA772950 AA932592 AA496722 AI186107 AA009748
 AA477144 AA788812 BE384172 AA009407 AA526549 D25270 AW882122 AW972929 BE174659
 322682 37364_1 AF063553 AI110679 AF090893
 307625 10562_13 AA768239 T98699 AW207784 AA343876 AW963055 AI299617
 314893 3084_2 AW969114 AA761093 AW082191 AA505065 AW087800 AI719655 AA576454 AW375968 AI804392
 323333 62251_1 AV651680 AA228883 AA367341 AW962458 AA628024 AW172426 AI767785 AA313012 AW963323
 300470 59496_1 T87841 AA233726 AV648314 BE545191 AW969738 AA579641 AA516077 AA483490 BE612779 AA460132 AA659710 AI149891
 AA113277 AI889233 AI028588 AA461487 AA074311 AA682750 AI421205 AA985248 AI753378 AI914588 AI493749 AA936668
 AA633392 AA722409 AI424537 AW609606 AW815447 AW268600 AW609594 AW601214 AW082930 AI752615 BE550576
 AI989665 AA046575 AI201331 AA169112 AA169113 AV648431 AV648389
 322738 26089_1 AF200496 AI343258 AI014548
 308337 3328_2 J00124 AA158848 AW452899 NM_000526 AW384139 BE140708 BE140690 H28274 BE140404 AW844922 BE157342
 AW580043 AW384049 BE157333 BE157179 H44127 BE140671 BE614947 AW380727 BE184532 AA808075 R73201
 AW949948 AW950242 BE183306 BE183297 AA587174 BE183243 AI591112 AI609229 AI590690 AW606369 AI609238
 AI608848 AI590885 AW084944 AI609220 AI609210 AA583890 AI609274 AI609226 AI608878 AA550914 AW170430 AI608947
 AI608606 R88146 M28646 AA587248 AA583985 AW872988 AA583993 AA586980 AI284481 AA584051 AA587024 AW800015
 AA587313 AI283394 AI143314 AA595434 AA583917 AA922332 AA584021 AA583576 AA862004 AW873168 AW796060
 AA862049 AW873161 AW079705 AI366769 AA583724 AA583889 D29065 AA113288 AW083705 AA584334 AA586711
 AA583558 AW117878 R72295 AA583842 AW996598 R73138 H28224 R88223 AA586985 AW369022 AA602252 AA641063
 R72845 AA861952 AA587149 AA587308 AW369033 AA584344 AW799955 AA583732 AW368990 AA862083 D29595 R53012
 AA587254 D29462 AA158849 R72649 BE181541 D29604 AI127631 D29297 H44051 AA583575 AA586762 D29122 AA583878
 AA595946 AW368880 AA587318 AW368881
 322774 104619_1 AA131111 AA132859 AA053057
 314938 337806_1 AA515635 AA516338 AI801993
 307783 697809_1 AI347274 AW844024
 301119 33384_1 BE621320 BE266806 BE276582 AW516729 AF142579 AW451687 AK000069 AA325236 BE168997 W73105 AA715365
 BE278873 AA808894 AA386371 AW517942 AW750993 BE140314 BE392384 BE621757 AA318192 BE548173 AW152607
 AW166898 AA352215 AW841506 T59802 AF147378 AA335719 AW956069 T59668 AA826362 AI961329 AI290469 AW197375
 AI805651 AA160748 AA581089 AI968889 AA581100 AA501478 AI621069 AA468534 AA503715 AA658457 AI144504 BE387827
 AA159880
 301163 427639_1 AA732066 AA807070
 324031 265007_1 AA376108 AA375646 AA376551 AW963816
 301178 431366_1 AA828385 AA769592 AA742234 AA742235
 324042 266490_1 BE387327 AA377589 AI903826
 324048 267284_1 AA378739 AW964174 AA570564 AI076833 AW265063 AW006805 AA480656 AW004789
 324064 421551_1 AL046841 AA721199 AL046079 AW137650
 323409 218874_1 AL135534 AA366767 AA313599 AA333787 AW966106 AW844387
 323426 188613_1 AA485236 AA830637 AA251401 AA749343
 324094 270098_1 BE395109 AW663898 AW237041 AI492154 BE046906 AI651285 AI983290 AW002590 AI201040 F32424 AA992272 AW271836
 316231 427772_1 AA732301 AA764985 AA732300
 323479 194627_1 AA278246 AW292815 AA278703
 322840 109637_1 AA083710 AA122195 AA081984 AA134650 AA080983 AA080954 AA062747 AA083876 AA079025 AA113855 AA074687
 AA078914 AA078873 AA074126
 322877 116942_1 AA079727 AA079728 AA824267
 308447 10607_2 AI659985
 324148 273755_1 AA393624 AI190160 AI342032 AI015092 AA992047 AA860917 AA400867
 300694 110146_1 AA063406 AA063407
 322907 5481_1 BE252579 BE255945 BE314749 BE260141 BE260121 AA084941 BE206830 BE256911 BE256464 BE277162 AA448932
 BE206992 AA158178 BE265680 BE164838 BE164881 AA411651 AA036706 AA411652 AA480595 R53714 AK000381
 AA191114 BE314072
 300707 114644_1 AA079132 AA080921 AA076662
 317010 485212_1 AA863389 AA863395 AI969882 AI695443
 324252 287622_1 AW629965 AW975427 AA421989 AI051821 AW748356 AW129223 AA715470
 300763 163257_1 BE000150 AA190753 AA760634 AI685862
 300781 23981_2 AA731209 AA236961 AW971508
 323676 220254_1 AI702835 AI758919 AI685405 AI952108 AI299207 AI400767 AW105389 AI952710 AA845312 AI784118 AI537315
 316473 439976_1 AA811452 AA829961 AA815116 AA764935 AW976998
 323699 222860_1 AW178750 AW178736 BE141842 AW178683 AW178714 AW178684 AW178679 AW178716 AW178685 AW178718 AW178717
 AW178681 BE141834 BE141835 AW178711 AW178735 AW178712 AW178734 AW178715 AW178680 AW178713 AW178677
 AW178719 AW178748 AW178710 BE141843 BE141844 AW751119 AW178682 AW178737 AW178749 AA318993 BE141841
 AI174911 AF116710 BE250634 BE513651 BE513483 AW973114 AW973111 BE407498 BE387872 BE255662 AW575394
 AW157150 BE383339 BE045072 BE382560 AA535472 BE389253 BE274463 BE076283 AW157403 W20446 AW663763 N83897
 AI816181 AI879111 AA603287 AA809812 T03060 AA531063 AI815578 AA534177 F26418 AA527007 AW157453 AA557931
 AA742784 AW163466 AA513251 AI816220 AI816077 AI929498 BE299421 AW163056 AA502024 AW160897 AA651678
 AA534185 AW663233 H46043 AI815950 AA635243 AW161304 AA532646 BE619905 AW163000 AI928982 AI929122 AA569189
 H94752 AW163120 BE619294 N84679 AA639280 AW161846 AA524657 N76560 H60985 AA318407 R98156 AA316834
 AA534172 AA353056 AA375240 D16959 AW328044 AA603503 AA531077 AA330098 AA244141 AA377880 AW161054
 AA070576 AA326867 AA370759 AA378306 AA055146 AA311016 AA356827 AW827213 AA318418 N84051 AA322649 T72970

AW630001 AA376419 AA343976 AA311126 F20273 AA308824 N84783 AA373006 AA374318 AA356480 AA300347 AA314040
 AW328346 AA092658 AA181308 C04940 AA329907 AA587591 AA300042 AA301309 AW674942 W21264 W47074 AA310460
 W31811 AW630251 AA332208 AA299335 AA360053 AA360318 AA328721 AA378343 AA299584 AA345747 T49611 AA376010
 AA186475 AW957009 AA305013 AI064911 AA330372 AV655922 AA314027 AA354481 AA313645 AA314699 AA314084
 AA358279 AA311170 AW327387 AW327464 D58829 AW973106 AA375740 AA308783 AA316940 AA315588 AA380257
 BE397919 AA181856 AI557351 N83566 AA315879 AA369434 AA357016 AA314419 AA130919 AA308111 AA314139 AA354095
 AA095733 AA247440 AA316663 AA307418 AA131136 AW157088 AA375200 AA316192 AA315616 AA360129 F26579
 AA363700 BE539203 AA379637 AA147978 AI340513 AA307861 AA467839 AA384626 AW328308 AW248834 AA379269
 BE621558 AA355664 AW404712 BE613747 AA507275 BE206816 AW270699 C13959 AW966785 AA310386 BE394115
 AA131219 BE385515 BE262339 AA095023 AA315277 AA364046 AA535741 AA188339 AA316095 BE312188 AA176667 T53669
 BE258138 BE258239 AA303587 BE272248 BE545416 BE250615 AA371845 AW839835 AA314570 AA330923 AA311279
 BE261310 AA320246 H95461 AA587557 AA308437 BE540153 BE390839 F25801 AA480575 N89472 AA302013 F29054
 AA375385 F19527 AI816119 AA227104 BE536936 BE535875 BE269659 BE536267 AA339654 AA771729 BE396514 BE263080
 BE312046 BE298027 AA771710 M13934 BE618296 AA807646 AI951409 BE613262 AA857346 BE294539 BE296371 F31870
 BE254168 BE621136 BE295564 BE612812 N88740 AA352787 AW475090 BE270398 BE618807 AI566936 NM_005617
 AW008274 BE392312 AI928878 AW162655 AI624147 AA854344 AW952982 AW085710 F01238 AA344919 AA641196
 AA720860 AA572870 AW161654 AI001113 AI862725 AI811592 AA320775 AI420790 AI207364 AI951381 BE270095 AI027794
 BE513425 BE252494 AA865409 BE294421 AI719767 AA897029 AI564328 AW628239 AI809839 AW082072 BE255143
 AI189653 AW515889 AA578771 AW162621 N86168 AA935172 BE384561 AW157031 BE295195 AI659958 AW263875
 AA533391 BE513648 AI445700 AI034465 H65716 AW272557 AW302286 BE271816 AW196996 AI953988 AW157372
 AA580376 AI191251 AA572856 AI027798 AA884282 BE268198 R92688 AW731956 AI261239 BE260070 BE253635 AA603422
 BE258354 AI810163 AA130398 AA861165 BE257787 BE408032 H96956 AA593399 BE275262 AA180066 BE395867 AI439795
 AA845816 AW572567 AA999943 AA301818 BE615972 T67509 AA152224 BE393104 AA857300 AA828978 AA812299
 AA834249 AW157807 BE253390 AA883769 BE382656 AA484099 AA759089 AA501594 AA742887 BE391312 AA304434
 AA091576 AW939788 AA989550 AA301655 AA374299 AI000013 AA379938 AA985668 AA293111 AA838481 AA302129
 BE255097 R48458 AA659479 AA311090 AW262218 AA864655 R70415 AA782420 F29372 BE301374 AA345410 AA152252
 AA664047 AA626811 AI092022 AA300592 AI204107 AA936560 AA349088 AI365000 AA311155 AA854688 AA176832
 AW338622 AW246720 AI096811 BE390455 AA181218 BE274363 AA320085 AA854819 AA379935 AA961683 AA706429
 AA301855 AA903668 AI167880 AA912490 AA736633 AA978322 AA306985 AA492120 AW613649 AI026088 AI500692
 AA642146 AA834125 AA970750 AA954809 AI937927 AA605094 AI000445 AW592871 AA642613 AI708961 AA864208
 AA935984 N78708 AW263613 AA379400 F30530 BE382934 AI347719 H44065 AA876331 AA642115 AW439014 AW613635
 AW592031 H02916 AI720155 AA661949 N24052 T72191 AI343917 AW000828 F20434 AI040902 AI189222 AW615066
 AI364998 AI833275 F20713 AA884055 AA603404 F32779 AI927611 AA582556 U91916 H44037 AA641501 AI718241 H44109
 AA971206 AA782740 AA311211 AA947800 N23272 AI590880 AI742000 AW651617 AI040892 AI051117 AA554857 AA782075
 R19307 AW515187 AA622350 AI284864 AI002194 AI339662 AA535783 AA480434 AI951550 W46973 AI936248 AA492016
 AA972511 AA071036 AW170504 AW629056 AA658282 AA843949 AA846986 AI335690 AI985054 AI335679 AI660582 F26201
 AA810379 AA187195 AI274712 AI300958 H99863 AA563821 AI973025 AI186080 AA533122 AI205703 AA166781 AA857765
 F37969 AA578216 F28780 AI972670 AI709163 AI749751 AI087008 AA186713 AA506638 AI298400 H62141 AA524656
 AA532581 AA136078 R48459 AI002336 AA617627 AA130399 AI870668 AI991186 AA293498 AW088368 AI929232 AA143219
 AA629414 AI859102 H73727 AA186706 AI581697 AA747261 AI718130 W73976 F26566 AI816041 AA633944 AA878094
 H61558 AI857355 H45978 F25943 AI879870 F27056 AA244085 AI927367 W69664 W69843 AI298014 N91111 AA229474
 AW969539 N95295 AW023874 AW572321 AA481820 AA580774 AI870680 AI568052 AI831105 AI750091 AI141652 AI833250
 AW001251 AA180067 AI554189 AI719251 AA807645 AI298013 T52779 AW264018 F21944 AI253714 AA342880 AA985284
 T49612 AW263695 AA508894 AA181908 AA533851 N84414 AI277062 T78929 AA534250 AA569444 R11589 AA022468 T60272
 AA582353 AA335709 AI929540 AW613761 BE327851 AA533776 W72345 AI601210 AA366049 AA719887 F22515 AI523442
 T07133 AA230206 AA827438 AA728986 AI718076 AA504069 AA469341 BE546614 AI434088 AW170241 T52780 AA629409
 BE543516 AA484074 W04709 AI582317 BE045496 AA737847 AA535491 AA628352 AA558076 AA864201 AW610533 AI707857
 R94198 AA522868 AA226911 AA857018 AA548787 AA627142 H65717 AW166287 AA564007 BE547258 AA330345 C15020
 AA166754 AW244086 AA844918 F32317 AI424155 AA228718 N89046 N91894 AA894498 AA995502 AA533354 BE222986
 F27737 AI887199 AA506272 AA558503 AA578345 F22227 AA352404 AA805843 N88511 AI628216 AW341732 AA300401
 AA648148 F19238 AI200285 BE041727 F29059 T92628 AW589349 F30549 AA653059 H61217 AA501652 AI919597 AA903957
 F31025 N34998 R96850 AA938689 AI919025 AI310209 AA975769 AW338225 AA342924 F25408 AA130863 AW087264 T72994
 AW873946 AW327429 AI186381 AW327428 AA974301 AW768990 AI690826 AA652111 AA467888 AA187218 AI183905
 AI424323 AA548057 AW051027 AW080306 AI803806 AA642861 F31183 AW406529 AI619660 AA918081 AA491673 F21729
 AI874177 AA715051 F33182 AA652773 AA659091 AW339904 AA662483 AA857275 AW105417 AA548056 AA601164
 AA622675 AA494257 AA036629 T60772 AA653018 AW673531 AI613161 AA668312 AI817429 AW195254 R93615 R69436
 F02292 AA995267 AA247239 AA320193 AA782878 AA994819 AA054936 AW151254 F17418 AA908823 AI890234 AA534130
 AI468869 AW149483 N22520 AA343231 AW001178 AA602740 AI352348 AA932611 AW273549 AI766324 AW118402
 AA888486 AA503847 AW300756 AA585120 AA496674 AA629998 AI619508 AI799389 T25968 AA535332 AA535126 AA467830
 AI915716 AA320648 AA585125 AA658579 AW451040 AI735214 F16590 AA284984 AA643858 AA283217 BE178572 AI921154
 AA344918 AA557543 AA308479 AA872892 AA481963 AA658578 AW004717 AA290824 H61178 AW474724 AA321490
 AA936492
 AI761307 BE161415 AW005281 AA558937 BE161404
 AI291330 AA452220 AA443354
 AA393739 AL138137 AA393798
 AW861185 AW991306 AI623237 AI018451 AA159072 BE294536 N40680 AA248594 AA332177 AA353889 AW136671
 AA063492 AW082601 AI734889 AI479298 AI690289 AA514475 AI827201 AA954932 AI375429 AW305231 AI078116 AI807586
 AI224855 AW025809 AA718988 AI093059 AI912915 AA456139 AI341411 N63437 N95744 AI830516 AA846245 N25902
 AW469026 AI042513 AI241692 AA988159 AW662812 C03567 AA594584 AW082516 BE068964 AW299374 AI636034
 BE172420 AB029022 NM_014914 AW896987 AA765269 BE077785 AA459768 AA436896 AL040331 AA285281 BE244301
 T54938 AA093121 F21778 AA150155 AW968251 AA258877 AW663766 AW470130 AI857358 AI469756 AI299480 AI672560
 AW089174 AW518770 AA081121 AW014387 AI869379 AA985193 AA152265 W94876
 AW499705 AW502537 AW503016
 BE615406 AA323714 BE515303 AA464826 AA453149 AA442802 BE387695 BE394179 BE392472 BE394406 BE393601
 BE394088 BE388690 BE395181
 AW300094 AA805026 AA700077 AI702882 AA327146

323770 230698_1 AA722425 AA329212 AI572177
 302138 228984_1 N83965 AA326737 H14153
 325007 428607_1 AA931484 AA758140 AI033284 AA931461 AA757895 AA877176 AA736429 R11591 AI017256
 302162 24588_1 AF119046 NM_014481 AJ011311 AB021260 BE091822 BE091819 BE280661 BE548576 BE531337 AW605371 BE547006
 BE076387 BE275532 AW386829 AW189348 AA554484 AW028935 AW080283 AW444648 AI538979 AI674393 N59092 C01178
 AI612817 AI347385 AI190577 AI918533 BE265083
 302183 25243_1 NM_002248 U69883 F11363 M62043 AA350009 AI937237 AI363154 AA351095 AA325431 D60120 D61063 D60321 C15510
 AW292489 BE504989 AW594619 AI825516 F09023
 324432 312487_1 AA464510 AA631257 AI740516 AI739132 AW972467 AI741376 AW068935 AI467852 AI752240 AI123717 AI754551 AW205510
 AW044211 AW028889 AW198033 AI538632 AA513096
 323808 247059_1 AW250114 Z43124 AA431421 AI879054 AA351616 AA351035 AL048999
 300982 361671_1 AA837754 AA581115
 323853 238221_1 AA393460 AA338940 AW966277 AA419006
 316664 455916_1 AI042101 AA805541 AA812130 AW977868
 323899 48373_1 AL042966 AW403294 BE294048 BE274337 BE261318 BE544865
 309470 1028089_1 AW118833
 308859 995_8 AI830787 BE563334
 302263 227972_1 AA325517 H19549 R53308
 302270 1734192_1 R56151 W91936
 302292 27735_1 AF067797 AB013456 NM_001169 AI791955 AW843925 AI732659 AA577625 AW083143 AW138645
 301644 867855_1 AW239364 AI792390
 301654 103655_1 H81795 Z42291 R20973 AA046920
 301660 171572_1 F13112 Z42752 T77015 AA211163
 324538 1156268_1 AW502082 AW502979 AW502807 AW501876
 301685 326972_1 W67730 Z44630 AA490699 W67596 W76661 R21207
 324560 1156518_1 AW502208 AW502366 AW502148
 324568 1135567_1 AW502311 AW502370 AW403858
 324575 65704_1 AW502257 AI014241 AA100360 BE298534
 308994 79433_1 BE261877 AI880051 BE242392
 302334 29269_1 AF120491 AF187963 NM_004980 AF205857 AF048713 AL049557
 301703 916575_1 AW301478 AW301560 AI889207
 301714 1534796_1 F06529 R19994
 302399 1570217_1 N79624 H18620
 301744 50221_6 BE277526 AW854299 AA356083 BE257389 F12667 T74316 BE251675
 301752 259807_1 F13486 T75247 AA368304
 301767 8416_1 AK001579 H15317 AW361892 R38240 R02257 R41005 T84341 AW963098 AW516794 AW664706 AI377637 BE463865 H15706
 AI452461 AW089869 AI986480 AA636063 AI123920 AI911424 AI123930 AI963282 AW170740 AA564654 AW136832
 AW468248 AI393655 AI656932 AI358006 AI968742 R38241 AA928629 R77428 AA705932 AA458491 AI755108 AA913331
 AI351287 AW044222 AA301591 R81470 AA344045
 301775 24697_1 AW250572 AW247670 BE067043 BE067049 AL080159 T48255 AI628030 AI401612 AW246476 AA365210 T48256 T81697
 H62983 AA909497 AI864565 AI801862 AI247137 Z25119
 316893 473541_1 AW979189 AA837332 AA856946 AA876935
 316897 474090_1 AA838114 AW629478 AA883713 AI620552
 303021 110136_1 BE277604 BE276408 BE265007 BE410545 BE407265 BE272589 BE263600 BE407970 BE303032 W39612 BE244678
 AA321272 BE244631 AW405664 AW673342 BE244379 BE280236
 303041 31134_1 AK000072 AW840683 AW843764 AW844444 AW844515 AW603469 AW862395 AI860838 AW511708 AF127035 NM_012128
 AK000138
 303042 5058_1 AW505345 AF129532 AF126028 AA852108 BE169359 R83701 Z43904 BE613543 AA283163 AA905463 AW067849 R13544
 R12337 R14020 H98970 AI474918 N56139 AL135669 AW067702 AW372065 AW631389 AA083416 AA287511 AA602923
 AA488914 AI167215 AW946829 R82855 AI948792 AA371333 AW953883 AW956152 C02539 AA298280 AI932587 AA022742
 AI983021 AA195252 N58991 R78733 AW083996 H39614 AI365249 AW615389 AI927744 AI089971 N52205 AA083417
 BE326666 BE349514 AI743785 AI640148 AI378211 AW181881 AI949484 W31374 AW628233 AA418406 AW068010 AI708085
 AI092696 AI089823 AI277828 AA022660 AI440527 AW054937 AW474104 AI017436 AI159819 AI356716 AW473140 AW316518
 N34522 AI675092 AI866697 AA864593 AW511185 AA488844 AA904975 N49111 Z39951 R37265 AI141362 T25856 R20664
 F03163 AI767927 AA805942 D79905 AI914645 AW190553 AI934213 AI458796 AA195385 R82854 W31965
 302445 16351_2 W37653 AW881001 AW840585 AW840696 N79647 AV648691 H25494 AW885394 AW001940 AI362793 N63970 H25448
 AI963184 AA324156 W37514
 302459 31751_1 AF169255 NM_006028 AF080582
 302488 32135_1 AC005551 AF161441 AA431001 AA336054 AW965560 AW376266 AA758808 AW024675 AA946948 AA306783 AA910368
 AA335971
 301855 33235_2 W25940 AF053356 AF053356
 301859 1799608_1 T61587 T61035
 324783 389615_1 AA640770 AI683112 AA913009
 316979 483302_1 AA861087 AI200951 AI026779
 303100 44550_1 T09353 U72943 U64597 R52598 R61404 R20022 R18898 U67037
 303106 85273_1 AA012877 AA021074
 303144 40757_1 AF202889 AF202890
 302514 2628_10 X58801 X58802 X58803 X58804 AI312844 AA283290 X51791 X86140 X51795 X86110 X86106 X86105 X86104 X86141
 AJ296352 AF020642
 303179 112488_1 AA071215 AA071444
 302535 1589284_1 H48676 W04984
 302569 17513_2 AC004472 BE312721 BE273942 F11928 T65358 BE612432 BE261576 BE179884
 318230 193526_1 AW407564 AA262049 W19405 AA504733 T12641 AW973724 AA558125 AW993087 T12640 T11447 AA521285 AI820042
 AA457028 AI674737 AI688648 N92749 AI439620 AI218005 AA731321 AA828303 T12590 AI685371 AA504636 AA825573
 AW172614 AA291292 AA649919 AW576505 AA262152 H29888 AA830757 AA910433 AA808481 AI971807 AI767874 AI216422
 AA831483 AI566351 H41305 AA879438 AA807123

324829 7288_14 AI537407 AW131277 AA714311 AW816039
 311004 344894_1 AW191647 AW973241 AA632846 AA533681 T51580
 309825 331299_2 AW293701 BE348286
 303215 130271_1 BE281058 BE276139 AW250314 BE336754 AA112498 BE265334 AW732954
 303265 155956_1 AA171403 AW160951
 303294 72494_1 AA205300 BE612585 AI393918
 302646 2628_31 X58808 AF071471
 324945 47710_1 AL360202 AA088768 R61018 T36114 AW966404 M85891 AW296810 AA421905 H29985 AI810129 AI798786 AI338041 H29886
 AA088702 R60901 AI648560 AA411400
 309912 14912_1 H19255 AA324634 BE398078 AW749970 AA309733 AA769449 BE501906 AI686211 AI280426 AI401680 AW235634 AI954773
 AI762656 AW082924 AI223790 AF160973 AI127758 AW009952 AI440473 AW136694 AW008937 AI492112 AW294956 H12044
 AA609256 AI400622 AA778657 AI342773 BE501767 BE048879 AI187333 AW025304 AI191550 AA383780 BE350769
 AW024606 AI244835 AA228447 AA983651 AA027332 AI167499 AA913695 AI479796 AA960843 AW272340 C02052 AI433299
 AB032994 AL136549 AI126781 AI339656 AA324178 AW274942 AW404411 AA351287 AW503975 AA978021 H19254
 AA826207 AA365760 AA887252 W35146 AW299327 AW593902 AA932287 AI940307 AW955721 M62008 AA034345 BE048271
 AA365723 AA682987 AA324179 T08342 BE396592 BE269097 BE242683 AA351288 AA317743 AA323517 AW950991
 BE169813 AW500399 AL119581 AW401530 AW501601 AW501500 AA663641 AW892664 AW501520 AW501448 AW501591
 AW500843 AW499580 BE396829 AA143673 AI834230 AW500792 AI909739 AW845214 BE140556 AW845213 AW500505
 AW500506 AW845216 AW574989 AI834238 AI929491 AW576513 BE245479 BE241953 AW505039 AI263367 H12043
 AA033638 AW339671 AW963748
 309963 22431_1 AW449073 NM_016507 AF227198 BE062563 AW893244 AI695667 AW370607 AW370608 AW505230 AL121377 T19010
 AA397553 AI138391 T86408 R78328 AA829647 AI797062 AW502286 AI703352 AI298289 AA730053 AA047200 AW083099
 AW370617 AI128124 AI264202 AI350744
 319000 1534458_1 Z44318 F06149 R20136 R14907
 319003 174731_1 R18085 AA219028 R17712 Z44345
 319027 6267_1 AK002182 AW842140 BE391303 AW807017 AW604195 AW604194 AK000527 AA716612 AW291848 C17004 D78698
 AA633316 AW085548 AW954620 AA351081 AW377003 AA594606 AA290880 R35913 Z44526 T74413 H39831 H03611 H70235
 AA410732 AA404618 AA026902 N87562 R49433 AI346545 H03501 AW189821 AA235590 AI188349 AW262971 AA283775
 AI431671 AA026903 AI246417 AI636152 AI370910 T74039 AI128930 BE208355 Z40426 AA291429 R01208 AI824714
 AW075793 AA576559
 302722 44456_1 U53530 L23958 AA775976 BE003131 AI903793
 303388 969232_1 AL039604 AL039497
 319055 167464_1 Z44855 AA196906 AA196723 BE278458 AA412305
 302776 23857_1 AJ133798 NM_014427 AJ133799 R19516 AA071126 AI278055 AA071125 AI915130 AI582322 AW070237 Z39757
 319091 1237615_1 BE392792 H55196 Z45264
 319098 922966_1 AI908374 Z45366 R11479 H79927
 317894 226420_1 AA323682 Z44357 F11306 R49705 R60252 T09440 T09172 H09876 F06094 R60848 H06625 T07793
 303405 215022_1 AA308601 AW411014
 303407 6848_4 AB040958 AA309616 AA322942 AA331675 BE257729 AW806959 AW860144 AW806968 AW512751 AI239617 R68424 R72046
 H85465 N28472 AI971920 AI459052 AI082821 H49714 AI218903 AA244036
 318504 1703724_1 T26453 Z44226 R20425
 318563 7543_1 AB037724 BE260227 R21318 BE538345 AW250501 AW403023 R46363 Z43008 R14654 AW953148 AW953149 T33110
 R20231 H30838 F05454 Z45790 AW965595 T08819 H06568 H29913 R16617 AW006449 AA588448 AI909629 R10832
 AW245067 AI479004 H29825 AI097108 AI829928 AI636607 AI079390 AA353858 AI374890 BE247041 R43324 R10833
 AA603730 AI298051 AI580953 AA400088 R16559 AI369715 AA401378 AW976688 BE245314 AW249837 AI869249 AA349796
 AA783040 AW474996 AI028378 R45633 AI864452 AA470470 AA629126 AI262201 H06513
 304161 34056_2 H71886
 311395 252948_1 R23313 R23323 Z25059 AA359123 AW965886 BE167187 AI808503
 303521 244029_2 AA746272 AA504079 AA347316 BE084755
 303535 972533_1 AL043430 N79419
 319207 1071625_1 R87679 H16883 F07785 AW245503
 302919 34022_1 AL137382 AA305545
 303592 29065_6 BE145971 BE146046 BE146316 BE146148 AA421129 AA382152 AW836960 AW836945 AW836851
 303596 270128_1 AW303377 AW270092 AA382636
 319264 247031_1 T65096 F12013 AA351004 F11787 T66093
 302972 47307_1 AF086321 W73400 W73375
 304211 21366_-11 N62228
 304241 84545_1 AA010976 AW611600
 303642 284260_1 AW299459 AA417112
 303650 290929_1 AA430709 AA427866
 319359 1541128_1 F13458 R17813 T74431
 319373 226757_2 R00371 R09720 R09711 AW873586 AI703426 AW016769 R36969 R00259 AI216256 R09712
 318728 323486_1 Z30201 AA486132 T72025
 312129 338029_1 T87431 AW300867 T87330 AA515973 AI242970
 312162 423491_1 AI660245 AI950027 AA971142 AI302981 AW771990 AA723809 AW195235
 303745 54759_3 AI142379 AA905379
 319403 1688716_1 T86043 R01431 T75579 T75580 T83765 T98413
 303778 174437_1 AW505368 AA218610 F11852 T65345 AA397806
 303782 2213_1 AA325129 AV655735 AW408703 AW505411 T64737
 319468 1691029_1 R06504 T99600 T95769
 318813 1540877_1 F13195 Z42617 T75318
 320042 551394_1 AI017510 T91374
 320083 1764305_1 T87761 R95025 W87407
 312217 382018_1 AA627706 F28433 D63189
 312251 193841_1 AA323400 AW968650 AA262398 H03952 AA824430
 312281 1563872_1 H46445 H22490 H19702 H46328

305064 11422_-7 AA636012
 303835 1305867_1 T05645 T32180 AW961890 T08680
 303849 43707_1 AA249439 BE256642 AW163324 AF012357 AL359617 H95481 AI217156 AI332310 AI016751 H94962 AW105657 AW082779
 AA815334 AA954302 AA628321 Z42118 AA737794 F08727 F06339 F07626 AI829971 T89928 AW970824 AW157525 AI979018
 AI537885 AI636077 AW439894 AI687692 AI476254 AI870810 AI860351 AI248264 Z40675 F05012 F02632 AA564443
 AW298565 BE091953 BE091884 F01656 BE091886 BE091841 BE091851 BE241581 AA403051
 320115 582314_-1 T93574
 320121 452027_1 AA780365 AA909233 AI275542
 318946 92484_1 AI122843 Z43800 R19718 R59259 N74752 W20097 N46928 AA215691 AW672684 AW672673 AL044945 H93163 H92772
 AW451096 AW675432 AW675425 AA844417 AW674797 AA855104 AA291320 AA770259 AI749837 AA034362 AW370463
 AI825998 AA027067 AA744373 AA732336 AW674014 AA291321 AA029285 AA766450 R59201 AA588329 AI168449 AA215692
 AI079651 Z39868 R05650 F03066 AA357760 AW955291 AI992075 AW020148 N90519
 312339 151127_1 AA524394 AW015969 AA158731 AI831401 AI955800 AW272596 AW272595 AI281799 R34231 R35558 AW378527
 304576 25108_1 AA329384 S49006 AW405735 AW404287 AW405848 AW405979 BE538908 H70947 AI814190 AA381896 AW582731
 AW975580 T94914 AW474500 AW869616 AW974125 AW946246 H44560 AW802184 AI538108 AW609912 AW865715
 BE007659 AA443571 AW376161 AW797783 AA713566 AW577973 AA745472 AW270172 AA910107 AA713717 AW364122
 AA533898 AI523353 AA715899 H44507 AW947263 AW390753 T89943 R66359 H44320 T64100 AA715879 R54661 AW579645
 H68597 AI499528 AI699010 AW605041 AW605043 AA236700 AI290767 H27472 AW079688 T69967 T87728 AW869468
 AW873389 AI250670 AA617786 AI566627 AW627605 AW302334 AA617836 AW793186 H16015 R83107 T85409 AA643479
 AA582449 AW794654 AI819995 AW865810 AW380149 AW793863 AI281629 T64021 AA501599 R49882 AA565066 R69406
 N23918 T59642 R54662 AW973199 R53006 AA401087 AA496563 AW934874 BE171294 AW793133 AI581595 AW605835
 AW605040 AW605055 AW605033 AW605058 AA291844 AW382472 AW605005 AA421881 AA513106 AA744190 AW386065
 AW613785 AW605829 AA580905 AW605027 AW364134 AA464027 BE012096 BE008565 AA809035 AA809154 AA911395
 AA713636 AA745324 AA826230 AW368498 AV646747 T89967 H61164 AI540661 AA721571 C02031 AA523762 AA523746
 AI287256 AW841164 AA962139 AW797014 AA515246 AW364140 H45842 T94267 T72111 R49771 T70151 H42664 R83656
 R83590 AW380297 AW380263 X95750 T57717 AW391436 AA293355 AW380185 X95749 X95748 X95747 AW796510
 AA318628 AI001043 AA744404 AA745567 AA650437 AA715526 AW392762 AA516228
 303958 10830_7 AL042931 T70163
 319668 17848_1 NM_002731 M34181 AA091596 AA090564 AW498491 AA383248 AA018979 AA352938 AL133918 T28731 AA984398 AL134676
 AW898293 M77877 AI124701 BE567802 AI288466 AA719614 BE622570
 320236 321288_1 AA528811 AA482942
 320258 217516_3 BE396475 AW814056 AA311866 H05207 R94015 AA504370 AW962851 T70351
 319793 1698018_1 R56360 R20336 R67291 R14290
 320360 259694_1 H12405 H12404 AA368159
 319886 22717_1 AK000906 AA603325 AI123244 AI742610 AI742621 AW451297 AI963292 N94395 AI122654 AI869312 AA693938 AI913241
 R69552 AI925715 AI243319 AI085752 AI094469 AI922008 AI521658 AI288451 AA627433 BE327863 AI417213 AA937953
 AW301143 AI827213 AW444808 AI056464 AA736786 AA968590 AI425075 AI420510 AI445367 AI866676 H25733 AI356146
 AI803734 AI194056 AI872656 AI222629 Z38818 H25937 AI547263 AI656165 AW590474 T73549 BE392068 H14735 H27088
 H45935 AA359427 AW167511
 306023 38159_2 BE463655 AA897764
 313257 452953_1 N92638 AA781521 AA846225
 305406 34836_-76 AA723860
 304831 13890_7 AA314337 AI805587 AA402097 AA293631 AA658356 BE566333 AI557276 AV651311 NM_001011 Z25749 AI525506 R97869
 BE546683 AA155861 AA532947 AA329269 H63470 AA187471 AV660956 AV650019 AA380909 AW327895 BE313243 N93984
 AA354585 W19057 AA428966 T55686 AW958123 AA315872 AA081305 AA083776 AW961442 AA352331 H00860 AA206205
 W21515 AA149180 H13044 AA372080 AV658875 AV658874 AA337727 BE276865 AA247683 AA209449 AA393619 AA147378
 AW404839 W19374 AW247081 AA311228 BE615971 AA308572 W01826 AA310230 AA412606 AA420575 AA362646 H70797
 AA525988 AA311440 BE564044 AW967302 AA302565 AA313021 AA312653 D52864 AA312582 AV654672 AA308096
 AA308509 AA308491 AA305867 AA306813 W75940 AV653876 AA365315 AW408185 AA308217 AA122395 AA314083
 AA315981 AA311782 AA310647 W46668 N31114 AA180871 AA187276 N72805 AA312418 AA304985 AA167580 AA307881
 AA310961 AW674912 AA310126 H82669 AA132497 AA809088 AA155963 AA640361 BE618580 AA229152 AW404970
 AA306621 AA308276 N98583 AV660766 AA654587 AA206190 AA312305 AA580740 AI568153 AI718253 AI860477 AI872388
 AA873460 AA405147 AA315435 AI129479 AI888709 AW583033 AW089596 AW264185 AI653503 AA858344 BE619226
 AA187721 AA306691 AW439857 BE616042 AI889905 AI862869 AA309960 AA307823 AI148769 BE619772 AA582168 AI963414
 AW168760 AW167856 BE619400 BE378974 BE619933 AW958117 W49703 AI951380 AA306263 AA583192 AA356605
 AA897095 AA149141 T53975 AI744255 AA845352 BE312890 AW961435 AW583101 W24684 BE619333 T96513 AI491903
 BE272256 AA315556 BE539380 BE619999 AW084687 BE465646 BE262138 AA999923 BE260616 BE276306 D55310 AI186578
 AI707735 AW404371 BE274614 AW512395 AA650425 AI439470 AA513739 AW404673 AW404664 M77233 AI970731 AI880754
 AI418821 AW273410 AA069936 AW058084 AA719351 AW404422 AW405314 AI523106 AA393107 BE408961 BE252375
 AA578681 BE513748 AI749494 N36979 N43025 D11774 AW391958 R34130 BE394953 AI865715 AI018059 N46292 AA908866
 AA907443 AW081633 AA622318 AW438511 BE262297 AA565643 AI018057 AI440067 AI719291 AA135054 BE222834
 AW262240 AA081120 AA442581 N86460 AA583569 AI061357 W72482 AA148278 AI186761 AA512934 AW615804 AA595332
 AI831069 AA778136 AA657641 AI433175 AA398698 AI735084 BE183158 AI566940 AW304785 AI401846 AA506149 AA102508
 AA736531 AI027939 AW000716 AA861339 AI027937 AA575877 AA639090 AW129111 AI421179 AA506553 AA936780
 AA972869 AA563975 AA582448 AI802748 AI471162 AA586422 N86248 AA528142 AA551225 AI566307 AI206730 AA513485
 AA363629 AA436824 AW575828 AA180774 AI001103 AA932070 AA613667 AI337566 AA582127 AW327319 AA610833
 AI333738 AI708124 AI349480 AI240444 AI225152 AA570790 AI539813 W80674 AI333517 AA181299 AA315527 AI719857
 BE087137 AW474616 AI510739 AA614724 AW337476 AW951820 AA149181 AA149142 AA523097 AA428873 AI708760
 AI978984 AA946913 AA844685 AI440225 AA306527 BE349026 AI659593 AA845752 AW327366 AA311945 AA595594 AI027199
 AI499554 AI262336 AA398535 AI333388 AW575598 AI472745 AI476623 AI150520 AW897766 AI864033 AW584030 AA148411
 BE348977 AA420550 AW768575 T27844 AI349314 AI371037 AI675707 AW102842 AI203978 AI719821 AW768495 AW021575
 AI686981 R36541 AI346551 AW888705 R25390 AA209335 AI342426 AA056446 AA582981 AA890201 AW026850 AA857587
 N91141 AW768541 T55235 AA401942 AA080860 AI291273 AI312669 AA412271 AA890649 AA846264 BE019907 BE090895
 T56904 H70798 AI500573 AW327642 F17734 AA157192 AA152417 AW327670 AA985481 H71524 AW439687 AA968516
 AW327857 AA405330 AI342315 H01239 AA878156 AA148279 H71525 N52399 AI991878 AA878100 N93956 H56020 AA132515
 W49704 H63414 AI717990 AI814318 AA912383 AA922317 R97819 AI860255 AI335093 AI187843 AW270357 AA187646

AI190237 AI991126 W07024 BE539453 AI819841 H75424 AA102446 AW026974 AI923973 AW001389 AA337759 N70772
 AW022155 AA336624 AI219252 N89590 AA664546 AW339690 AA651993 AA608735 H65064 AA857788 T81916 AA860215
 AI031685 AA133689 AA186954 R16825 N27213 AA857155 N69981 AA318664 AI735334 H82411 AI460293 AA205819
 AW803086 AI922965 N33363 AA580622 AA664756 AA651961 AI201624 AI066494 AA834187 AA187722 AA652066 W80675
 AW051553 AW263699 R34131 AA340971 AA364263 AI824574 AI356913 AI439263 AA205822 AI540881 AA640625 AI206794
 AI198883 AA167581 AA970474 AA299068 AA157088 N90120 AI371330 AA090914 AI889887 AI274617 AA730747 AI745000
 AW265227 AI358313 AA122396 AA501489 AA918963 AA953637 AI434343 AI707767 AA603889 W04799 T55604 AA614231
 AA071264 AA083777 AI880809 AI185259 AA747112 AA908459 AA134970 AI192649 BE046107 AI358698 AA310968 AW517574
 AA984892 W46578 AW105597 AA224970 AA747937 T96514 AI472689 AA283670 AI186789 F35482 AW873463 AW361039
 AA583072 AI872660 AA040277 AA224895 N85343 AA484723 AA937597 AI304419 AA228409 AA501488 AA664896 AA664966
 AA482963 AA736806 AA528814 AA927560 AA328094 N83225 AA582536 AA938377 AA916871 AA507716 AA101182 AI720885
 AA876858 AA483322 AA362647 N75592 N23917 AI193949 N74054 AI352629 D51754 AI570783 AA470923 AW975162
 AA328256 AA659768 AI919411 W40458 F00799 AA147346 AA728856 AA528675 AI676101 AA523785 T52866 AA533842
 AW516442 AA554875 AA886066 AW518472 AA971169 AA908345 AI561318 AA482746 AA482735 AA482882 AA188350
 AA629989 AA482917 AW263351 T52867 D52318 AI696386 AA689276 AI719128 AI719124 AA541702 X85626 AA640165
 AA228408 AI832575 AI143550 AI281727 N73099 AA733095 AI749387 X85625 AA640766 AA652170 AA652139 AW606146
 AA649563 T25406 AA327330 AA080984 X74803 AA746016 AW957997 AI005578 BE547070 AA886825 AA927742 AI927866
 AA528573 AA665260 AW270340 AI698507 AA501524 AA483113 AA506345 N91789 AI933429 AW904843 BE092709 BE093487
 BE093472 BE092712 F22641 N80062 AW455220 BE079292
 AW408392 AW847299 AW847302 T86065 T85884 T77135
 W23285 H42714 F25381 F37215
 AA081495 R87345 H43858 BE266428 BE263090
 NM_005897 AF156857 AA346876 BE545147 AI003306 N45644 AW889728 BE007236
 NM_003658 AF031924 AJ243512 AI792204 AI675861 AI915798 AI733498 AI823489 AI370544 AI696665 AA991537
 AA774834 AK001079 BE293936 AW372365 BE271898 F00113 AA424108 AI950409 W70049 N56481 BE048416 W70050
 AI619669 AL040446 AA996189 AA962427 W37166 AA179135 Z21574 N64837 BE562818
 BE259406 BE379716 AA147786 BE300171 BE267161 BE515287 AU076914 AW374229 AA069647 BE561555 D53431 D54395
 AA191250 D52650 BE208576 BE566731 BE387383 AA373416 R23516 T68691 T69334 AA355791 R02636 BE566591
 BE407444 AI982546 H49682 AA094446 BE515225 D54740 AA095798 AA196716 AA353034 AW955137 D53869 AA100150
 AA188091 AI524940 D54982 AA090373 D53479 AA247363 BE567604 BE391813 N41527 BE410575 AA380139 BE616028
 AW881909 AW963736 BE276064 BE380156 BE566181 BE567132 BE561903 AI205098 X52851 AW881897 BE616573
 BE298397 AA127519 R88890 BE616648 BE279162 BE559666 BE514563 BE312454 BE407312 BE276098 BE394047
 BE267326 BE276908 BE565569 BE385054 BE265740 BE409229 H44489 AA207193 AI525570 BE304612 BE396965 BE386123
 BE264758 BE266121 AA215851 BE295137 BE512683 BE388849 AA223494 BE263350 BE408879 BE386132 BE382906
 BE271789 BE539264 BE378507 BE567995 BE208471 Y00052 BE256484 BE260931 AL021395 BE260620 BE512892 AI906447
 BE615419 BE560786 BE279517 H46528 BE258084 BE535992 BE274774 BE274916 BE260585 BE563269 BE249941
 BE264782 BE408521 BE312750 BE559964 AA147099 T70141 AV661600 AA581711 AA186462 T69259 AA521058 AA563932
 BE397758 T68848 BE514531 H50191 AA641322 AI869370 AA653502 T70072 AW139957 AA069924 AI953984 C06029
 AA190399 AA617735 AA085181 AA506423 AI470746 C05982 BE077432 AW945661 BE272794 AA011065 AA922406 BE183113
 AA564289 AA374410 AI264729 AW957628 T68610 AA143328 AW381780 AW381880 AA135191 AA857453 AA112231
 AA011066 F36776 AW798236 H00395 BE272608 AW798123 AA532416 AI936732 BE183271 AA129828 AA741102 BE164382
 AW799104 AW997926 AA211136 AW601437 AW602618 H11277 AA083462 AA056516 AW364819 R01694 AA086193
 BE171120 BE093136 AW796864 AA663009 AW605266 AA247458 AW796905 BE171125 AW392363 BE171106 BE171110
 AW796810 AW796854 AW578648 AI221714 AW151499 AW937186 BE293542 BE249842 AW363879 AI701218 AW084288
 AA489447 AW798124 AW798256 AA658272 U46266
 AA329384 S49006 AW405735 AW404287 AW405848 AW405979 BE538908 H70947 AI814190 AA381896 AW582731
 AW975580 T94914 AW474500 AW869616 AW974125 AW946246 H44560 AW802184 AI538108 AW609912 AW865715
 BE007659 AA443571 AW376161 AW797783 AA713566 AW577973 AA745472 AW270172 AA910107 AA713717 AW364122
 AA533898 AI523353 AA715899 H44507 AW947263 AW390753 T89943 R66359 H44320 T64100 AA715879 R54661 AW579645
 H68597 AI499528 AI699010 AW605041 AW605043 AA236700 AI290767 H27472 AW079688 T69967 T87728 AW869468
 AW873389 AI250670 AA617786 AI566627 AW627605 AW302334 AA617836 AW793186 H16015 R83107 T85409 AA643479
 AA582449 AW794654 AI819995 AW865810 AW380149 AW793863 AI281629 T64021 AA501599 R49882 AA565066 R69406
 N23918 T59642 R54662 AW973199 R53006 AA401087 AA496563 AW934874 BE171294 AW793133 AI581595 AW605835
 AW605040 AW605055 AW605033 AW605058 AA291844 AW382472 AW605005 AA421881 AA513106 AA744190 AW386065
 AW613785 AW605829 AA580905 AW605027 AW364134 AA464027 BE012096 BE008565 AA809035 AA809154 AA911395
 AA713636 AA745324 AA826230 AW368498 AV646747 T89967 H61164 AI540661 AA721571 C02031 AA523762 AA523746
 AI287256 AW841164 AA962139 AW797014 AA515246 AW364140 H45842 T94267 T72111 R49771 T70151 H42664 R83656
 R83590 AW380297 AW380263 X95750 T57717 AW391436 AA293355 AW380185 X95749 X95748 X95747 AW796510
 AA318628 AI001043 AA744404 AA745567 AA650437 AA715526 AW392762 AA516228
 AA431366 AA490423 H96381 AA361614 H56121 AA354669
 X58799 AF071472
 BE245833 BE539992 AI380940 AW952644 AA535470 R84610
 AA010267 AA720674 AA010209
 AA837782 AA828713 H84206 AW979069
 BE260893 AA078319 R85057 AW803024 H85811 AA078293
 AB033072 AW163387 AW161566 T08007 AW161909 AW157331
 AB033100 AA347036 BE260325 AW961669 AL047207 AA347037 AI766894 AA601045 AI559897 AW139033 AW274622
 AW172884 AW089070 AA804340 AW798925
 AA078493
 AW972301 AW474412 AJ227863 AA516297 AA641949 AW995029
 AW003360 AI971548 AA017585 X80306 X91133 AJ276100 X91132 AF064499 AF064495 AF063768 X83713 AW951310
 AW975565 AA721610 AA715972
 H54398 AA700844 AW895023 BE549308 AW834812 AA299525 AW957027 AA001789 BE219218 R73244
 AL137357 AW173064 AW662837 AI222955 AI138884 AW438842 AA883686 AA978208 AA653137 AA906477 AI150554
 BE295082 BE243550
 319900 1138215_1
 321121 1545647_1
 321132 117535_1
 320503 25164_1
 320586 26170_1
 305557 41560_1
 304978 28800_7
 304983 25108_1
 321223 249691_1
 321240 2628_30
 321286 236538_2
 313476 83849_1
 312854 467476_1
 321304 115882_1
 321321 32811_1
 321325 28266_1
 321354 116028_2
 321359 41877_1
 320727 36759_63
 320767 18895_2
 322012 22619_2
 306406 AA971973

306426 AA975039
306443 AA976950
306511 AA988891
320965 266751_1 H18166 R86173 H19851
306531 AA991423
306546 AA993109
306549 AA993796
306558 AA994743
306590 AI000246
306591 AI000248
329464 c_y_hs
336695 CH22_4181FG_48_4_
329496 c10_p2
336705 CH22_4209FG_63_2_
336717 CH22_4234FG_81_1_
306668 AI004890
306739 AI028393
306791 AI042387
329665 c14_p2
336883 CH22_4625FG_322_2_
336898 CH22_4647FG_330_1_
308016 AI445116
308082 AI473682
338177 CH22_6725FG_LINK_EM:AC00
308092 AI474896
308097 AI475411
306801 AI052653
306809 AI057134
336908 CH22_4670FG_343_2_
336917 CH22_4688FG_346_4_
306839 AI077385
306866 AI086683
306881 AI088695
308115 AI479071
308127 AI492187
308138 AI494446
306919 AI096832
306930 AI124518
329824 c14_p2
329839 c14_p2
306975 AI127042
308258 AI565612
308282 AI569456
308311 AI581855
308382 AI624301
308385 AI625428
308406 AI634885
308449 AI660854
308465 AI672480
308517 AI689279
308539 AI694191
308544 AI695133
308548 AI695484
338648 CH22_7413FG_LINK_EM:AC00
308572 AI707882
338668 CH22_7441FG_LINK_EM:AC00
308582 AI709056
338679 CH22_7453FG_LINK_EM:AC00
308598 AI719237
338686 CH22_7461FG_LINK_EM:AC00
308601 AI719930
338703 CH22_7483FG_LINK_EM:AC00
338705 CH22_7485FG_LINK_EM:AC00
338725 CH22_7521FG_LINK_EM:AC00
338747 CH22_7561FG_LINK_EM:AC00
308676 AI761036
338770 CH22_7593FG_LINK_EM:AC00
308695 AI763350
308707 AI769997
308718 AI798009
308851 AI829820
308954 AI868958
308961 AI870248
333043 CH22_269FG_70_4_LINK_EM:A
333054 CH22_280FG_73_8_LINK_EM:A
308991 AI879831

303582 647662_1 AA377444 AJ458965
305018 AA627127
305030 AA629988
305046 AA632201
335131 CH22_2463FG_497_15_LINK_E
335157 CH22_2493FG_501_7_LINK_EM
305071 AA640579
335163 CH22_2499FG_502_7_LINK_EM
305080 AA641485
335174 CH22_2510FG_504_4_LINK_EM
305093 AA642917
305116 AA649244
335200 CH22_2538FG_508_9_LINK_EM
335201 CH22_2539FG_508_10_LINK_E
335217 CH22_2556FG_512_3_LINK_EM
305134 AA653159
305145 AA653589
328015 c_6_hs
328016 c_6_hs
335234 CH22_2573FG_515_3_LINK_EM
335236 CH22_2577FG_515_8_LINK_EM
328025 c_6_hs
335247 CH22_2589FG_516_8_LINK_EM
305167 AA663080
305168 AA663105
328031 c_6_hs
335262 CH22_2604FG_520_3_LINK_EM
335265 CH22_2607FG_521_1_LINK_EM
335266 CH22_2608FG_521_2_LINK_EM
328053 c_6_hs
305197 AA666301
335281 CH22_2623FG_524_4_LINK_EM
335284 CH22_2626FG_526_6_LINK_EM
328098 c_6_hs
303929 AW470753
303933 AW471472
326806 c20_hs
326808 c20_hs
326857 c20_hs
326874 c20_hs
326876 c20_hs
326884 c20_hs
335311 CH22_2654FG_532_4_LINK_EM
305234 AA670431
335320 CH22_2664FG_534_7_LINK_EM
328109 c_6_hs
335331 CH22_2675FG_535_4_LINK_EM
335339 CH22_2686FG_535_16_LINK_E
305259 AA679225
335340 CH22_2687FG_535_17_LINK_E
335344 CH22_2691FG_536_3_LINK_EM
335348 CH22_2695FG_537_4_LINK_EM
335349 CH22_2696FG_539_2_LINK_EM
305264 AA679505
328134 c_6_hs
335371 CH22_2720FG_543_9_LINK_EM
335377 CH22_2726FG_543_17_LINK_E
328171 c_6_hs
326942 c21_hs
326943 c21_hs
326957 c21_hs
326981 c21_hs
326997 c21_hs
305335 AA704235
335421 CH22_2772FG_551_1_LINK_EM
328221 c_6_hs
328224 c_6_hs
328228 c_6_hs
335448 CH22_2799FG_562_5_LINK_EM
305361 AA708902
335451 CH22_2802FG_562_9_LINK_EM
328236 c_6_hs
335455 CH22_2806FG_562_15_LINK_E
328243 c_6_hs
335468 CH22_2819FG_567_4_LINK_EM
335470 CH22_2821FG_568_3_LINK_EM

335482 CH22_2834FG_570_11_LINK_E
335485 CH22_2837FG_570_17_LINK_E
328271 c_6_hs
328276 c_7_hs
328277 c_7_hs
328282 c_7_hs
305403 AA723748
335517 CH22_2872FG_571_34_LINK_E
328305 c_7_hs
335523 CH22_2878FG_572_3_LINK_EM
335527 CH22_2882FG_572_7_LINK_EM
305443 AA736653
328314 c_7_hs
335536 CH22_2891FG_574_2_LINK_EM
305454 AA738413
328328 c_7_hs
305464 AA742425
335565 CH22_2921FG_579_1_LINK_EM
335566 CH22_2922FG_580_1_LINK_EM
305486 AA748889
335585 CH22_2943FG_581_24_LINK_E
335587 CH22_2945FG_581_26_LINK_E
335593 CH22_2951FG_581_32_LINK_E
335606 CH22_2964FG_582_3_LINK_EM
305536 AA770682
305547 AA773111
335634 CH22_2994FG_584_14_LINK_E
328420 c_7_hs
328428 c_7_hs
335651 CH22_3011FG_590_2_LINK_EM
335652 CH22_3012FG_590_3_LINK_EM
328436 c_7_hs
328444 c_7_hs
335667 CH22_3027FG_590_18_LINK_E
328462 c_7_hs
328467 c_7_hs
335687 CH22_3048FG_596_2_LINK_EM
335690 CH22_3051FG_596_5_LINK_EM
328474 c_7_hs
335692 CH22_3053FG_596_7_LINK_EM
335693 CH22_3054FG_596_8_LINK_EM
328484 c_7_hs
335700 CH22_3061FG_598_1_LINK_EM
305621 AA789095
305632 AA805276
335720 CH22_3081FG_599_23_LINK_E
335721 CH22_3082FG_599_24_LINK_E
328504 c_7_hs
328506 c_7_hs
328507 c_7_hs
335733 CH22_3095FG_601_3_LINK_EM
335739 CH22_3102FG_601_10_LINK_E
335745 CH22_3108FG_601_16_LINK_E
335747 CH22_3111FG_601_20_LINK_E
335750 CH22_3115FG_602_4_LINK_EM
335755 CH22_3122FG_604_4_LINK_EM
328544 c_7_hs
335768 CH22_3137FG_607_2_LINK_EM
305686 AA812726
328552 c_7_hs
335774 CH22_3143FG_607_10_LINK_E
328557 c_7_hs
328558 c_7_hs
335777 CH22_3146FG_607_13_LINK_E
305697 AA814956
335782 CH22_3151FG_609_4_LINK_EM
335783 CH22_3152FG_610_3_LINK_EM
328569 c_7_hs
335787 CH22_3156FG_611_3_LINK_EM
328570 c_7_hs
328581 c_7_hs
328582 c_7_hs
328592 c_7_hs
337011 CH22_4876FG_427_6_
337023 CH22_4894FG_433_12_
337032 CH22_4910FG_438_3_

337069 CH22_4967FG_448_2_
337092 CH22_5016FG_465_12_
337093 CH22_5017FG_465_18_
337094 CH22_5018FG_465_19_
337097 CH22_5028FG_471_1_
305700 AA815428
335806 CH22_3178FG_616_8_LINK_EM
335817 CH22_3189FG_618_5_LINK_EM
328607 c_7_hs
335827 CH22_3200FG_620_1_LINK_EM
335831 CH22_3204FG_620_5_LINK_EM
335832 CH22_3205FG_620_6_LINK_EM
328620 c_7_hs
328624 c_7_hs
328636 c_7_hs
335863 CH22_3238FG_629_8_LINK_EM
305782 AA844730
305787 AA845035
328662 c_7_hs
335895 CH22_3272FG_635_3_LINK_EM
337100 CH22_5031FG_472_3_
337114 CH22_5060FG_494_17_
337121 CH22_5096FG_519_1_
337132 CH22_5112FG_526_3_
337168 CH22_5188FG_562_28_
307085 AI160868
337170 CH22_5190FG_564_1_
337172 CH22_5192FG_565_2_
307090 AI161024
305803 AA846052
305808 AA853958
305816 AA854776
335902 CH22_3279FG_635_10_LINK_E
335920 CH22_3297FG_636_16_LINK_E
305841 AA860348
305867 AA864572
335956 CH22_3334FG_647_3_LINK_DJ
305877 AA865649
335968 CH22_3347FG_652_1_LINK_DJ
335971 CH22_3350FG_652_4_LINK_DJ
335975 CH22_3354FG_652_9_LINK_DJ
335980 CH22_3360FG_653_2_LINK_DJ
328768 c_7_hs
328770 c_7_hs
335993 CH22_3373FG_656_6_LINK_DJ
335998 CH22_3379FG_656_16_LINK_D
335999 CH22_3380FG_657_1_LINK_DJ
328791 c_7_hs
337203 CH22_5256FG_591_3_
337204 CH22_5261FG_595_1_
307120 AI184343
307140 AI185762
307177 AI188864
305903 AA873085
305925 AA877883
328803 c_7_hs
330002 c16_p2
328810 c_7_hs
328820 c_7_hs
330021 c16_p2
305967 AA886428
328835 c_7_hs
305971 AA886874
328841 c_7_hs
305984 AA887654
328851 c_7_hs
328859 c_7_hs
330057 c17_p2
330058 c17_p2
305999 AA889603
307215 AI193189
307262 AI202100
307318 AI208577
307380 AI222985
307433 AI244895
307437 AI245683

307556 AI281651
307558 AI281998
337645 CH22_5960FG_LINK_EM:AC00
337657 CH22_5976FG_LINK_EM:AC00
307574 AI283549
307588 AI285535
307592 AI285739
337685 CH22_6020FG_LINK_EM:AC00
337695 CH22_6033FG_LINK_EM:AC00
337697 CH22_6037FG_LINK_EM:AC00
307606 AI290006

307629 AI300246
307642 AI302103
307643 AI302124
307646 AI302236
307703 AI318588
307728 AI335557
307752 AI339447
307799 AI351112
309005 AI884454
307864 AI367417
307877 AI368880
307899 AI380270
309108 AI925949
309169 AI949216
309181 AI951727
307904 AI381019
307912 AI382224
307918 AI383496
307954 AI419692
307961 AI421059
307992 AI434166
309206 AI961962
309233 AI971416
309245 AI972447
309247 AI972768
309275 AI989570
309324 AW015373
309333 AW025709
309343 AW028652
309351 AW057547
309403 AW082954
309533 AW151131
309592 AW172384
325271 c11_hs
325285 c11_hs
325289 c11_hs
309600 AW182066
309605 AW182800
309759 AW268822
309767 AW271805
309815 AW292760
309859 AW298760
302681 31257_1 X97550 X97552
302683 31326_1 X85153 T63701
309958 AW444488
309977 AW451663
309985 AW452919
302727 32493_1 L10141 L10151 L10148 L09095
302747 32813_1 AF062275 L03830
304022 T02990
304055 R07994
304056 R08577
304060 T61464
304125 H40976
304127 H42981
304134 H54627
304195 N35382
302952 39444_1 AF103179 U82961
302996 41196_1 AF054663 AF124197 R70292
304269 AA069029
304324 AA137045
304330 AA157834
304424 AA293494
304465 AA421948

304467 AA424703
 304480 AA430373
 304485 AA434076
 304487 AA434241
 304559 AA488050
 304575 AA496437
 304605 AA513225
 304612 AA514207
 304623 AA521331
 304635 AA523976
 304667 AA535602
 304674 AA541735
 304675 AA541740
 304693 AA554263
 304696 AA554758
 304707 AA564846
 304731 AA576085
 304734 AA576428
 304745 AA577771
 304746 AA577793
 306009 AA894560
 306012 AA896989
 306053 AA905312
 306081 AA908472
 306090 AA908609
 304811 AA584361
 304813 AA584540
 304817 AA584712
 304833 AA586504
 304841 AA587541
 304887 AA599355
 306137 AA916176
 306180 AA922503
 306183 AA922622
 306193 AA923457
 304918 AA602697
 304968 AA614308
 306200 AA926816
 306220 AA928363
 306221 AA928686
 306300 AA937573
 320789 252516_1
 306351 AA961356
 330435 41165_1
 330436 10605_34

R78712 AA603646 R78713
 U63836 AW842139 X74956 U78550 AW840802 X74954 AW388241 AW842709 AF253321 X74955 X74370 AW363799
 BE073386 AI791962 AA587390 AW840865
 BE259039 W29128 AW410299 X72990 BE246492 NM_005243 X66899 AI909006 AW248151 AL031186 AA012966 BE273549
 BE311429 BE253102 Y07848 BE538102 BE256863 BE261240 BE312156 BE618412 BE257322 BE620446 AW806629
 AA376777 AA325384 BE256808 BE251039 BE257878 BE275352 AA357169 AW403562 AA204995 AA093259 W95953
 BE256279 BE336683 BE252465 BE251266 AA380754 BE294942 AA380941 AA380999 BE297164 BE249995 BE294719
 BE295372 AI270673 BE305132 BE563752 BE295357 AI525421 BE263980 AA057505 AA020915 BE266318 BE206948
 AI474020 BE296420 BE297374 BE408545 BE019366 BE407372 BE266180 BE279437 R58233 T19567 BE300738 AW381179
 AA357571 AW361285 AA436908 AA301019 AA301022 N20202 BE408777 BE548638 BE167415 AA071260 BE088429
 BE280092 W23117 T19568 R51681 AW402216 W22784 BE185607 AI457224 BE544120 AL134874 S72620 AA375079 D51319
 AW818280 BE514686 AW853024 BE563744 AA300469 T07592 BE622190 BE272834 W21781 BE315450 BE542367 BE393120
 AA988441 H55137 BE562296 BE622502 BE395960 AA329733 AA332348 AI768317 AA456866 AI497832 AW878437 AA857042
 U18018 BE621418 AI818790 AI949507 BE397693 AI885545 AI858854 AI355147 BE169028 S62138 AW732191 AA856891
 BE266060 X71427 BE268557 AF095890 AW001288 AI799634 AI623498 AA071346 BE547662 BE261446 AI564543 BE559759
 U35622 BE314249 BE264915 AI638591 AI538385 AW090025 BE384754 AI888689 AW778800 AI925273 AA075797 AW949130
 AV660275 AW438697 AI587137 AI524121 AA806249 AW628247 AA808241 AI244388 AI761125 AW117672 AA911782
 AI129250 AA654447 H55291 BE258050 BE206162 W95867 AA857187 AI871378 AI660103 AW103827 AI220929 AW149949
 BE465561 AI302857 AW168841 D82190 AW249814 AI623432 AI687358 AW951077 R51592 W60458 AI092863 AW474693
 D12765 AI911646 D82208 D82187 AW074031 AI358527 AW338497 AA970893 AW072573 AA205364 AI858886 AA012830
 AW148763 AI863056 AA548656 BE250325 AI016994 AI864005 BE046122 AI497746 C75340 R58896 D82141 AW168240
 C19048 AI741090 D29465 AI222365 AA948288 AI583522 AW572212 AI091290 AA582727 AA579897 AA570629 W60883
 AW516989 AL038160 AA577334 AI865872 AA994043 AA922583 AA464778 AA209178 AI829479 AI370235 BE246529
 AA384177 AA456255 AI699730 W60654 AL035744 AA862042 R32756 AI886886 AA993087 AI289479 AA627840 AA464184
 AI619503 R32755 AW075358 AI432315 AA457024 AA020865 R92132 AA454629 AA746059 AA454643 AA456240 AA826984
 BE163738 AI806470 AI991074 AI802560 AA587095 AA558714 AA968521 N87780 AI538246 N71794 AV661738 AI368903
 AA362570 AI989445 AI674962 S75762 BE245204 AA975296 D20123 AW005704 AA693328 AA582270 AI918474 AW205707
 AI696299 AA220990 AA101538 T29030 H27201 AW262526 AI610530 AA126840 AA126790 X92120 AW367868 BE299644
 BE299451 AA476561 BE300044 AA134363 BE295222 AA307504 N42337 AA319098 N39502 AW964461 N57241 BE299049
 N86332 R51156 AA085859 T75212 AA133939 AA147129 AA156161 BE543953 BE538848 AA133676 BE299745 AA135050
 AA218535 AW406401 AW411287 BE410528 C01410 NM_004083 BE314959 AA836413 AA085862 AW024370 AA471059
 AW467508 AA001025 AI828231 AA633221 T95517 AA147038 AA476447 AW027012 AW078627 BE513200 AI192297
 AA886279 AW081806 AA316185 AA010506 AI269929 W93139 AI682935 AA609555 AA378028 AI093877 AA999997 AA730698
 AI143923 AW575315 AA890550 AA494353 AW576601 AI796336 AA826130 AA609207 AI539618 AI088539 AI089090 AA825505

AA632978 AA015892 AW204713 AA156495 AA824613 AA133630 N29826 AA527476 AI633352 T27908 AA134364 AA133940
AW043601 H37775 AA772375 AA057871 AA047888 AA054225 H86568 AA001511 H25718 AW189507 AA165589 AA054433
H85549 AA165486 AA058972 AA454911 AA464064 AA493802 AA428253 R85508 AW302469 AI611812 BE162582 F11073
T95518 N26811 AI783929 H40669 AW611745 AI658803 R51042 R45276 AA528386 AA782875 AW880218 AL138391 AA314536
AW949338 AA149466 AA149552 AI346513 AA216776 BE349131 AW007654 AI141803 AA622688 AI185131 AW057635
AA101539 AA627986 H27202 AI536847 W93084 AI973148 AI246788 AW572108 AI469414 AA454835 AA612707 AA430746
AI084991 AA010400 AA856636 AA463928 AI248310 R07170 AA834033 D12244 AI655670 AA054350 AA639480 AI702067
AI475389
330527 14658_-15 S77356
330833 103550_1 AA046804 AA046821
330855 111881_1 AA070316 AA079318
332099 genbank_AA608983 AA608983
332240 genbank_N54803 N54803

TABLE 1-20B

Table 1-20B, shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Tables 1-20. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
332792	Dunham, I. et al.	Plus	73381-73768
332843	Dunham, I. et al.	Plus	1142859-1143494
332909	Dunham, I. et al.	Plus	1946582-1946735
332920	Dunham, I. et al.	Plus	2007562-2007785
332947	Dunham, I. et al.	Plus	2431726-2432006
332949	Dunham, I. et al.	Plus	2436245-2436348
332958	Dunham, I. et al.	Plus	2516164-2516310
332992	Dunham, I. et al.	Plus	2699997-2701093
332993	Dunham, I. et al.	Plus	2701550-2701685
333004	Dunham, I. et al.	Plus	2759056-2759165
333006	Dunham, I. et al.	Plus	2762853-2762953
333007	Dunham, I. et al.	Plus	2763569-2763709
333132	Dunham, I. et al.	Plus	3358040-3358153
333133	Dunham, I. et al.	Plus	3360058-3360195
333139	Dunham, I. et al.	Plus	3369495-3369571
333152	Dunham, I. et al.	Plus	3612171-3612354
333205	Dunham, I. et al.	Plus	3942727-3943009
333221	Dunham, I. et al.	Plus	3978070-3978187
333225	Dunham, I. et al.	Plus	3992229-3992386
333245	Dunham, I. et al.	Plus	4157587-4157668
333248	Dunham, I. et al.	Plus	4162041-4162139
333261	Dunham, I. et al.	Plus	4336597-4337752
333272	Dunham, I. et al.	Plus	4381561-4382212
333281	Dunham, I. et al.	Plus	4506230-4506342
333283	Dunham, I. et al.	Plus	4514226-4514360
333288	Dunham, I. et al.	Plus	4516841-4516939
333298	Dunham, I. et al.	Plus	4581537-4581947
333306	Dunham, I. et al.	Plus	5396233-5396310
333382	Dunham, I. et al.	Plus	4905796-4905913
333403	Dunham, I. et al.	Plus	4925140-4925256
333420	Dunham, I. et al.	Plus	4954302-4954465
333428	Dunham, I. et al.	Plus	4973869-4974007
333464	Dunham, I. et al.	Plus	5210762-5211300
333465	Dunham, I. et al.	Plus	5211385-5211858
333488	Dunham, I. et al.	Plus	5396233-5396310
333515	Dunham, I. et al.	Plus	5564299-5564851
333520	Dunham, I. et al.	Plus	5586133-5586296
333566	Dunham, I. et al.	Plus	5954226-5954473
333567	Dunham, I. et al.	Plus	5959139-5959515
333571	Dunham, I. et al.	Plus	6007916-6008058
333572	Dunham, I. et al.	Plus	6026896-6027189
333576	Dunham, I. et al.	Plus	6090345-6090721
333577	Dunham, I. et al.	Plus	6123950-6124281
333580	Dunham, I. et al.	Plus	6142935-6143145
333587	Dunham, I. et al.	Plus	6250599-6250966
333588	Dunham, I. et al.	Plus	6255445-6255779
333591	Dunham, I. et al.	Plus	6285884-6286251
333592	Dunham, I. et al.	Plus	6297731-6297976
333593	Dunham, I. et al.	Plus	6304132-6304428
333594	Dunham, I. et al.	Plus	6308990-6309450
333599	Dunham, I. et al.	Plus	6337885-6338255
333600	Dunham, I. et al.	Plus	6355629-6355925
333601	Dunham, I. et al.	Plus	6360075-6360442
333607	Dunham, I. et al.	Plus	6504431-6504690
333608	Dunham, I. et al.	Plus	6510834-6511130

333619	Dunham, I. et.al.	Plus	6562799-6562926
333623	Dunham, I. et.al.	Plus	6584559-6584956
333625	Dunham, I. et.al.	Plus	6603020-6603310
333626	Dunham, I. et.al.	Plus	6614174-6614467
333627	Dunham, I. et.al.	Plus	6620584-6620903
333628	Dunham, I. et.al.	Plus	6629004-6629233
333629	Dunham, I. et.al.	Plus	6636915-6637205
333631	Dunham, I. et.al.	Plus	6650904-6651011
333632	Dunham, I. et.al.	Plus	6651520-6651658
333635	Dunham, I. et.al.	Plus	6663683-6663973
333637	Dunham, I. et.al.	Plus	6674968-6675134
333640	Dunham, I. et.al.	Plus	6688350-6688624
333642	Dunham, I. et.al.	Plus	6708760-6709139
333643	Dunham, I. et.al.	Plus	6728053-6728343
333646	Dunham, I. et.al.	Plus	6739110-6739379
333647	Dunham, I. et.al.	Plus	6772502-6772779
333648	Dunham, I. et.al.	Plus	6787465-6787782
333650	Dunham, I. et.al.	Plus	6796852-6797128
333652	Dunham, I. et.al.	Plus	6809455-6809573
333653	Dunham, I. et.al.	Plus	6811130-6811392
333654	Dunham, I. et.al.	Plus	6816731-6816993
333656	Dunham, I. et.al.	Plus	6822087-6822406
333657	Dunham, I. et.al.	Plus	6831369-6831445
333658	Dunham, I. et.al.	Plus	6835282-6835474
333668	Dunham, I. et.al.	Plus	7011009-7011223
333670	Dunham, I. et.al.	Plus	7027945-7028181
333680	Dunham, I. et.al.	Plus	7071730-7071794
333682	Dunham, I. et.al.	Plus	7076641-7076760
333698	Dunham, I. et.al.	Plus	7205279-7205383
333710	Dunham, I. et.al.	Plus	7230314-7230476
333717	Dunham, I. et.al.	Plus	7308714-7308815
333727	Dunham, I. et.al.	Plus	7373219-7373311
333785	Dunham, I. et.al.	Plus	7775317-7775415
333791	Dunham, I. et.al.	Plus	7795972-7796082
333859	Dunham, I. et.al.	Plus	8041203-8041359
333875	Dunham, I. et.al.	Plus	8135505-8136179
333879	Dunham, I. et.al.	Plus	8146919-8147062
333891	Dunham, I. et.al.	Plus	8156437-8156709
333918	Dunham, I. et.al.	Plus	8307124-8307215
333929	Dunham, I. et.al.	Plus	8479486-8479580
333932	Dunham, I. et.al.	Plus	8489124-8489205
333983	Dunham, I. et.al.	Plus	8813593-8813668
333987	Dunham, I. et.al.	Plus	8824245-8824376
333997	Dunham, I. et.al.	Plus	8866668-8867255
334010	Dunham, I. et.al.	Plus	8996696-8998236
334015	Dunham, I. et.al.	Plus	9055452-9055595
334017	Dunham, I. et.al.	Plus	9139516-9139634
334026	Dunham, I. et.al.	Plus	9196549-9196681
334030	Dunham, I. et.al.	Plus	9288463-9288782
334044	Dunham, I. et.al.	Plus	9373898-9374065
334047	Dunham, I. et.al.	Plus	9428152-9428211
334055	Dunham, I. et.al.	Plus	9662077-9662270
334063	Dunham, I. et.al.	Plus	9731991-9732085
334066	Dunham, I. et.al.	Plus	9739568-9739680
334068	Dunham, I. et.al.	Plus	9746279-9746477
334076	Dunham, I. et.al.	Plus	9801613-9801693
334091	Dunham, I. et.al.	Plus	9872327-9872527
334106	Dunham, I. et.al.	Plus	10261155-10261841
334109	Dunham, I. et.al.	Plus	10267679-10267864
334111	Dunham, I. et.al.	Plus	10279365-10279531
334115	Dunham, I. et.al.	Plus	10316414-10316608
334118	Dunham, I. et.al.	Plus	10344273-10344384
334120	Dunham, I. et.al.	Plus	10402389-10403196
334135	Dunham, I. et.al.	Plus	10457085-10457183
334235	Dunham, I. et.al.	Plus	12983601-12983703
334239	Dunham, I. et.al.	Plus	13056569-13056693
334244	Dunham, I. et.al.	Plus	13159198-13159302
334257	Dunham, I. et.al.	Plus	13213243-13213429
334260	Dunham, I. et.al.	Plus	13223819-13223968
334298	Dunham, I. et.al.	Plus	13424763-13425914
334342	Dunham, I. et.al.	Plus	13646844-13646980
334354	Dunham, I. et.al.	Plus	13702598-13702747
334430	Dunham, I. et.al.	Plus	14269664-14270102
334435	Dunham, I. et.al.	Plus	14275597-14275689
334451	Dunham, I. et.al.	Plus	14315572-14315741
334504	Dunham, I. et.al.	Plus	14510206-14510398

334510	Dunham, I. et.al.	Plus	14522303-14522418
334518	Dunham, I. et.al.	Plus	14630584-14630669
334525	Dunham, I. et.al.	Plus	14781066-14781137
334528	Dunham, I. et.al.	Plus	14787558-14787675
334529	Dunham, I. et.al.	Plus	14788825-14788971
334565	Dunham, I. et.al.	Plus	14989033-14989353
334568	Dunham, I. et.al.	Plus	14992698-14993210
334590	Dunham, I. et.al.	Plus	15033247-15033753
334612	Dunham, I. et.al.	Plus	15170470-15170535
334626	Dunham, I. et.al.	Plus	15299954-15300077
334661	Dunham, I. et.al.	Plus	15477716-15477786
334664	Dunham, I. et.al.	Plus	15501941-15502119
334666	Dunham, I. et.al.	Plus	15504203-15504279
334676	Dunham, I. et.al.	Plus	15516334-15516412
334677	Dunham, I. et.al.	Plus	15517449-15517560
334719	Dunham, I. et.al.	Plus	15778859-15779028
334730	Dunham, I. et.al.	Plus	15967830-15967934
334797	Dunham, I. et.al.	Plus	16383231-16383458
334819	Dunham, I. et.al.	Plus	16758514-16758711
334855	Dunham, I. et.al.	Plus	18402556-18402735
334900	Dunham, I. et.al.	Plus	19315678-19315743
334906	Dunham, I. et.al.	Plus	19323493-19323590
334907	Dunham, I. et.al.	Plus	19336829-19336938
334914	Dunham, I. et.al.	Plus	19495158-19495275
334915	Dunham, I. et.al.	Plus	19505267-19506101
334935	Dunham, I. et.al.	Plus	20108247-20108373
335019	Dunham, I. et.al.	Plus	20689525-20689582
335036	Dunham, I. et.al.	Plus	20755250-20756375
335049	Dunham, I. et.al.	Plus	20877184-20877309
335081	Dunham, I. et.al.	Plus	21113871-21113937
335131	Dunham, I. et.al.	Plus	21449834-21450003
335157	Dunham, I. et.al.	Plus	21543302-21544341
335163	Dunham, I. et.al.	Plus	21583508-21583655
335174	Dunham, I. et.al.	Plus	21631301-21631447
335180	Dunham, I. et.al.	Plus	21641226-21641603
335188	Dunham, I. et.al.	Plus	21669118-21669328
335189	Dunham, I. et.al.	Plus	21673403-21673472
335193	Dunham, I. et.al.	Plus	21692208-21692362
335200	Dunham, I. et.al.	Plus	21743499-21743881
335201	Dunham, I. et.al.	Plus	21745249-21745664
335284	Dunham, I. et.al.	Plus	22272583-22272712
335311	Dunham, I. et.al.	Plus	22501602-22501676
335320	Dunham, I. et.al.	Plus	22542132-22542246
335371	Dunham, I. et.al.	Plus	22849529-22849808
335377	Dunham, I. et.al.	Plus	22869909-22870188
335421	Dunham, I. et.al.	Plus	23250433-23250498
335448	Dunham, I. et.al.	Plus	23477532-23477831
335451	Dunham, I. et.al.	Plus	23480611-23480711
335455	Dunham, I. et.al.	Plus	23486127-23486216
335468	Dunham, I. et.al.	Plus	23787245-23787367
335470	Dunham, I. et.al.	Plus	23812877-23813365
335482	Dunham, I. et.al.	Plus	24087956-24088114
335485	Dunham, I. et.al.	Plus	24098953-24099123
335517	Dunham, I. et.al.	Plus	24226461-24226531
335536	Dunham, I. et.al.	Plus	24498783-24499762
335565	Dunham, I. et.al.	Plus	24881886-24882470
335585	Dunham, I. et.al.	Plus	24988240-24988405
335587	Dunham, I. et.al.	Plus	24991457-24991618
335593	Dunham, I. et.al.	Plus	25037253-25037370
335634	Dunham, I. et.al.	Plus	25163837-25164042
335651	Dunham, I. et.al.	Plus	25317560-25317696
335652	Dunham, I. et.al.	Plus	25325625-25325883
335667	Dunham, I. et.al.	Plus	25345735-25345856
335687	Dunham, I. et.al.	Plus	25445952-25446064
335690	Dunham, I. et.al.	Plus	25455442-25455625
335692	Dunham, I. et.al.	Plus	25468557-25468725
335693	Dunham, I. et.al.	Plus	25471363-25471524
335700	Dunham, I. et.al.	Plus	25512222-25512890
335720	Dunham, I. et.al.	Plus	25596542-25596646
335721	Dunham, I. et.al.	Plus	25599118-25599228
335733	Dunham, I. et.al.	Plus	25686486-25686626
335739	Dunham, I. et.al.	Plus	25698550-25698826
335745	Dunham, I. et.al.	Plus	25718164-25718332
335747	Dunham, I. et.al.	Plus	25723304-25723494
335783	Dunham, I. et.al.	Plus	25941882-25942040
335968	Dunham, I. et.al.	Plus	27743843-27744029

335971	Dunham, I. et.al.	Plus	27752808-27753017
335975	Dunham, I. et.al.	Plus	27801321-27801391
335993	Dunham, I. et.al.	Plus	28006396-28006571
335998	Dunham, I. et.al.	Plus	28026247-28026356
336011	Dunham, I. et.al.	Plus	28570760-28570900
336035	Dunham, I. et.al.	Plus	29016748-29017410
336049	Dunham, I. et.al.	Plus	29124451-29124606
336055	Dunham, I. et.al.	Plus	29166352-29166573
336072	Dunham, I. et.al.	Plus	29269409-29269575
336075	Dunham, I. et.al.	Plus	29343938-29344050
336081	Dunham, I. et.al.	Plus	29372270-29372407
336083	Dunham, I. et.al.	Plus	29379738-29379881
336084	Dunham, I. et.al.	Plus	29380664-29380792
336086	Dunham, I. et.al.	Plus	29385594-29385713
336087	Dunham, I. et.al.	Plus	29387122-29387253
336088	Dunham, I. et.al.	Plus	29389001-29389124
336089	Dunham, I. et.al.	Plus	29401421-29401625
336090	Dunham, I. et.al.	Plus	29413020-29413162
336091	Dunham, I. et.al.	Plus	29415486-29415617
336092	Dunham, I. et.al.	Plus	29438816-29438948
336094	Dunham, I. et.al.	Plus	29567934-29568099
336102	Dunham, I. et.al.	Plus	29681500-29681687
336124	Dunham, I. et.al.	Plus	30053441-30053500
336125	Dunham, I. et.al.	Plus	30056541-30056622
336127	Dunham, I. et.al.	Plus	30058870-30059029
336128	Dunham, I. et.al.	Plus	30059294-30059367
336171	Dunham, I. et.al.	Plus	30223877-30224048
336214	Dunham, I. et.al.	Plus	30561988-30562044
336306	Dunham, I. et.al.	Plus	33172949-33173281
336316	Dunham, I. et.al.	Plus	33338776-33338919
336333	Dunham, I. et.al.	Plus	33673947-33677345
336387	Dunham, I. et.al.	Plus	34013939-34014124
336442	Dunham, I. et.al.	Plus	34187937-34188061
336481	Dunham, I. et.al.	Plus	34231611-34231720
336489	Dunham, I. et.al.	Plus	34239511-34239619
336498	Dunham, I. et.al.	Plus	34267340-34267424
336502	Dunham, I. et.al.	Plus	34268953-34269083
336516	Dunham, I. et.al.	Plus	34296068-34296249
336548	Dunham, I. et.al.	Plus	34353881-34354826
336590	Dunham, I. et.al.	Plus	2569428-2570275
336593	Dunham, I. et.al.	Plus	4617967-4618783
336606	Dunham, I. et.al.	Plus	16170215-16170415
336623	Dunham, I. et.al.	Plus	167287-167616
336632	Dunham, I. et.al.	Plus	983890-985529
336633	Dunham, I. et.al.	Plus	985591-986221
336634	Dunham, I. et.al.	Plus	986296-986670
336635	Dunham, I. et.al.	Plus	987908-988364
336637	Dunham, I. et.al.	Plus	989276-990813
336638	Dunham, I. et.al.	Plus	991906-993240
336654	Dunham, I. et.al.	Plus	1588782-1588858
336665	Dunham, I. et.al.	Plus	2007241-2007363
336695	Dunham, I. et.al.	Plus	2464609-2464739
336705	Dunham, I. et.al.	Plus	2817668-2817723
336751	Dunham, I. et.al.	Plus	4499629-4499739
336753	Dunham, I. et.al.	Plus	4509509-4509601
336757	Dunham, I. et.al.	Plus	4541167-4541466
336759	Dunham, I. et.al.	Plus	4560526-4560699
336808	Dunham, I. et.al.	Plus	6251639-6251761
336813	Dunham, I. et.al.	Plus	6436416-6436719
336827	Dunham, I. et.al.	Plus	6773762-6774057
336833	Dunham, I. et.al.	Plus	6856506-6856634
336836	Dunham, I. et.al.	Plus	7077262-7077326
336878	Dunham, I. et.al.	Plus	9200300-9200399
336898	Dunham, I. et.al.	Plus	10138365-10138458
336917	Dunham, I. et.al.	Plus	11228329-11228403
336924	Dunham, I. et.al.	Plus	11525273-11525527
336934	Dunham, I. et.al.	Plus	11854506-11854792
336958	Dunham, I. et.al.	Plus	13203550-13203973
336968	Dunham, I. et.al.	Plus	13660250-13660530
336985	Dunham, I. et.al.	Plus	14785058-14785225
337032	Dunham, I. et.al.	Plus	16949229-16949306
337121	Dunham, I. et.al.	Plus	22050289-22050370
337132	Dunham, I. et.al.	Plus	22255234-22255437
337168	Dunham, I. et.al.	Plus	23503596-23504240
337170	Dunham, I. et.al.	Plus	23533763-23534008
337172	Dunham, I. et.al.	Plus	23608358-23608526

337218	Dunham, I. et.al.	Plus	26126466-26126565
337219	Dunham, I. et.al.	Plus	26129629-26130053
337236	Dunham, I. et.al.	Plus	27114318-27114571
337238	Dunham, I. et.al.	Plus	27141465-27141776
337259	Dunham, I. et.al.	Plus	27674026-27674142
337291	Dunham, I. et.al.	Plus	28823308-28823412
337298	Dunham, I. et.al.	Plus	29002509-29002806
337304	Dunham, I. et.al.	Plus	29131691-29131823
337333	Dunham, I. et.al.	Plus	30281383-30281673
337338	Dunham, I. et.al.	Plus	30427592-30427775
337345	Dunham, I. et.al.	Plus	30649387-30649467
337355	Dunham, I. et.al.	Plus	30832838-30833042
337363	Dunham, I. et.al.	Plus	30942712-30942840
337396	Dunham, I. et.al.	Plus	31585902-31586067
337402	Dunham, I. et.al.	Plus	31691134-31691482
337403	Dunham, I. et.al.	Plus	31692319-31692611
337425	Dunham, I. et.al.	Plus	32072241-32072334
337426	Dunham, I. et.al.	Plus	32076190-32076349
337427	Dunham, I. et.al.	Plus	32078958-32079076
337435	Dunham, I. et.al.	Plus	32255716-32255844
337484	Dunham, I. et.al.	Plus	33238033-33238176
337489	Dunham, I. et.al.	Plus	33295724-33295872
337503	Dunham, I. et.al.	Plus	33385583-33385857
337504	Dunham, I. et.al.	Plus	33386053-33386236
337522	Dunham, I. et.al.	Plus	33963188-33963979
337544	Dunham, I. et.al.	Plus	34268412-34268495
337548	Dunham, I. et.al.	Plus	34472882-34472957
337562	Dunham, I. et.al.	Plus	278105-278281
337564	Dunham, I. et.al.	Plus	285643-285788
337586	Dunham, I. et.al.	Plus	952102-952250
337628	Dunham, I. et.al.	Plus	2013838-2014032
337657	Dunham, I. et.al.	Plus	2844851-2845055
337685	Dunham, I. et.al.	Plus	3547161-3547245
337695	Dunham, I. et.al.	Plus	3609670-3609808
337697	Dunham, I. et.al.	Plus	3644971-3645195
337756	Dunham, I. et.al.	Plus	3975015-3975172
337781	Dunham, I. et.al.	Plus	4116049-4116265
337797	Dunham, I. et.al.	Plus	4325712-4325811
337835	Dunham, I. et.al.	Plus	4792299-4792423
337843	Dunham, I. et.al.	Plus	4984966-4985082
337865	Dunham, I. et.al.	Plus	5377705-5377861
337870	Dunham, I. et.al.	Plus	5442516-5442636
337904	Dunham, I. et.al.	Plus	5685819-5686012
337918	Dunham, I. et.al.	Plus	6031241-6031358
337930	Dunham, I. et.al.	Plus	6393566-6393692
337947	Dunham, I. et.al.	Plus	6675643-6675781
337951	Dunham, I. et.al.	Plus	6766321-6766382
337954	Dunham, I. et.al.	Plus	6831483-6831620
337964	Dunham, I. et.al.	Plus	7032720-7032802
338043	Dunham, I. et.al.	Plus	8222138-8222430
338054	Dunham, I. et.al.	Plus	8429258-8429382
338062	Dunham, I. et.al.	Plus	8578852-8579012
338080	Dunham, I. et.al.	Plus	9212114-9212220
338090	Dunham, I. et.al.	Plus	9488619-9488858
338096	Dunham, I. et.al.	Plus	9698397-9698469
338120	Dunham, I. et.al.	Plus	10765673-10765820
338123	Dunham, I. et.al.	Plus	10815824-10815886
338124	Dunham, I. et.al.	Plus	10860311-10860471
338177	Dunham, I. et.al.	Plus	12781530-12781724
338239	Dunham, I. et.al.	Plus	14669918-14670016
338278	Dunham, I. et.al.	Plus	16168714-16168840
338280	Dunham, I. et.al.	Plus	16171884-16172039
338326	Dunham, I. et.al.	Plus	17358806-17358964
338336	Dunham, I. et.al.	Plus	17453324-17453448
338344	Dunham, I. et.al.	Plus	17780512-17780623
338411	Dunham, I. et.al.	Plus	19299273-19299522
338412	Dunham, I. et.al.	Plus	19340661-19340737
338491	Dunham, I. et.al.	Plus	21168430-21168556
338514	Dunham, I. et.al.	Plus	21379420-21379655
338516	Dunham, I. et.al.	Plus	21382180-21382383
338521	Dunham, I. et.al.	Plus	21471358-21471476
338522	Dunham, I. et.al.	Plus	21471617-21471711
338526	Dunham, I. et.al.	Plus	21551136-21551250
338527	Dunham, I. et.al.	Plus	21552237-21553280
338529	Dunham, I. et.al.	Plus	21635616-21635867
338579	Dunham, I. et.al.	Plus	22774968-22775132

338596	Dunham, I. et.al.	Plus	23078273-23078348
338648	Dunham, I. et.al.	Plus	24091259-24091434
338679	Dunham, I. et.al.	Plus	24684836-24684940
338703	Dunham, I. et.al.	Plus	25219881-25220046
338705	Dunham, I. et.al.	Plus	25231397-25231551
338747	Dunham, I. et.al.	Plus	26336372-26336460
338770	Dunham, I. et.al.	Plus	26784513-26784714
338809	Dunham, I. et.al.	Plus	27271920-27272000
338830	Dunham, I. et.al.	Plus	27759923-27760055
338880	Dunham, I. et.al.	Plus	28420713-28420826
338895	Dunham, I. et.al.	Plus	28598893-28599135
338896	Dunham, I. et.al.	Plus	28618487-28618552
338911	Dunham, I. et.al.	Plus	28804184-28804445
338925	Dunham, I. et.al.	Plus	28883892-28884036
338952	Dunham, I. et.al.	Plus	29418831-29418968
338959	Dunham, I. et.al.	Plus	29478431-29478589
338970	Dunham, I. et.al.	Plus	29645468-29645613
339081	Dunham, I. et.al.	Plus	30927871-30928080
339116	Dunham, I. et.al.	Plus	31462304-31462382
339164	Dunham, I. et.al.	Plus	32207441-32207802
339246	Dunham, I. et.al.	Plus	32844518-32844586
339271	Dunham, I. et.al.	Plus	32999935-33000078
339304	Dunham, I. et.al.	Plus	33323712-33323821
339309	Dunham, I. et.al.	Plus	33366900-33367198
339312	Dunham, I. et.al.	Plus	33378992-33379172
339356	Dunham, I. et.al.	Plus	33573387-33573517
339357	Dunham, I. et.al.	Plus	33575210-33575416
339360	Dunham, I. et.al.	Plus	33579433-33579593
339384	Dunham, I. et.al.	Plus	33950591-33950697
339413	Dunham, I. et.al.	Plus	34268734-34268875
339419	Dunham, I. et.al.	Plus	34359680-34359777
332854	Dunham, I. et.al.	Minus	1283611-1283053
332859	Dunham, I. et.al.	Minus	1358943-1358861
332896	Dunham, I. et.al.	Minus	1631641-1631422
332995	Dunham, I. et.al.	Minus	2708847-2708685
333014	Dunham, I. et.al.	Minus	2772479-2772387
333043	Dunham, I. et.al.	Minus	2920906-2920781
333054	Dunham, I. et.al.	Minus	2995314-2995219
333069	Dunham, I. et.al.	Minus	3040771-3040661
333074	Dunham, I. et.al.	Minus	3054171-3054008
333101	Dunham, I. et.al.	Minus	3208966-3208908
333140	Dunham, I. et.al.	Minus	3377220-3376309
333142	Dunham, I. et.al.	Minus	3474264-3474145
333175	Dunham, I. et.al.	Minus	3768113-3768051
333216	Dunham, I. et.al.	Minus	3967627-3967512
333219	Dunham, I. et.al.	Minus	3968531-3968423
333220	Dunham, I. et.al.	Minus	3969363-3968789
333240	Dunham, I. et.al.	Minus	4100495-4100281
333242	Dunham, I. et.al.	Minus	4104544-4104259
333251	Dunham, I. et.al.	Minus	4168970-4168870
333252	Dunham, I. et.al.	Minus	4172550-4172390
333257	Dunham, I. et.al.	Minus	4300724-4300578
333258	Dunham, I. et.al.	Minus	4301348-4301269
333271	Dunham, I. et.al.	Minus	4377786-4377589
333294	Dunham, I. et.al.	Minus	4538728-4538642
333296	Dunham, I. et.al.	Minus	4550766-4550644
333312	Dunham, I. et.al.	Minus	4638794-4638635
333313	Dunham, I. et.al.	Minus	4639397-4639277
333323	Dunham, I. et.al.	Minus	4655333-4655166
333329	Dunham, I. et.al.	Minus	4661779-4661672
333339	Dunham, I. et.al.	Minus	4679691-4679610
333346	Dunham, I. et.al.	Minus	4704564-4704466
333355	Dunham, I. et.al.	Minus	4727555-4727460
333408	Dunham, I. et.al.	Minus	4936879-4936661
333423	Dunham, I. et.al.	Minus	4958233-4957593
333424	Dunham, I. et.al.	Minus	4959694-4958713
333441	Dunham, I. et.al.	Minus	2708847-2708685
333466	Dunham, I. et.al.	Minus	2708847-2708685
333495	Dunham, I. et.al.	Minus	5404039-5403881
333496	Dunham, I. et.al.	Minus	5404643-5404523
333541	Dunham, I. et.al.	Minus	5859241-5859098
333545	Dunham, I. et.al.	Minus	5885539-5885064
333561	Dunham, I. et.al.	Minus	5903659-5903590
333568	Dunham, I. et.al.	Minus	5965072-5964999
333581	Dunham, I. et.al.	Minus	6151638-6151159
333582	Dunham, I. et.al.	Minus	6158522-6158322

333665	Dunham, I. et.al.	Minus	6975471-6975215
333713	Dunham, I. et.al.	Minus	7289490-7289337
333730	Dunham, I. et.al.	Minus	7489326-7489007
333737	Dunham, I. et.al.	Minus	7551981-7551842
333762	Dunham, I. et.al.	Minus	7679466-7679343
333815	Dunham, I. et.al.	Minus	7871914-7871764
333895	Dunham, I. et.al.	Minus	8193845-8193735
333903	Dunham, I. et.al.	Minus	8216956-8216810
333910	Dunham, I. et.al.	Minus	8230221-8230116
333944	Dunham, I. et.al.	Minus	8557051-8556936
333965	Dunham, I. et.al.	Minus	8627484-8626258
334035	Dunham, I. et.al.	Minus	9323508-9323292
334125	Dunham, I. et.al.	Minus	10433521-10432612
334137	Dunham, I. et.al.	Minus	10461063-10460708
334172	Dunham, I. et.al.	Minus	11644142-11644008
334175	Dunham, I. et.al.	Minus	11668659-11668597
334191	Dunham, I. et.al.	Minus	11932215-11932091
334196	Dunham, I. et.al.	Minus	11966322-11966182
334198	Dunham, I. et.al.	Minus	12032364-12032146
334215	Dunham, I. et.al.	Minus	12670395-12670077
334237	Dunham, I. et.al.	Minus	12994394-12993954
334254	Dunham, I. et.al.	Minus	13199268-13198999
334304	Dunham, I. et.al.	Minus	13455315-13455219
334358	Dunham, I. et.al.	Minus	13724372-13724201
334396	Dunham, I. et.al.	Minus	14164482-14164340
334399	Dunham, I. et.al.	Minus	14186289-14186163
334418	Dunham, I. et.al.	Minus	14237235-14237028
334470	Dunham, I. et.al.	Minus	14389581-14389442
334474	Dunham, I. et.al.	Minus	14391920-14391809
334476	Dunham, I. et.al.	Minus	14394777-14394589
334496	Dunham, I. et.al.	Minus	14480743-14480669
334540	Dunham, I. et.al.	Minus	14832365-14832224
334548	Dunham, I. et.al.	Minus	14837304-14837150
334560	Dunham, I. et.al.	Minus	14980648-14980485
334591	Dunham, I. et.al.	Minus	15035270-15035057
334593	Dunham, I. et.al.	Minus	15036374-15036242
334625	Dunham, I. et.al.	Minus	15244936-15243666
334650	Dunham, I. et.al.	Minus	15371251-15371178
334682	Dunham, I. et.al.	Minus	15520806-15520668
334690	Dunham, I. et.al.	Minus	15603055-15602918
334691	Dunham, I. et.al.	Minus	15615920-15611418
334745	Dunham, I. et.al.	Minus	16049960-16049653
334752	Dunham, I. et.al.	Minus	16118059-16117848
334759	Dunham, I. et.al.	Minus	16134427-16134207
334760	Dunham, I. et.al.	Minus	16136658-16136578
334764	Dunham, I. et.al.	Minus	16151208-16151104
334766	Dunham, I. et.al.	Minus	16154663-16154529
334779	Dunham, I. et.al.	Minus	16276881-16276815
334782	Dunham, I. et.al.	Minus	16291693-16291574
334783	Dunham, I. et.al.	Minus	16293336-16293226
334784	Dunham, I. et.al.	Minus	16294548-16294360
334785	Dunham, I. et.al.	Minus	16295583-16295408
334788	Dunham, I. et.al.	Minus	16301237-16301081
334793	Dunham, I. et.al.	Minus	16330748-16330681
334804	Dunham, I. et.al.	Minus	16428342-16428208
334823	Dunham, I. et.al.	Minus	16851360-16851189
334827	Dunham, I. et.al.	Minus	16905877-16905684
334836	Dunham, I. et.al.	Minus	17215581-17215418
334842	Dunham, I. et.al.	Minus	17464352-17464181
334946	Dunham, I. et.al.	Minus	20140514-20140410
334948	Dunham, I. et.al.	Minus	20141727-20141583
334955	Dunham, I. et.al.	Minus	20151753-20151684
334958	Dunham, I. et.al.	Minus	20156046-20155932
334966	Dunham, I. et.al.	Minus	20169171-20169079
334969	Dunham, I. et.al.	Minus	20188176-20188020
334970	Dunham, I. et.al.	Minus	20195886-20195554
335000	Dunham, I. et.al.	Minus	20455403-20455348
335002	Dunham, I. et.al.	Minus	20479143-20479008
335009	Dunham, I. et.al.	Minus	20602011-20601951
335068	Dunham, I. et.al.	Minus	20955606-20955458
335090	Dunham, I. et.al.	Minus	21192979-21190943
335092	Dunham, I. et.al.	Minus	21298638-21298571
335108	Dunham, I. et.al.	Minus	21324221-21324030
335115	Dunham, I. et.al.	Minus	21388250-21388146
335116	Dunham, I. et.al.	Minus	21388573-21388414
335217	Dunham, I. et.al.	Minus	21801622-21801195

335234	Dunham, I. et al.	Minus	21904287-21904080
335236	Dunham, I. et al.	Minus	21915016-21914870
335247	Dunham, I. et al.	Minus	21944287-21944209
335262	Dunham, I. et al.	Minus	22065821-22065630
335265	Dunham, I. et al.	Minus	22102127-22102000
335266	Dunham, I. et al.	Minus	22108492-22108411
335281	Dunham, I. et al.	Minus	22237614-22237503
335331	Dunham, I. et al.	Minus	22556823-22556708
335339	Dunham, I. et al.	Minus	22569208-22569045
335340	Dunham, I. et al.	Minus	22570500-22570342
335344	Dunham, I. et al.	Minus	22600566-22600498
335348	Dunham, I. et al.	Minus	22646377-22646122
335349	Dunham, I. et al.	Minus	22661861-22661271
335523	Dunham, I. et al.	Minus	24235282-24235175
335527	Dunham, I. et al.	Minus	24241519-24241370
335566	Dunham, I. et al.	Minus	24892522-24891998
335606	Dunham, I. et al.	Minus	25056719-25055010
335750	Dunham, I. et al.	Minus	25732501-25731972
335755	Dunham, I. et al.	Minus	25763806-25763747
335768	Dunham, I. et al.	Minus	25819821-25819690
335774	Dunham, I. et al.	Minus	25883733-25883572
335777	Dunham, I. et al.	Minus	25885770-25885599
335782	Dunham, I. et al.	Minus	25908578-25908440
335787	Dunham, I. et al.	Minus	25947022-25946835
335806	Dunham, I. et al.	Minus	26217475-26217146
335817	Dunham, I. et al.	Minus	26321875-26321750
335827	Dunham, I. et al.	Minus	26380557-26380472
335831	Dunham, I. et al.	Minus	26321526-26321349
335832	Dunham, I. et al.	Minus	26383701-26383583
335863	Dunham, I. et al.	Minus	26693017-26692763
335895	Dunham, I. et al.	Minus	26975307-26975239
335902	Dunham, I. et al.	Minus	26985491-26985358
335920	Dunham, I. et al.	Minus	27034927-27034811
335956	Dunham, I. et al.	Minus	27653729-27653635
335980	Dunham, I. et al.	Minus	27846751-27846614
335999	Dunham, I. et al.	Minus	28033986-28033848
336000	Dunham, I. et al.	Minus	28105547-28105354
336029	Dunham, I. et al.	Minus	28732042-28731966
336142	Dunham, I. et al.	Minus	30135157-30135054
336149	Dunham, I. et al.	Minus	30148185-30148059
336161	Dunham, I. et al.	Minus	30169370-30169185
336177	Dunham, I. et al.	Minus	30306638-30303284
336198	Dunham, I. et al.	Minus	30459668-30459460
336199	Dunham, I. et al.	Minus	30461245-30461040
336200	Dunham, I. et al.	Minus	30462971-30462895
336202	Dunham, I. et al.	Minus	30468933-30468781
336203	Dunham, I. et al.	Minus	30470796-30470653
336227	Dunham, I. et al.	Minus	30902014-30901946
336231	Dunham, I. et al.	Minus	30967656-30967471
336232	Dunham, I. et al.	Minus	30977707-30977645
336238	Dunham, I. et al.	Minus	31160083-31159959
336243	Dunham, I. et al.	Minus	31402237-31402104
336246	Dunham, I. et al.	Minus	31425669-31425253
336279	Dunham, I. et al.	Minus	32103203-32102860
336280	Dunham, I. et al.	Minus	32103588-32103497
336294	Dunham, I. et al.	Minus	32946997-32946890
336295	Dunham, I. et al.	Minus	32950291-32950162
336328	Dunham, I. et al.	Minus	33584461-33584201
336347	Dunham, I. et al.	Minus	33843218-33843104
336351	Dunham, I. et al.	Minus	33865890-33865681
336397	Dunham, I. et al.	Minus	34021504-34021389
336400	Dunham, I. et al.	Minus	34023437-34023298
336402	Dunham, I. et al.	Minus	34024090-34023981
336406	Dunham, I. et al.	Minus	34030774-34030564
336417	Dunham, I. et al.	Minus	34047771-34047675
336455	Dunham, I. et al.	Minus	34209155-34209018
336463	Dunham, I. et al.	Minus	34212236-34211968
336479	Dunham, I. et al.	Minus	34218224-34218139
336510	Dunham, I. et al.	Minus	34277046-34276928
336538	Dunham, I. et al.	Minus	34329270-34329189
336584	Dunham, I. et al.	Minus	34516566-34516468
336599	Dunham, I. et al.	Minus	11736500-11734418
336615	Dunham, I. et al.	Minus	26020622-26016546
336616	Dunham, I. et al.	Minus	26021027-26020848
336618	Dunham, I. et al.	Minus	25799-25612
336645	Dunham, I. et al.	Minus	1351268-1351168

336653	Dunham, I. et.al.	Minus	1568327-1568216
336657	Dunham, I. et.al.	Minus	1705497-1705415
336717	Dunham, I. et.al.	Minus	3297417-3297352
336772	Dunham, I. et.al.	Minus	5129939-5129785
336795	Dunham, I. et.al.	Minus	5681580-5681460
336796	Dunham, I. et.al.	Minus	5683253-5683016
336854	Dunham, I. et.al.	Minus	7884839-7884767
336858	Dunham, I. et.al.	Minus	8200946-8200789
336862	Dunham, I. et.al.	Minus	8394593-8394369
336863	Dunham, I. et.al.	Minus	8396673-8396425
336883	Dunham, I. et.al.	Minus	9322767-9322554
336908	Dunham, I. et.al.	Minus	10791347-10791256
336927	Dunham, I. et.al.	Minus	11548111-11547937
336929	Dunham, I. et.al.	Minus	11603040-11602908
336978	Dunham, I. et.al.	Minus	14241223-14241030
336981	Dunham, I. et.al.	Minus	14478638-14478472
336984	Dunham, I. et.al.	Minus	14725450-14725309
336994	Dunham, I. et.al.	Minus	15104752-15104656
336999	Dunham, I. et.al.	Minus	15389579-15388897
337011	Dunham, I. et.al.	Minus	16106423-16106080
337023	Dunham, I. et.al.	Minus	16346174-16346065
337069	Dunham, I. et.al.	Minus	19014379-19014222
337092	Dunham, I. et.al.	Minus	20140132-20139980
337093	Dunham, I. et.al.	Minus	20145693-20145570
337094	Dunham, I. et.al.	Minus	20146915-20146778
337097	Dunham, I. et.al.	Minus	20498648-20497686
337100	Dunham, I. et.al.	Minus	20543830-20543751
337114	Dunham, I. et.al.	Minus	21328259-21328050
337203	Dunham, I. et.al.	Minus	25349286-25349156
337204	Dunham, I. et.al.	Minus	25419024-25418931
337225	Dunham, I. et.al.	Minus	26607638-26607468
337244	Dunham, I. et.al.	Minus	27362048-27361952
337279	Dunham, I. et.al.	Minus	28430185-28430033
337289	Dunham, I. et.al.	Minus	28756246-28756163
337316	Dunham, I. et.al.	Minus	29657129-29656997
337431	Dunham, I. et.al.	Minus	32110529-32110475
337432	Dunham, I. et.al.	Minus	32199134-32198922
337445	Dunham, I. et.al.	Minus	32292380-32292228
337451	Dunham, I. et.al.	Minus	32408680-32408576
337452	Dunham, I. et.al.	Minus	32415187-32415117
337455	Dunham, I. et.al.	Minus	32434517-32434425
337456	Dunham, I. et.al.	Minus	32438887-32438828
337513	Dunham, I. et.al.	Minus	33478692-33478562
337514	Dunham, I. et.al.	Minus	33484408-33484339
337517	Dunham, I. et.al.	Minus	33795568-33795385
337590	Dunham, I. et.al.	Minus	982397-982246
337592	Dunham, I. et.al.	Minus	1007791-1007634
337604	Dunham, I. et.al.	Minus	1329838-1329759
337606	Dunham, I. et.al.	Minus	1346786-1346617
337612	Dunham, I. et.al.	Minus	1570235-1570142
337645	Dunham, I. et.al.	Minus	5141462-5141329
337704	Dunham, I. et.al.	Minus	3658670-3658545
337706	Dunham, I. et.al.	Minus	3672056-3671922
337760	Dunham, I. et.al.	Minus	4008389-4008037
337768	Dunham, I. et.al.	Minus	4050134-4049973
337771	Dunham, I. et.al.	Minus	4060797-4060707
337778	Dunham, I. et.al.	Minus	4087301-4087157
337787	Dunham, I. et.al.	Minus	4135097-4135025
337816	Dunham, I. et.al.	Minus	4523203-4523090
337821	Dunham, I. et.al.	Minus	4538189-4538075
337848	Dunham, I. et.al.	Minus	5053964-5053829
337911	Dunham, I. et.al.	Minus	5866504-5866154
337913	Dunham, I. et.al.	Minus	6149843-6149786
337974	Dunham, I. et.al.	Minus	7153401-7153085
337984	Dunham, I. et.al.	Minus	7282160-7282020
338069	Dunham, I. et.al.	Minus	8728655-8728580
338087	Dunham, I. et.al.	Minus	9362067-9361878
338113	Dunham, I. et.al.	Minus	10481242-10481089
338132	Dunham, I. et.al.	Minus	10989617-10989530
338140	Dunham, I. et.al.	Minus	11237977-11237876
338151	Dunham, I. et.al.	Minus	11519629-11519501
338221	Dunham, I. et.al.	Minus	14183649-14183568
338223	Dunham, I. et.al.	Minus	14287001-14286830
338235	Dunham, I. et.al.	Minus	14484254-14484179
338271	Dunham, I. et.al.	Minus	16048151-16047985
338285	Dunham, I. et.al.	Minus	16275030-16274895

338306	Dunham, I. et.al.	Minus	16966519-16968247
338325	Dunham, I. et.al.	Minus	17241596-17241507
338368	Dunham, I. et.al.	Minus	18272087-18272025
338381	Dunham, I. et.al.	Minus	18534404-18534234
338431	Dunham, I. et.al.	Minus	19747608-19747496
338450	Dunham, I. et.al.	Minus	20172384-20172200
338451	Dunham, I. et.al.	Minus	20174286-20174193
338486	Dunham, I. et.al.	Minus	21063152-21063049
338508	Dunham, I. et.al.	Minus	21308161-21307923
338576	Dunham, I. et.al.	Minus	22676619-22676368
338591	Dunham, I. et.al.	Minus	22959271-22959182
338593	Dunham, I. et.al.	Minus	22992718-22992531
338594	Dunham, I. et.al.	Minus	23026144-23026029
338668	Dunham, I. et.al.	Minus	24500606-24500442
338686	Dunham, I. et.al.	Minus	24836463-24836246
338725	Dunham, I. et.al.	Minus	25904148-25904017
338819	Dunham, I. et.al.	Minus	27539222-27539058
338829	Dunham, I. et.al.	Minus	27739328-27739163
338843	Dunham, I. et.al.	Minus	27899321-27899045
338934	Dunham, I. et.al.	Minus	29036147-29036048
338976	Dunham, I. et.al.	Minus	29867484-29867259
338990	Dunham, I. et.al.	Minus	30019967-30019837
339019	Dunham, I. et.al.	Minus	30498278-30498118
339032	Dunham, I. et.al.	Minus	30613407-30613275
339033	Dunham, I. et.al.	Minus	30621102-30620830
339037	Dunham, I. et.al.	Minus	30634104-30633988
339044	Dunham, I. et.al.	Minus	30721853-30721740
339071	Dunham, I. et.al.	Minus	30885702-30885511
339127	Dunham, I. et.al.	Minus	31688232-31688072
339130	Dunham, I. et.al.	Minus	31743961-31743767
339181	Dunham, I. et.al.	Minus	32321697-32321571
339188	Dunham, I. et.al.	Minus	32347554-32347250
339193	Dunham, I. et.al.	Minus	32415060-32414928
339196	Dunham, I. et.al.	Minus	32431422-32431097
339208	Dunham, I. et.al.	Minus	32491714-32491657
339213	Dunham, I. et.al.	Minus	32496590-32496440
339215	Dunham, I. et.al.	Minus	32502559-32502383
339220	Dunham, I. et.al.	Minus	32519184-32519081
339230	Dunham, I. et.al.	Minus	32729004-32728929
339251	Dunham, I. et.al.	Minus	32894314-32894216
339256	Dunham, I. et.al.	Minus	32926055-32925967
339266	Dunham, I. et.al.	Minus	32976148-32976041
339268	Dunham, I. et.al.	Minus	32984700-32984500
339280	Dunham, I. et.al.	Minus	33114230-33114010
339340	Dunham, I. et.al.	Minus	33485220-33485144
339342	Dunham, I. et.al.	Minus	33494677-33494541
339344	Dunham, I. et.al.	Minus	33503675-33503520
339363	Dunham, I. et.al.	Minus	33589964-33589665
339365	Dunham, I. et.al.	Minus	33641615-33641446
339401	Dunham, I. et.al.	Minus	34045393-34045138
339424	Dunham, I. et.al.	Minus	34392464-34392311
339435	Dunham, I. et.al.	Minus	34538987-34538876
337884			
337885			
337895			
337898			
329611	3962478	Minus	11780-11875
329496	3983518	Plus	13570-13686
325310	5866864	Minus	17256-17357
325320	5866870	Minus	33200-33646
325338	5866883	Minus	62747-62928
325271	5866901	Plus	87318-87378
325285	5866903	Plus	107772-107864
325289	5866903	Minus	129715-129877
325300	5866908	Minus	7940-8059
325304	5866910	Minus	37468-37884
329630	6729060	Minus	167326-167511
325369	5866920	Minus	1018736-1018830
325359	5866920	Plus	392668-392781
325408	5866921	Plus	599118-599289
325409	5866921	Plus	599438-599655
325410	5866921	Plus	615477-615580
325393	5866921	Minus	350513-350691
325396	5866921	Plus	476868-477200
325433	5866936	Minus	480706-480826
325448	5866941	Minus	392834-392982

325464	5866947	Plus	323995-324279
325480	5866957	Plus	20558-21112
325482	5866957	Plus	47957-48078
325510	5866974	Plus	219958-220917
325524	5866981	Minus	117837-117997
325513	6017035	Minus	34295-34490
325519	6017036	Minus	186804-186915
325571	6552439	Minus	184952-185135
329638	3779004	Minus	4636-5127
325623	5867000	Plus	84366-84472
325636	5867002	Minus	149928-150033
325677	5867017	Minus	58414-58518
325691	5867021	Plus	65467-65629
325690	5867021	Plus	7391-7530
325702	5867028	Plus	139925-140061
325703	5867028	Plus	155806-156098
325790	6381957	Minus	105385-105524
325783	6456780	Plus	102815-102957
325695	6552446	Minus	199599-199778
325726	6552447	Plus	154262-154623
325742	6552448	Minus	38225-38306
325760	6552449	Plus	343394-343549
325801	6552451	Plus	49269-49542
325803	6552451	Plus	53355-53558
325649	6588011	Minus	215659-215815
325710	6682473	Plus	204538-204822
325712	6682473	Plus	208541-208926
325755	6682474	Plus	406603-407037
325751	6682474	Plus	130437-130520
325763	6682475	Minus	327530-327910
325791	6682476	Plus	344059-344841
329782	5912597	Plus	123410-123499
329779	6002090	Minus	195353-195669
329760	6048280	Minus	51419-51528
329752	6065777	Plus	132916-133335
329737	6065779	Plus	70136-70236
329735	6065780	Plus	63923-64213
329719	6065785	Plus	46970-47762
329725	6065785	Plus	133747-133842
329705	6065790	Minus	63183-63724
329665	6272129	Plus	91791-91891
329793	6522661	Minus	96556-96698
329824	6630758	Minus	126072-126254
329839	6672062	Plus	34377-34537
329853	6682295	Plus	68945-69009
329870	6706435	Minus	5729-5870
329879	6466518	Minus	12266-12356
329902	6634760	Plus	106906-106984
325851	5867067	Minus	51751-51981
325886	5867087	Plus	194694-194915
325887	5867087	Plus	195052-195485
326005	5867112	Minus	7827-8117
325945	5867138	Minus	123079-124086
325953	5867140	Minus	4721-4901
325965	5867147	Plus	216364-216516
325966	5867147	Plus	217235-217356
325977	6249602	Plus	60638-60759
325835	6552452	Minus	81182-81414
329995	4567166	Minus	150014-150315
329948	5540101	Minus	134056-134261
329940	6165199	Minus	33718-33882
329921	6165205	Minus	33759-33891
330002	6623963	Plus	46097-46158
330021	6671889	Plus	120938-121032
326162	5867168	Minus	5870-6291
326070	5867175	Plus	132181-132731
326029	5867176	Minus	112558-112669
326033	5867178	Plus	37261-37333
326039	5867179	Minus	15157-15227
326122	5867194	Plus	144397-144683
326136	5867202	Minus	155973-156065
326194	5867213	Plus	75271-75522
326206	5867219	Plus	113881-115080
326218	5867226	Minus	259784-259920
326224	5867230	Plus	21528-21667
326240	5867260	Plus	94843-96127

326253	5867263	Minus	222216-222341
326249	5867263	Minus	80253-80323
326266	5867264	Plus	337993-338192
326304	5867277	Minus	367450-367559
326309	5867277	Plus	614150-614294
326310	5867277	Plus	621555-621698
326338	6056311	Minus	161972-162333
326343	6525295	Minus	2699-2777
326344	6525295	Minus	3207-3365
326073	6682495	Minus	248865-249009
330057	6478962	Plus	75145-75287
330058	6634847	Plus	100602-100963
330061	6721261	Plus	4254-4388
326539	5867307	Plus	198357-198504
326545	5867307	Plus	600850-601425
326549	5867307	Plus	698004-698069
326552	5867308	Minus	6988-7107
326554	5867308	Plus	16259-18271
326559	5867310	Plus	159233-159439
326577	5867317	Plus	215987-216127
326380	5867327	Plus	32474-32668
326412	5867362	Minus	9263-9436
326417	5867362	Plus	89132-89383
326418	5867365	Plus	23609-23745
326423	5867369	Minus	142311-142500
326458	5867400	Plus	128045-128147
326459	5867400	Plus	137590-138212
326506	5867435	Minus	9368-9509
326509	6682496	Plus	92406-92680
330112	6015238	Plus	32059-32163
330086	6015293	Plus	29518-29662
330080	6015314	Minus	4890-4972
330082	6015314	Plus	27158-27296
330064	6165044	Minus	5619-5696
330063	6165044	Minus	948-1025
330065	6165044	Minus	9876-9948
326646	5867562	Plus	100426-100608
326688	5867582	Plus	104875-105531
326708	5867593	Minus	39203-39310
326710	5867593	Minus	80204-80468
326746	5867611	Plus	129366-129565
326793	5867631	Plus	136295-136518
326603	6056312	Minus	50323-50575
326806	6469835	Plus	101628-102149
326783	6525298	Plus	196378-196863
326668	6552455	Plus	146726-146838
326725	6552456	Minus	223005-223125
326857	6552460	Minus	120142-120345
326763	6598307	Plus	239690-239902
326808	6682504	Minus	65107-65214
326874	6682507	Minus	4643-4888
326876	6682507	Minus	46203-46499
326884	6682511	Plus	33403-33479
326997	5867660	Minus	71389-72147
327009	5867664	Plus	933145-933266
327015	5867664	Plus	1030457-1030534
326942	6004446	Minus	88675-88785
326943	6004446	Minus	89242-89427
326957	6469836	Plus	37529-37694
327049	6531965	Minus	1924026-1924110
327051	6531965	Plus	2222592-2222717
327056	6531965	Plus	2374323-2374751
327059	6531965	Plus	2421032-2421799
327067	6531965	Minus	3726023-3726668
327089	6531965	Plus	5238983-5239187
327037	6531965	Minus	387854-388045
327123	6531971	Minus	23980-24340
327125	6531971	Plus	48884-48975
326981	6588016	Plus	105091-106038
330139	4210430	Plus	112089-112450
330153	4325335	Plus	146951-147475
330130	6002196	Minus	241903-241967
327203	5867447	Plus	36485-36577
327206	5867447	Plus	177855-178031
327259	5867454	Plus	87268-87438
327264	5867461	Plus	47014-47367

327273	5867466	Plus	73451-73549
327274	5867470	Minus	84027-84128
327277	5867473	Minus	165616-165715
327278	5867473	Minus	166350-166439
327289	5867481	Plus	49296-49536
327304	5867494	Plus	20664-20850
327315	5867508	Minus	78409-79245
327246	5867547	Plus	136212-136325
327155	5867549	Plus	90343-90876
327159	5867550	Minus	8219-8331
327334	5902477	Minus	142655-142745
327341	6017016	Minus	122906-123014
327185	6117805	Minus	3287-3451
327309	6456757	Minus	10219-10457
327263	6525274	Minus	153814-154920
327362	6552412	Minus	62459-62805
327413	5867750	Plus	101410-101508
327418	5867750	Minus	153453-153547
327430	5867754	Plus	1320-1403
327431	5867754	Plus	1853-1958
327472	5867775	Plus	74628-74937
327487	5867785	Minus	146220-146326
327379	5867795	Plus	1368-1820
327461	6004455	Plus	209031-209210
327532	6469818	Plus	71994-72137
330170	6648220	Plus	103280-103849
330166	6648220	Plus	86542-86867
327544	5867797	Minus	18105-18332
327564	5867811	Plus	13850-14018
327566	5867811	Plus	33383-33901
327581	5867825	Plus	5318-5434
327585	5867825	Plus	85660-85764
327605	6004463	Plus	199214-199579
327710	5867860	Minus	131012-131790
327610	5867868	Minus	174109-174278
327624	5867871	Minus	37699-37788
327641	5867890	Plus	13583-13702
327646	5867894	Minus	3043-3258
327614	6525283	Plus	3634-4001
327736	5867940	Minus	37781-37887
327739	5867942	Minus	182187-182548
327740	5867943	Plus	25716-26077
327743	5867944	Minus	155930-156098
327755	5867955	Minus	61969-62145
327772	5867964	Minus	26185-26285
327774	5867964	Minus	127659-127899
327823	5867968	Minus	170359-170433
327827	5867968	Minus	201918-202048
327833	5867968	Minus	303618-303732
327805	5867968	Plus	19952-20019
327809	5867968	Plus	54610-54761
327816	5867968	Minus	79202-79552
327790	5867977	Plus	19822-19985
327791	5867977	Plus	22491-22610
327793	5867979	Plus	18874-19254
327845	6531962	Plus	193402-193549
327846	6531962	Plus	195216-195373
330204	6013606	Plus	86663-86811
330189	6165182	Minus	26732-26991
330239	6671857	Plus	117484-118092
330266	6671885	Minus	129505-129832
330275	6671904	Plus	103585-103716
330280	6671910	Plus	2109-2377
330286	6671913	Minus	31050-31171
327999	5867994	Plus	94710-94841
328109	5868020	Minus	353895-354525
328098	5868020	Minus	261745-261920
328134	5868039	Plus	72354-72487
328171	5868071	Plus	101102-101224
328221	5868099	Minus	37489-37829
328224	5868101	Plus	105563-105832
328228	5868105	Minus	21488-21596
328236	5868117	Plus	13864-14371
327864	5868130	Plus	59139-59358
327888	5868149	Minus	51964-52120
327899	5868156	Minus	102288-102697

327925	5868172	Minus	118396-118490
327927	5868173	Plus	50989-51246
327937	5868192	Minus	33127-33485
327946	5868206	Plus	44102-44319
327982	5868216	Plus	30307-30527
327990	5868218	Minus	36225-36503
328015	5902482	Minus	477679-478113
328016	5902482	Minus	507572-508519
328025	5902482	Minus	931937-932171
328031	5902482	Plus	1176372-1177283
328053	5902482	Minus	2709850-2710010
328243	6056292	Plus	1-243
328271	6552415	Plus	39015-39098
328592	5868227	Minus	252407-252565
328570	5868231	Plus	89210-89816
328607	5868233	Minus	246798-246944
328620	5868241	Minus	15651-15788
328624	5868246	Minus	120666-120836
328791	5868309	Plus	171592-171929
328810	5868327	Plus	101730-101914
328820	5868330	Plus	90446-90602
328835	5868339	Plus	88053-88461
328282	5868353	Plus	72692-72819
328314	5868371	Minus	288397-288505
328328	5868375	Plus	169210-169407
328420	5868411	Plus	53612-53886
328428	5868417	Plus	13599-13780
328436	5868417	Plus	203760-203904
328444	5868420	Plus	65393-66103
328462	5868433	Plus	49649-49768
328467	5868434	Minus	15954-16073
328474	5868446	Minus	128777-128970
328484	5868454	Minus	21974-22140
328504	5868471	Plus	47064-47217
328506	5868471	Plus	60716-60830
328507	5868473	Minus	199637-199990
328544	5868486	Plus	145659-145829
328552	5868489	Plus	47328-47607
328557	5868489	Plus	138094-138161
328558	5868489	Plus	143648-144108
328276	6004471	Plus	13282-13450
328277	6004471	Minus	279901-280181
328662	6004473	Plus	1184773-1184855
328636	6004473	Plus	192484-192543
328803	6004475	Minus	291716-291948
328305	6004478	Minus	34730-34851
328569	6004480	Plus	232896-233243
328581	6006033	Minus	121249-121400
328582	6006033	Minus	134177-134282
328768	6017031	Minus	223741-224238
328770	6017031	Minus	363933-364166
328841	6381920	Minus	5214-5479
328851	6381923	Plus	2502-2606
328859	6381928	Plus	69045-69138
328860	6381928	Plus	83265-83366
328863	6381929	Minus	29313-29506
328868	6381930	Plus	112825-112993
328876	6525286	Plus	94053-94185
328886	6588003	Plus	31068-31429
328888	6588003	Minus	111901-111999
328936	5868500	Minus	1352202-1352259
328938	5868500	Plus	1522923-1522986
328971	6478806	Minus	23976-24105
330338	5457162	Plus	48406-48518
330327	5919194	Plus	121561-121683
330319	5932415	Plus	49095-50132
328974	5868520	Plus	31557-31668
328981	5868527	Minus	105677-105764
328989	5868535	Plus	182088-182198
330363	3126882	Minus	61838-61901
330370	6580495	Plus	10826-11669
329041	5868564	Plus	141592-141785
329078	5868597	Plus	326798-326860
329097	5868624	Plus	12002-12170
329107	5868626	Plus	101063-101190
329114	5868650	Minus	23792-23910

329116	5868650	Minus	43389-43493
329164	5868691	Plus	62305-62517
329187	5868713	Plus	29909-30175
329201	5868718	Plus	79266-79539
329221	5868727	Minus	105837-105894
329246	5868732	Minus	250541-250792
329254	5868733	Plus	4133-4214
329326	5868806	Plus	155884-155992
329330	5868806	Minus	340278-340403
329382	5868868	Plus	41401-41655
329384	5868869	Minus	116524-116662
329386	6004484	Plus	160502-161110
329140	6017060	Plus	290842-290905
329182	6056331	Minus	662206-663423
329018	6249620	Plus	103950-104034
329319	6381976	Plus	721390-721470
329392	6478815	Plus	109786-109854
329029	6525302	Plus	281445-282490
329401	6682544	Plus	21342-24014
329406	6682547	Plus	47249-47395
329411	6682549	Minus	84558-84835
329429	5868882	Minus	97008-97091
329436	5868883	Plus	230265-230528
329464	6456788	Minus	4437-4538

TABLE 21:
310 GENES UP-REGULATED IN COLON CANCER DERIVED LIVER METASTASES COMPARED TO NORMAL COLON TISSUE

Table 21 shows 310 genes up-regulated in colon cancer derived liver metastases compared to normal colon tissue. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer derived liver metastases to "average" normal colon tissues was greater than or equal to 3.0. The "average" colon cancer derived liver metastases level was set to the 50th percentile. The "average" normal colon tissue level was set to the 50th percentile.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	Genes up mets vs normal

Pkey	ExAccn	UnigeneID	Unigene Title	R1
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	26.72
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	16.36
409041	AB033025	Hs.50081	KIAA1199 protein	13.94
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	13.90
432314	AA533447	Hs.312989	ESTs	12.24
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	11.60
443162	T49951	Hs.9029	DKFZP434G032 protein	9.52
436385	BE551618	Hs.144097	ESTs	9.20
418662	AI801098	Hs.151500	ESTs	9.00
433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	8.90
412093	BE242691	Hs.14947	ESTs	8.74
442369	AI565071	Hs.159983	ESTs	8.40
426101	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	8.39
435937	AA830893	Hs.119769	ESTs	8.22
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	8.22
432572	AI660840	Hs.191202	ESTs, Weakly similar to ALUE_HUMAN II	7.96
440524	R71264	Hs.16798	ESTs	7.94
424878	H57111	Hs.221132	ESTs	7.88
430433	AA478883	Hs.273766	ESTs	7.82
410245	C17908	Hs.194125	ESTs	7.78
417315	AI080042	Hs.336901	ribosomal protein S24	7.76
430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	7.76
432435	BE218886	Hs.282070	ESTs	7.74
426818	AA554827	Hs.289115	DKFZp434A0131 protein	7.58
419145	N99638		gb:za39g11.r1 Soares fetal liver spleen	7.56
444838	AV651680	Hs.208558	ESTs	7.54
428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	7.48
446682	AW205632	Hs.211198	ESTs	7.26
421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	7.19
440116	AI798851	Hs.283108	hemoglobin, gamma G	7.12
450230	AW016607	Hs.201582	ESTs	7.08
456332	AA228357		gb:nc39d05.r1 NCI_CGAP_Pr2 Homo sapiens	7.04
421814	L12350	Hs.108623	thrombospondin 2	6.89
440774	AI420611	Hs.127832	ESTs	6.86
428065	AI634046	Hs.157313	ESTs	6.78
422330	D30783	Hs.115263	epiregulin	6.72
413950	AA249096	Hs.32793	ESTs	6.67
438011	BE466173	Hs.145696	splicing factor (CC1.3)	6.62
421057	T58283	Hs.10450	Homo sapiens cDNA: FLJ22063 fis, clone H	6.58
428698	AA852773	Hs.334838	KIAA1866 protein	6.40
408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	6.38
425787	AA363867	Hs.155029	ESTs	6.38
435812	AA700439	Hs.188490	ESTs	6.32
448974	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	6.28
418875	W19971	Hs.233459	ESTs	6.22
407284	AI539227	Hs.214039	hypothetical protein FLJ23556	6.17
408243	Y00787	Hs.624	interleukin 8	6.12
434936	AI285970	Hs.183817	ESTs	6.12

412088	AI689496	Hs.108932	ESTs	6.04
450377	AB033091	Hs.74313	KIAA1265 protein	6.00
407618	AW054922	Hs.53478	Homo sapiens cDNA FLJ12366 fis, clone MA	5.98
408296	AL117452	Hs.44155	DKFZP586G1517 protein	5.94
456999	AA319798	Hs.298581	eukaryotic translation elongation factor	5.90
432559	AW452948	Hs.257631	ESTs	5.88
423349	AF010258	Hs.127428	homeo box A9	5.84
436100	AA704806	Hs.143842	ESTs, Weakly similar to 2004399A chromos	5.84
453204	R10799	Hs.191990	ESTs	5.84
429183	AB014604	Hs.197955	KIAA0704 protein	5.78
427882	AA640987	Hs.193767	ESTs	5.72
447033	AI357412	Hs.157601	ESTs	5.70
428054	AI948688	Hs.266619	ESTs	5.66
414504	AW069181	Hs.115175	sterile-alpha motif and leucine zipper c	5.64
442806	AW294522	Hs.149991	ESTs	5.64
418259	AA215404	Hs.137289	ESTs	5.60
434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	5.60
419999	AI760942	Hs.191754	ESTs	5.58
431749	AL049263	Hs.306292	Homo sapiens mRNA; cDNA DKFZp564F133 (fr	5.58
422790	AA809875	Hs.25933	ESTs	5.56
440980	AL042005	Hs.1117	tripeptidyl peptidase II	5.48
432451	AW972771	Hs.292471	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.46
438578	AA811244	Hs.164168	ESTs	5.44
410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	5.42
426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific,	5.42
450164	AI239923	Hs.30098	ESTs	5.40
438899	AF085833	Hs.135624	ESTs	5.38
432945	AL043683	Hs.8173	hypothetical protein FLJ10803	5.36
437176	AW176909	Hs.42346	calcineurin-binding protein calsarcin-1	5.34
419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	5.33
407966	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	5.30
447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	5.26
419682	H13139	Hs.92282	paired-like homeodomain transcription fa	5.26
421097	AI280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	5.22
443373	AI792868	Hs.135365	ESTs	5.22
412059	AA317962	Hs.249721	ESTs, Moderately similar to PC4259 ferri	5.21
443651	W22152	Hs.282929	ESTs	5.21
411274	NM_002776	Hs.69423	kallikrein 10	5.17
421999	U50535	Hs.110630	Human BRCA2 region, mRNA sequence CG006	5.17
426981	AL044675	Hs.173081	KIAA0530 protein	5.14
431319	AA873350	Hs.302232	ESTs	5.10
434966	AA657494		gb:nt66f04.s1 NCI_CGAP_Pr3 Homo sapiens	5.10
418830	BE513731	Hs.88959	hypothetical protein MGC4816	5.08
428290	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	5.07
408784	AW971350	Hs.63386	ESTs	5.04
411975	AI916058	Hs.144583	ESTs	5.02
409760	AA302840		gb:EST10534 Adipose tissue, white I Homo	4.97
420717	AA284447	Hs.271887	ESTs	4.96
417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	4.95
434442	AA737415	Hs.152826	ESTs	4.94
441328	AI982794	Hs.159473	ESTs	4.92
438962	BE046594		gb:hr41c11.x1 NCI_CGAP_RDF2 Homo sapiens	4.92
451277	AK001123	Hs.26176	hypothetical protein FLJ10261	4.92
438406	BE273296	Hs.254467	Homo sapiens cDNA FLJ13255 fis, clone OV	4.90
424950	AA602917	Hs.156974	ESTs	4.88
436823	AW749865	Hs.293645	ESTs, Weakly similar to I38022 hypotheti	4.87
444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	4.82
444301	AK000136	Hs.10760	asporin (LRR class 1)	4.80
445390	AI222165	Hs.144923	ESTs	4.80
439608	AW864696	Hs.301732	hypothetical protein MGC5306	4.78
450506	NM_004460	Hs.418	fibroblast activation protein, alpha	4.78
432682	AI376400	Hs.159588	ESTs	4.76
426086	T94907	Hs.188572	ESTs	4.76
435981	H74319	Hs.188620	ESTs	4.74
432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	4.72
435756	AI418466	Hs.33665	ESTs	4.72
447982	H22953	Hs.137551	ESTs	4.72
449509	AA001615	Hs.84561	ESTs	4.72
407946	AA226495	Hs.154292	ESTs	4.70
426215	AW963419	Hs.155223	stanniocalcin 2	4.70
414783	AW069569	Hs.278270	inactive progesterone receptor, 23 kD	4.68
417601	NM_014735	Hs.82292	KIAA0215 gene product	4.68
438461	AW075485	Hs.286049	phosphoserine aminotransferase	4.68
449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	4.68
426501	AW043782	Hs.293616	ESTs	4.67
409024	AW883529	Hs.173830	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.67

439848	AW979249		gb:EST391359 MAGE resequences, MAGP Homo	4.66
424762	AL119442	Hs.183684	eukaryotic translation initiation factor	4.66
442007	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	4.62
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	4.62
432409	AA806538	Hs.130732	KIAA1575 protein	4.60
452220	BE158006	Hs.212296	ESTs	4.60
442577	AA292998	Hs.163900	ESTs	4.58
434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	4.58
414271	AK000275	Hs.75871	protein kinase C binding protein 1	4.58
433854	AA610649	Hs.333239	ESTs	4.56
431315	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	4.53
434220	AI174777	Hs.283039	Homo sapiens PRO2492 mRNA, complete cds	4.50
457752	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	4.50
449941	AW450536	Hs.209260	ESTs	4.48
415116	AA160363	Hs.269956	ESTs	4.47
414386	X00442	Hs.75990	haptoglobin	4.47
422956	BE545072	Hs.122579	hypothetical protein FLJ10461	4.44
423974	AL118754		gb:DKFZp761P1910_r1 761 (synonym: hamy2)	4.44
449618	AI076459	Hs.15978	KIAA1272 protein	4.44
428279	AA425310	Hs.155766	ESTs, Weakly similar to A47582 B-cell gr	4.42
430573	AA744550	Hs.136345	ESTs	4.42
430929	AA489166	Hs.156933	ESTs	4.40
433530	BE349534	Hs.281789	ESTs	4.40
446099	T93096	Hs.17126	hypothetical protein MGC15912	4.40
447082	T85314	Hs.42644	thioredoxin-like	4.39
407168	R45175	Hs.117183	ESTs	4.38
417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	4.38
408380	AF123050	Hs.44532	diubiquitin	4.36
431379	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	4.36
406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	4.34
419317	AA236282	Hs.172318	ESTs	4.32
450295	AI766732	Hs.210628	ESTs	4.32
423578	AW960454	Hs.222830	ESTs	4.31
419553	N34145	Hs.250614	ESTs, Moderately similar to ZN91_HUMAN Z	4.31
429512	AA453987	Hs.144802	ESTs	4.30
426848	H72531	Hs.36190	ESTs	4.30
429831	AA564489	Hs.137526	ESTs	4.30
433735	AA608955	Hs.109653	ESTs	4.30
450546	AA010200	Hs.175551	ESTs	4.27
421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	4.27
413243	AA769266	Hs.193657	ESTs	4.26
433230	AW136134	Hs.220277	ESTs	4.22
439717	W94472	Hs.59529	ESTs, Moderately similar to ALU1_HUMAN A	4.20
439362	AI954880	Hs.134604	ESTs	4.19
450157	AW961576	Hs.60178	ESTs	4.17
451690	AW451469	Hs.209990	ESTs	4.17
418661	NM_001949	Hs.1189	E2F transcription factor 3	4.16
443135	AI376331	Hs.156103	ESTs	4.16
443148	AI034357	Hs.211194	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.16
407765	AW076027	Hs.257711	ESTs, Moderately similar to ALU8_HUMAN A	4.14
428825	AI084336	Hs.128783	ESTs, Weakly similar to I38022 hypotheti	4.14
447519	U46258	Hs.339665	ESTs	4.14
439451	AF086270	Hs.278554	heterochromatin-like protein 1	4.12
450219	AI826999	Hs.224624	ESTs	4.12
431451	AA761378	Hs.192013	ESTs	4.11
432917	NM_014125	Hs.279812	PRO0327 protein	4.10
431328	AA502999	Hs.291591	ESTs	4.09
425992	AA367069	Hs.100636	ESTs	4.08
404571				4.06
420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	4.06
421114	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	4.06
432731	R31178	Hs.287820	fibronectin 1	4.06
433588	AI056872	Hs.133386	ESTs	4.06
434658	AI624436	Hs.310286	ESTs	4.06
444040	AF204231	Hs.182982	golgin-67	4.06
444984	H15474	Hs.132898	fatty acid desaturase 1	4.06
438543	AA810141	Hs.192182	ESTs	4.05
413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	4.04
434575	AI133446	Hs.299964	Homo sapiens clone FLB7723 PRO2055 mRNA,	4.04
430256	AA470152	Hs.192195	ESTs	4.04
424839	AA740632	Hs.120850	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.02
429048	AI372949	Hs.44241	Homo sapiens cDNA: FLJ21447 fis, clone C	4.02
449429	AA054224	Hs.59847	ESTs	4.02
410762	AF226053	Hs.66170	HSKM-B protein	4.00
418876	AA740616		gb:ny97f11.s1 NCL CGAP_GCB1 Homo sapiens	4.00
425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	4.00

429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	4.00
431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.00
435008	AF150262	Hs.162898	ESTs	4.00
431361	AW971375	Hs.292921	ESTs	3.97
444816	Z48633	Hs.283742	H.sapiens mRNA for retrotransposon	3.96
434701	AA460479	Hs.321707	KIAA0742 protein	3.96
413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	3.95
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	3.92
428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	3.91
435714	AA699325	Hs.269880	ESTs	3.86
447514	AI809314	Hs.208501	ESTs, Weakly similar to B34087 hypothei	3.86
453818	BE256832	Hs.10711	hypothetical protein FLJ13449	3.85
433586	T85301		gb:yd78d06.s1 Soares fetal liver spleen	3.85
440638	AI376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	3.85
417819	AI253112	Hs.133540	ESTs	3.84
409596	BE244200	Hs.55075	KIAA0410 gene product	3.83
423129	L44396	Hs.124106	Homo sapiens cDNA FLJ11941 fis, clone HE	3.83
453884	AA355925	Hs.36232	KIAA0186 gene product	3.83
431193	AW749505	Hs.296770	KIAA1719 protein	3.81
409262	AK000631	Hs.52256	hypothetical protein FLJ20624	3.80
425568	AW963118	Hs.161784	ESTs	3.78
441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.77
428079	AA421020	Hs.208919	ESTs	3.77
412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	3.76
435354	AA678267	Hs.117115	ESTs	3.75
436535	AW295687	Hs.254420	ESTs	3.74
420439	AW270041	Hs.193053	eukaryotic translation initiation factor	3.72
436090	AI640635	Hs.116468	EST	3.71
416265	AA177088	Hs.190065	ESTs	3.70
417715	AW969587	Hs.86366	ESTs	3.67
435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	3.67
438607	AW080237	Hs.252884	ESTs	3.66
408194	AA601038	Hs.191797	ESTs, Weakly similar to S65657 alpha-1C-	3.65
417211	T97617	Hs.269092	ESTs	3.60
435538	AB011540	Hs.4930	low density lipoprotein receptor-related	3.59
410390	AA876905	Hs.125286	ESTs	3.58
438818	AW979008	Hs.222487	ESTs	3.57
431416	AA532718	Hs.178604	ESTs	3.57
433517	AW022133	Hs.189838	ESTs	3.56
428355	BE256452	Hs.2257	vitronectin (serum spreading factor, som	3.56
432954	AI076345	Hs.214199	ESTs	3.53
434466	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	3.53
421933	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	3.52
422082	AA016188	Hs.111244	hypothetical protein	3.52
437135	AL038624	Hs.208752	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.49
424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	3.49
434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	3.49
407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	3.48
417670	R07785		gb:yf15c06.r1 Soares fetal liver spleen	3.48
431615	AW295859	Hs.235860	ESTs	3.48
429355	AW973253	Hs.292689	ESTs	3.45
430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	3.45
432929	AW207166	Hs.191265	ESTs	3.44
437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	3.44
445674	BE410347	Hs.13063	transcription factor CA150	3.42
408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3.42
408908	BE296227	Hs.250822	serine/threonine kinase 15	3.41
432235	AA531129	Hs.190297	ESTs	3.41
453985	N44545	Hs.251865	ESTs	3.41
415736	AA827082	Hs.291872	ESTs	3.38
430220	BE378277	Hs.152230	ESTs	3.37
426510	AW861225	Hs.194637	BANP homolog, SMAR1 homolog	3.37
412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	3.36
411573	AB029000	Hs.70823	KIAA1077 protein	3.33
413816	AW958181	Hs.189998	ESTs	3.32
428057	AI343641	Hs.185798	ESTs	3.32
436280	AI690734	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.31
449365	AW968261	Hs.118913	ESTs, Moderately similar to T46371 hypot	3.31
440659	AF134160	Hs.7327	claudin 1	3.30
436110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypothei	3.29
433862	D86960	Hs.3610	KIAA0205 gene product	3.29
424624	AB032947	Hs.151301	Ca2+-dependent activator protein for secr	3.29
439955	AW203959	Hs.149532	ESTs	3.28
417333	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	3.28
436150	AW510927	Hs.125243	ESTs	3.27
414900	AW452420	Hs.248678	ESTs	3.26

439349	AI660898	Hs.195602	ESTs	3.25
428255	AI627478	Hs.187670	ESTs	3.24
436217	T53925	Hs.107	fibrinogen-like 1	3.24
429083	Y09397	Hs.227817	BCL2-related protein A1	3.24
422244	Y08890	Hs.113503	karyopherin (importin) beta 3	3.22
430178	AW449612	Hs.152475	ESTs	3.21
413810	AW197644	Hs.19107	ESTs	3.20
428728	NM_016625	Hs.191381	hypothetical protein	3.20
437151	AA745618	Hs.194637	BANP homolog, SMAR1 homolog	3.19
427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	3.19
438378	AW970529	Hs.86434	hypothetical protein FLJ21816	3.19
439943	AW083789	Hs.124620	ESTs	3.18
439280	AI125436	Hs.48752	ESTs	3.18
452336	AA960961	Hs.305953	zinc finger protein 83 (HPF1)	3.17
433713	AW976511	Hs.112592	ESTs	3.16
414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	3.14
407328	AA508857	Hs.187748	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.14
432722	AA830532	Hs.326150	ESTs	3.14
419457	AA243146	Hs.209334	ESTs, Moderately similar to S23A_HUMAN P	3.11
449987	AW079749	Hs.184719	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.11
418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	3.09
409969	AW514668	Hs.194258	ESTs, Moderately similar to ALU5_HUMAN A	3.08
436299	AK000767	Hs.5111	hypothetical protein FLJ20729	3.08
406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	3.07
408242	AA251594	Hs.43913	PIBF1 gene product	3.07
444614	R44284	Hs.2730	heterogeneous nuclear ribonucleoprotein	3.06
459407	N92114		gb:za22h11.r1 Soares fetal liver spleen	3.05
433972	AI878910	Hs.3688	cisplatin resistance-associated overexpr	3.04
427704	AW971063	Hs.292882	ESTs	3.03
440255	AI932285	Hs.160569	ESTs	3.03
424542	AI860558	Hs.272009	ESTs, Weakly similar to ALU2_HUMAN ALU S	3.03
413822	R08950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.02
433944	AL117518	Hs.3686	KIAA0978 protein	3.01
440428	BE560954		gb:601347719F1 NIH_MGC_8 Homo sapiens cD	3.00

TABLE 21A

Table 21A shows the accession numbers for those pkeys lacking unigeneID's for Table 21A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT Number Accession

409760	115373_1	AA302840 T93016 T92950 AA077551
413497	1373771_1	BE177661 H06215 BE144709 BE144829
417670	1692163_1	R07785 T85948 T86972
418876	179960_1	AA740616 AA654854 AA229923
419145	182217_1	N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815
423974	233842_1	AL118754 AA333202 H38001
430068	312849_1	AA464964 M85405 AA947566
432340	345248_1	AA534222 AA632632 T81234
433586	370470_1	T85301 AW517087 AA601054 BE073959
434280	382816_1	BE005398 AA628622 AA994155
434966	396504_1	AA657494 AI582663 AI581639
438962	467390_1	BE046594 BE046667 AA828585 AI207343
439848	477806_1	AW979249 D63277 AA846968
440428	49370_1	BE560954
440638	499025_1	AI376551 T87714 AA897445
456332	179104_1	AA228357 AW841786 AW841716

TABLE 21B

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
404571	7249169	Minus	112450-112648

TABLE 22: 177 GENES DOWN-REGULATED IN COLON CANCER DERIVED LIVER METASTASES COMPARED TO NORMAL COLON TISSUE

Table 22 shows 177 genes down-regulated in colon cancer derived liver metastases compared to normal colon tissue. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer derived liver metastases to "average" normal colon tissues was less than or equal to 0.25. The "average" colon cancer derived liver metastases level was set to the 50th percentile. The "average" normal adult tissue level was set to the 50th percentile.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Genes down mets vs. normal

Pkey	ExAccn	UnigeneID	Unigene Title	R1
425196	AL037915	Hs.155097	carbonic anhydrase II	0.03
414522	AW518944	Hs.76325	step II splicing factor SLU7	0.03
409153	W03754	Hs.50813	hypothetical protein FLJ20022	0.03
452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	0.03
424326	NM_014479	Hs.145296	disintegrin protease	0.04
414798	AJ286323	Hs.97411	hypothetical protein MGC12335	0.04
432150	AK000224	Hs.272789	hypothetical protein FLJ20217	0.04
425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	0.05
437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	0.05
447513	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A	0.05
414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	0.06
428934	AF039401	Hs.194659	chloride channel, calcium activated, fam	0.06
432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	0.07
431727	AW293464	Hs.162031	ESTs	0.07
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	0.07
414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	0.08
412047	AA934589	Hs.49696	ESTs	0.08
412056	T28160	Hs.778	guanylate cyclase activator 1B (retina).	0.08
422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	0.08
450684	AA872605	Hs.25333	interleukin 1 receptor, type II	0.09
418935	T28499	Hs.89485	carbonic anhydrase IV	0.09
433658	L03678	Hs.156110	immunoglobulin kappa constant	0.09
422260	AA315993	Hs.105484	regenerating gene type IV	0.09
433336	AF017986	Hs.31386	secreted frizzled-related protein 2	0.09
426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	0.09
441888	AI733306	Hs.128071	hypothetical protein FLJ21302	0.10
440624	AF017987	Hs.7306	secreted frizzled-related protein 1	0.10
420929	AI694143	Hs.296251	programmed cell death 4	0.10
429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	0.10
417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	0.10
414802	AI793107	Hs.27018	Ris	0.10
424566	M16801	Hs.1790	nuclear receptor subfamily 3, group C, m	0.11
421996	AW583807	Hs.1460	glucagon	0.11
423371	AU076819	Hs.1650	solute carrier family 26, member 3	0.11
406741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	0.11
414176	BE140638	Hs.75794	endothelial differentiation, lysophospha	0.11
408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	0.11
424527	AW138558	Hs.267158	ESTs, Weakly similar to I54374 gene NF2	0.12
426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	0.12
453967	AW009077	Hs.232947	ESTs	0.12
425920	AL049977	Hs.162209	claudin 8	0.13
408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiester	0.13
457407	AA505035	Hs.195651	ESTs	0.13
446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	0.14
422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	0.14
409196	NM_001874	Hs.334873	carboxypeptidase M	0.14
416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	0.14
406636	L12064		gb:Homo sapiens (clone WR4.12VL) anti-th	0.14

457982	AW856093	Hs.183617	ESTs	0.14
407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	0.14
430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	0.14
424885	AI333771	Hs.82204	ESTs	0.14
423555	AW958201	Hs.178589	hepatocellular carcinoma antigen gene 52	0.14
444237	AA336878	Hs.9842	Human DNA sequence from clone RP4-788L20	0.14
445848	AA774824	Hs.13377	Homo sapiens clone 23649 and 23755 unkno	0.14
451062	AL110125	Hs.25910	Homo sapiens mRNA; cDNA DKFZp564C1416 (f	0.14
436485	X59135	Hs.156110	immunoglobulin kappa constant	0.14
423655	AA722425	Hs.182785	ESTs, Moderately similar to 1207289A rev	0.15
417332	AW972717	Hs.288462	hypothetical protein FLJ21511	0.15
427506	AK000134	Hs.179100	hypothetical protein FLJ20127	0.15
430712	AW044647	Hs.196284	ESTs	0.15
421666	AL035250	Hs.1408	endothelin 3	0.16
425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	0.16
429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	0.16
433745	AF075320	Hs.28980	hypothetical protein FLJ14540	0.16
450085	AW293791	Hs.60162	Homo sapiens cDNA: FLJ21528 fis, clone C	0.16
417820	D87449	Hs.82635	UDP-glucuronic acid/UDP-N-acetylgalactos	0.16
406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	0.16
426488	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	0.16
436327	AA813075	Hs.120181	ESTs	0.16
408873	AL046017	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	0.16
429524	AB033037	Hs.205293	KIAA1211 protein	0.16
447023	AA356764	Hs.17109	integral membrane protein 2A	0.17
424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	0.17
410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	0.17
432563	NM_013261	Hs.198468	peroxisome proliferative activated recep	0.17
406897	M57417		gb:Homo sapiens mucin (mucin) mRNA, part	0.17
451096	BE383234	Hs.25925	Homo sapiens, clone MGC:15393, mRNA, com	0.17
447726	AL137638	Hs.19368	matrilin 2	0.17
409549	AB029015	Hs.54886	phospholipase C, epsilon 2	0.17
433334	AI927208	Hs.231958	matrix metalloproteinase 28	0.17
425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	0.17
407360	X13075		gb:Human 2a12 mRNA for kappa-immunoglobu	0.17
430627	U61148	Hs.247685	atonal homolog 1 (Drosophila)	0.17
418807	NM_004944	Hs.88646	deoxyribonuclease I-like 3	0.18
453399	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	0.18
422994	AW891802	Hs.296276	ESTs	0.18
432134	AI816782	Hs.122583	hypothetical protein FLJ21934	0.18
400417	X72475			0.18
443506	H10661	Hs.192124	ESTs, Weakly similar to I38022 hypotheti	0.18
428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	0.18
451928	AI823801	Hs.30315	CTCL tumor antigen se57-1	0.18
429576	BE242628	Hs.209061	sudD (suppressor of blmD6, Aspergillus n	0.18
422106	D84239	Hs.111732	Fc fragment of IgG binding protein	0.19
430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFZp434H1235 (f	0.19
452852	AK001972	Hs.30822	hypothetical protein FLJ11110	0.19
421904	BE143533	Hs.109309	hypothetical protein FLJ20035	0.19
417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	0.19
417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	0.19
452802	AU076403	Hs.323468	electron-transferring-flavoprotein dehyd	0.19
450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	0.19
420061	AW024937	Hs.29410	ESTs	0.19
426828	NM_000020	Hs.172670	activin A receptor type II-like 1	0.19
408190	AB032963	Hs.43577	ATPase, Class I, type 8B, member 2	0.19
437682	AA476652	Hs.94952	Homo sapiens cDNA: FLJ23371 fis, clone H	0.19
449110	H56112		gb:yq95f07.r1 Soares fetal liver spleen	0.19
446727	AB011095	Hs.16032	KIAA0523 protein	0.19
408395	BE072425	Hs.44579	hypothetical protein FLJ20199	0.20
423541	AA296922	Hs.129778	gastrointestinal peptide	0.20
410850	AW362867	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	0.20
412420	AL035668	Hs.73853	bone morphogenetic protein 2	0.20
423942	AF209704	Hs.135723	glycolipid transfer protein	0.20
421832	NM_016098	Hs.108725	HSPC040 protein	0.20
459046	AA910339	Hs.26216	LOC50627	0.20
421360	AA297012	Hs.103839	erythrocyte membrane protein band 4.1-II	0.20
438091	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m	0.20
403047				0.20
421712	AK000140	Hs.107139	hypothetical protein	0.20
427333	AF067797	Hs.176658	aquaporin 8	0.20
421964	X73079	Hs.288579	polymeric immunoglobulin receptor	0.20
438089	W05391	Hs.83623	nuclear receptor subfamily 1, group I, m	0.21
445200	AA084460	Hs.12409	somatostatin	0.21
404854				0.21
426390	AA377299	Hs.90431	ESTs	0.21

403381				0.21
449833	R82252	Hs.106106	protein kinase (cAMP-dependent, catalytic)	0.21
457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	0.21
435730	AB020635	Hs.4984	KIAA0828 protein	0.21
431518	AA743462	Hs.165337	ESTs	0.21
412589	R28660	Hs.24305	ESTs	0.21
432584	AA928829	Hs.47099	hypothetical protein FLJ21212	0.21
426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	0.21
429143	AA333327	Hs.197335	plasma glutamate carboxypeptidase	0.21
414429	R51494	Hs.71818	ESTs	0.22
439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	0.22
406697	M21388	Hs.123017	Human unproductively rearranged Ig mu-ch	0.22
406663	U24683	Hs.302063	immunoglobulin heavy constant mu	0.22
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	0.22
417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	0.22
430107	AA465293	Hs.105069	ESTs	0.22
424273	W40460	Hs.144442	phospholipase A2, group X	0.22
419559	Y07828	Hs.91096	ring finger protein	0.22
413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	0.22
407243	AA058357	Hs.74466	cardioembryonic antigen-related cell ad	0.22
433906	AI167816	Hs.43355	ESTs	0.22
446203	Z47553	Hs.14286	flavin containing monooxygenase 5	0.22
403740				0.22
405701				0.22
413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	0.22
419577	L36531	Hs.91296	Integrin, alpha 8	0.23
451820	AW058357	Hs.337353	ESTs	0.23
424897	D63216	Hs.153684	frizzled-related protein	0.23
422880	AF228704	Hs.121524	glutathione reductase	0.23
430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	0.23
430753	AI432401	Hs.2659	fibrinogen-like 2	0.23
409060	AI815867	Hs.50130	necdin (mouse) homolog	0.23
412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	0.24
414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	0.24
417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	0.24
414589	AA149791	Hs.68864	ESTs, Weakly similar to phosphatidylseri	0.24
427167	AI239607	Hs.99196	hypothetical protein MGC11324	0.24
440630	BE561430	Hs.239388	Human DNA sequence from clone RP1-304B14	0.24
423044	AA320829	Hs.97266	protocadherin 18	0.24
441931	BE564830	Hs.23744	hypothetical protein FLJ12899	0.24
443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	0.24
405441				0.24
407241	M34516		gb:Human omega light chain protein 14.1	0.24
415165	AW887604	Hs.78065	complement component 7	0.24
426447	AV655843	Hs.169919	electron-transfer-flavoprotein, alpha po	0.24
410748	BE383816	Hs.12532	chromosome 1 open reading frame 21	0.24
436032	AA150797	Hs.109276	latexin protein	0.24
414256	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr	0.24
414197	W44877	Hs.55501	ESTs	0.24
406836	AW514501	Hs.156110	immunoglobulin kappa constant	0.24
437083	AW082597	Hs.244862	ESTs	0.25
421709	AA159394	Hs.107056	CED-6 protein	0.25
426512	AW511656	Hs.170177	Meis1 (mouse) homolog	0.25

TABLE 22A

Table 22A shows the accession numbers for those pkeys lacking unigeneID's for Tables 21A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset Identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT Number Accession

449110 798430_1 H56112 H58047 A1630710 N58742

TABLE 22B

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
403047	3540153	Minus	59793-59968
403381	9438267	Minus	26009-26178
403740	7630882	Plus	86504-87227
404854	7143420	Plus	14260-14537
405441	7408124	Plus	100952-101283
405701	4263751	Plus	93243-93364

TABLE 23: 175 GENES UP-REGULATED IN COLON CANCER DERIVED LIVER METASTASES COMPARED TO COLON CANCER PRIMARY TUMOR SAMPLES CLASSIFIED AS DUKE'S B SURVIVOR

Table 23 shows 175 genes up-regulated in colon cancer derived liver metastases compared to colon cancer primary tumor samples classified as Duke's B stage with a positive survival outcome (Duke's B survivor). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer derived liver metastases to "average" Duke's B survivor was greater than or equal to 3.0. The "average" colon cancer derived liver metastases level was set to the 50th percentile. The "average" Duke's B survivor level was set to the 50th percentile.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	Genes up liver metastases vs Duke's B survivors

Pkey	ExAccn	UnigeneID	Unigene Title	R1
426101	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	9.06
432572	AI660840	Hs.191202	ESTs, Weakly similar to ALUE_HUMAN IIII	7.96
424878	H57111	Hs.221132	ESTs	7.88
428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	7.48
407284	AI539227	Hs.214039	hypothetical protein FLJ23556	7.45
439943	AW083789	Hs.124620	ESTs	7.00
442369	AI565071	Hs.159983	ESTs	7.00
415116	AA160363	Hs.269956	ESTs	6.98
433517	AW022133	Hs.189838	ESTs	6.70
437176	AW176909	Hs.42346	calcineurin-binding protein calsarcin-1	6.68
440524	R71264	Hs.16798	ESTs	6.62
408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	6.38
448974	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f6.28	6.28
412088	AI689496	Hs.108932	ESTs	6.04
417670	R07785		gb:rf15c06.r1 Soares fetal liver spleen	5.95
440774	AI420611	Hs.127832	ESTs	5.91
426086	T94907	Hs.188572	ESTs	5.90
436100	AA704806	Hs.143842	ESTs, Weakly similar to 2004399A chromos	5.84
453204	R10799	Hs.191990	ESTs	5.84
407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	5.67
432435	BE218886	Hs.282070	ESTs	5.61
434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	5.60
421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	5.54
407328	AA508857	Hs.187748	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.51
440980	AL042005	Hs.1117	tripeptidyl peptidase II	5.48
443651	W22152	Hs.282929	ESTs	5.42
412668	AA456195	Hs.10056	hypothetical protein FLJ14621	5.29
444838	AV651680	Hs.208558	ESTs	5.24
433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	5.11
430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	5.11
434966	AA657494		gb:nt66f04.s1 NCI_CGAP_Pr3 Homo sapiens	5.10
426897	AW976570	Hs.97387	ESTs	5.08
432954	AI076345	Hs.214199	ESTs	5.07
431416	AA532718	Hs.178604	ESTs	5.00
420717	AA284447	Hs.271887	ESTs	4.96
424950	AA602917	Hs.156974	ESTs	4.94
438962	BE046594		gb:hn41c11.x1 NCI_CGAP_RDF2 Homo sapiens	4.92
419999	AI760942	Hs.191754	ESTs	4.89
435812	AA700439	Hs.188490	ESTs	4.86
418662	AI801098	Hs.151500	ESTs	4.79
428065	AI634046	Hs.157313	ESTs	4.77
407618	AW054922	Hs.53478	Homo sapiens cDNA FLJ12366 fis, clone MA	4.75
435981	H74319	Hs.188620	ESTs	4.74
419145	N99638		gb:za39g11.r1 Soares fetal liver spleen	4.73
432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	4.72
447982	H22953	Hs.137551	ESTs	4.72

449509	AA001615	Hs.84561	ESTs	4.72
407946	AA226495	Hs.154292	ESTs	4.70
438607	AW080237	Hs.252884	ESTs	4.68
438406	BE273296	Hs.254467	Homo sapiens cDNA FLJ13255 fis, clone OV	4.62
426818	AA554827	Hs.289115	DKFZp434A0131 protein	4.62
452220	BE158006	Hs.212296	ESTs	4.60
436823	AW749865	Hs.293645	ESTs, Weakly similar to I38022 hypotheti	4.60
433854	AA610649	Hs.333239	ESTs	4.56
413816	AW958181	Hs.189998	ESTs	4.52
428079	AA421020	Hs.208919	ESTs	4.52
421097	AI280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	4.50
417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	4.48
423974	AL118754		gb:DKFZp761P1910_r1 761 (synonym: hamy2)	4.44
449618	AI076459	Hs.15978	KIAA1272 protein	4.44
431615	AW295859	Hs.235860	ESTs	4.44
418876	AA740616		gb:ny97f11.s1 NCL CGAP_GCB1 Homo sapiens	4.43
428279	AA425310	Hs.155766	ESTs, Weakly similar to A47582 B-cell gr	4.42
430573	AA744550	Hs.136345	ESTs	4.42
430929	AA489166	Hs.156933	ESTs	4.40
446099	T93096	Hs.17126	hypothetical protein MGC15912	4.40
439362	AI954880	Hs.134604	ESTs	4.38
421999	U50535	Hs.110630	Human BRCA2 region, mRNA sequence CG006	4.35
434220	AI174777	Hs.283039	Homo sapiens PRO2492 mRNA, complete cds	4.33
432925	AA878324	Hs.192734	ESTs	4.32
417819	AI253112	Hs.133540	ESTs	4.30
426848	H72531	Hs.36190	ESTs	4.30
429831	AA564489	Hs.137526	ESTs	4.30
433735	AA608955	Hs.109653	ESTs	4.30
418884	AA230228	Hs.59197	ESTs	4.28
413243	AA769266	Hs.193657	ESTs	4.26
431749	AL049263	Hs.306292	Homo sapiens mRNA; cDNA DKFZp564F133 (fr	4.23
428054	AI948688	Hs.266619	ESTs	4.22
413967	AW204431	Hs.117853	ESTs, Weakly similar to I38022 hypotheti	4.22
433230	AW136134	Hs.220277	ESTs	4.22
421057	T58283	Hs.10450	Homo sapiens cDNA: FLJ22063 fis, clone H	4.22
423578	AW960454	Hs.222830	ESTs	4.21
439717	W94472	Hs.59529	ESTs, Moderately similar to ALU1_HUMAN A	4.20
443696	AW607444	Hs.134622	ESTs	4.20
432722	AA830532	Hs.326150	ESTs	4.18
435756	AI418466	Hs.33665	ESTs	4.14
428825	AI084336	Hs.128783	ESTs, Weakly similar to I38022 hypotheti	4.14
439451	AF086270	Hs.278554	heterochromatin-like protein 1	4.12
445943	AW898533	Hs.181574	ESTs	4.12
450219	AI826999	Hs.224624	ESTs	4.12
431379	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	4.11
432451	AW972771	Hs.292471	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.10
443148	AI034357	Hs.211194	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.08
450177	AI698091	Hs.107845	ESTs	4.08
420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	4.06
421114	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	4.06
432731	R31178	Hs.287820	fibronectin 1	4.06
433588	AI056872	Hs.133386	ESTs	4.06
434658	AI624436	Hs.310286	ESTs	4.06
444040	AF204231	Hs.182982	golgin-67	4.06
429512	AA453987	Hs.144802	ESTs	4.06
443349	AI052572	Hs.269864	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.04
439867	AA847510	Hs.161292	ESTs	4.04
425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	4.02
431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.00
432125	AW972667	Hs.287510	Homo sapiens cDNA FLJ12300 fis, clone MA	4.00
435468	AW362803	Hs.166271	ESTs	3.97
412059	AA317962	Hs.249721	ESTs, Moderately similar to PC4259 ferri	3.95
446682	AW205632	Hs.211198	ESTs	3.95
441328	AI982794	Hs.159473	ESTs	3.92
455778	BE088746		gb:CM2-BT0693-210300-123-d09 BT0693 Homo	3.90
438996	AW748336	Hs.168052	KIAA0421 protein	3.86
418303	AA215701	Hs.186541	ESTs, Weakly similar to I38022 hypotheti	3.85
444816	Z48633	Hs.283742	H.sapiens mRNA for retrotransposon	3.84
429355	AW973253	Hs.292689	ESTs	3.83
438578	AA811244	Hs.164168	ESTs	3.83
432945	AL043683	Hs.8173	hypothetical protein FLJ10803	3.83
435318	T97301	Hs.18026	ESTs	3.82
449941	AW450536	Hs.209260	ESTs	3.80
424915	R42755	Hs.23096	ESTs	3.76
449987	AW079749	Hs.184719	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.76
416265	AA177088	Hs.190065	ESTs	3.75

413497	BE177661	gb:RC1-HT0598-020300-011-h02 HT0598 Homo	3.74
412093	BE242691	Hs.14947 ESTs	3.74
413822	R08950	Hs.272044 ESTs, Weakly similar to ALU1_HUMAN ALU S	3.73
431915	AK000777	Hs.272197 Homo sapiens cDNA FLJ20770 fis, clone CO	3.68
434442	AA737415	Hs.152826 ESTs	3.63
434959	AW974949	Hs.186564 ESTs, Weakly similar to I38022 hypotheti	3.63
427704	AW971063	Hs.292882 ESTs	3.62
426510	AW861225	Hs.194637 BANP homolog, SMAR1 homolog	3.60
435714	AA699325	Hs.269880 ESTs	3.60
432598	AI341227	Hs.157106 ESTs	3.57
438543	AA810141	Hs.192182 ESTs	3.55
422068	AI807519	Hs.104520 Homo sapiens cDNA FLJ13694 fis, clone PL	3.54
418259	AA215404	Hs.137289 ESTs	3.54
428290	AI932995	Hs.183475 Homo sapiens clone 25061 mRNA sequence	3.49
419457	AA243146	Hs.209334 ESTs, Moderately similar to S23A_HUMAN P	3.47
439312	AA833902	Hs.270745 ESTs	3.47
408784	AW971350	Hs.63386 ESTs	3.45
456332	AA228357	gb:nc39d05.r1 NCI_CGAP_Pr2 Homo sapiens	3.45
424762	AL119442	Hs.183684 eukaryotic translation initiation factor	3.44
442884	AI076570	Hs.134053 ESTs	3.44
421023	AW449855	Hs.96557 Homo sapiens cDNA FLJ12727 fis, clone NT	3.43
434575	AI133446	Hs.299964 Homo sapiens clone FLB7723 PRO2055 mRNA,	3.42
430433	AA478883	Hs.273766 ESTs	3.39
419317	AA236282	Hs.172318 ESTs	3.38
448710	T62926	Hs.304184 ESTs	3.37
439322	H72245	Hs.188635 ESTs	3.37
430332	R51790	Hs.239483 Human clone 23933 mRNA sequence	3.35
411755	BE327036	Hs.117494 ESTs	3.33
427882	AA640987	Hs.193767 ESTs	3.28
438899	AF085833	Hs.135624 ESTs	3.28
436535	AW295687	Hs.254420 ESTs	3.25
434936	AI285970	Hs.183817 ESTs	3.22
451730	AF095687	Hs.26937 brain and nasopharyngeal carcinoma suscep	3.18
447514	AI809314	Hs.208501 ESTs, Weakly similar to B34087 hypotheti	3.18
413672	BE156536	gb:QV0-HT0368-310100-091-h10 HT0368 Homo	3.16
435073	AA664078	gb:ac04a05.s1 Stratagene lung (937210) H	3.13
450295	AI766732	Hs.210628 ESTs	3.13
419341	N71463	Hs.118888 ESTs, Weakly similar to ALU1_HUMAN ALU S	3.13
434495	AW352170	Hs.129086 Homo sapiens cDNA FLJ12007 fis, clone HE	3.12
408113	T82427	Hs.194101 Homo sapiens cDNA: FLJ20869 fis, clone A	3.12
456437	AI924228	Hs.115185 ESTs, Moderately similar to PC4259 ferri	3.12
421489	AI922821	Hs.32433 ESTs	3.12
436090	AI640635	Hs.116468 EST	3.11
450230	AW016607	Hs.201582 ESTs	3.11
438011	BE466173	Hs.145696 splicing factor (CC1.3)	3.09
418720	AI381687	Hs.39526 ESTs	3.09
433102	AI343966	Hs.158528 ESTs	3.08
436150	AW510927	Hs.125243 ESTs	3.05
440116	AI798851	Hs.283108 hemoglobin, gamma G	3.04
414900	AW452420	Hs.248678 ESTs	3.04
435937	AA830893	Hs.119769 ESTs	3.02
424848	AI263231	Hs.327090 EST	3.02
435354	AA678267	Hs.117115 ESTs	3.00

TABLE 23A

Table 23A show the accession numbers for those pkeys lacking unigeneID's for tables 1-20A, 21A, 22A, and 23A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT Number Accession

413497	1373771_1	BE177661 H06215 BE144709 BE144829
413672	1382512_1	BE156536 BE156439 BE156700 BE156449 BE156653 BE156533 BE156524 BE156670 BE156721 BE156723
417670	1692163_1	R07785 T85948 T86972
418876	179960_1	AA740616 AA654854 AA229923
419145	182217_1	N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815
423974	233842_1	AL118754 AA333202 H38001
432340	345248_1	AA534222 AA632632 T81234
434966	396504_1	AA657494 AI582663 AI581639
435073	399701_1	AA664078 AW363313 AA805009
438962	467390_1	BE046594 BE046667 AA828585 AI207343
455778	1364506_1	BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952
456332	179104_1	AA228357 AW841786 AW841716

TABLE 24: 34 GENES DOWN-REGULATED IN COLON CANCER DERIVED LIVER METASTASES COMPARED TO COLON CANCER PRIMARY TUMOR SAMPLES CLASSIFIED AS DUKE'S B SURVIVOR

Table 24 shows 34 genes down-regulated in colon cancer derived liver metastases compared to colon cancer primary tumor samples classified as Duke's B stage with a positive survival outcome (Duke's B survivor). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer derived liver metastases to "average" Duke's B survivor was greater than or equal to 0.25. The "average" colon cancer derived liver metastases level was set to the 50th percentile. The "average" Duke's B survivor level was set to the 50th percentile.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Genes down liver metastases vs Duke's B survivors

Pkey	ExAccn	UnigeneID	Unigene Title	R1
414522	AW518944	Hs.76325	step II splicing factor SLU7	0.05
416768	AA363733	Hs.1032	regenerating Islet-derived 1 alpha (panc	0.07
409153	W03754	Hs.50813	hypothetical protein FLJ20022	0.07
414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	0.11
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	0.11
424326	NM_014479	Hs.145296	disintegrin protease	0.11
428934	AF039401	Hs.194659	chloride channel, calcium activated, fam	0.12
417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	0.12
422260	AA315993	Hs.105484	regenerating gene type IV	0.12
425196	AL037915	Hs.155097	carbonic anhydrase II	0.13
433336	AF017986	Hs.31386	secreted frizzled-related protein 2	0.13
450685	L15533	Hs.423	pancreatitis-associated protein	0.14
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antag	0.15
414798	AI286323	Hs.97411	hypothetical protein MGC12335	0.16
452852	AK001972	Hs.30822	hypothetical protein FLJ11110	0.17
447513	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A	0.17
423541	AA296922	Hs.129778	gastrointestinal peptide	0.17
425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	0.18
406636	L12064		gb:Homo sapiens (clone WR4.12VL) anti-th	0.18
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	0.18
428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	0.19
414812	X72755	Hs.77367	monokine induced by gamma interferon	0.20
452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	0.20
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	0.21
408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	0.21
453064	R40334	Hs.89463	potassium large conductance calcium-acti	0.21
431727	AW293464	Hs.162031	ESTs	0.22
433658	L03678	Hs.156110	immunoglobulin kappa constant	0.22
442064	AI422867	Hs.88594	ESTs	0.22
417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	0.22
430280	AA361258	Hs.237868	interleukin 7 receptor	0.23
452877	AI250789	Hs.32478	ESTs	0.23
410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	0.24
402408				0.24

TABLE 24B

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402408	9796239	Minus	110326-110491

TABLE 25:

Table 25 depicts Seq ID No., UnigeneID, UnigeneTitle, Pkey, and ExAccn for all of the sequences in Table 26. Seq ID No links the nucleic acid and protein sequence information in Table 26 to Table 25.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 Seq.ID.No.: Sequence Identification Number found in Table 26

Pkey	ExAccn	UnigeneID	Unigene Title	Seq ID No.
426101	AL049987		Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1-4
419145	N99638		gb	5 & 6
426818	AA554827	Hs.340046	DKFZp434A0131 protein	7 & 8
421057	T58283		Homo sapiens cDNA	9
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	10 & 11
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	12 & 13
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	14 & 15
443162	T49951	Hs.9029	DKFZP434G032 protein	16 & 17
436385	BE551618	Hs.144097	ESTs	18-20
447033	AI357412	Hs.157601	ESTs	21 & 22
439608	AW864696	Hs.301732	hypothetical protein MGC5306	23-27
449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	28 & 29
442577	AA292998	Hs.163900	ESTs	30 & 31
429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	32 & 33
424566	M16801	Hs.1790	nuclear receptor subfamily 3, group C, m	34 & 35
457407	AA505035	Hs.345911	ESTs	36
430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	37 & 38
417332	AW972717	Hs.288462	hypothetical protein FLJ21511	39 & 40

TABLE 25A

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT Number Accession

409041 10962_2 AB033025 AL359061 AL045836 AI751521 AI752804 AI752650 AA853580 AI752290 AA853460 AI752769 AA852309
 AA853785 AA853219 AW068503 AI752069 AL049389 AW068368 BE439518 W52813 BE141833 AI940574 AI750606 AL109718
 AA242845 AA315795 AA307741 AW954603 AI752070 AA350794 AI752649 AA307755 AW951677 AA298896 BE439692
 AA852453 AW068826 AW853984 AA418236 AA639417 AW290917 AI750592 AI752768 AL045837 AI926513 AW262903
 BE439819 AI459360 AW339074 AW295181 AW029483 AI750945 AI750659 AI752525 AI147688 BE440122 AI751522 AI473816
 AI752291 AI694639 AI925816 AA599476 AA242752 AW021892 AI755098 AW469299 AW769363 AA853579 AI784082
 AA852454 AI925501 AA976657 AW150473 AW166734
 417332 166755_1 AW972717 AA523805 AI962905 AI373245 AW235545 AI812045 AW589434 AI826824 AW572339 AI377551 AA195718
 AI868470
 419145 182217_1 N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815
 421057 198849_1 T58283 AA765038 AA283052 H99396 AA814751 AI032674 N81016 N81017 BE222349 AA830545
 424566 2408_1 M16801 NM_000901 D57171 AL041328 AF068623 AI201179 AA151766 AA568349 AI698649 AI692765 BE327401 AA744953
 AA744951 AW361986 AV651840 T29894 AW945146 AW945145 W24096 AI183952 AI458972 AW190993 AI765359 AI634663
 AI741201 AW418944 AI767551 AA679687 AW772342 AW629508 BE504300 AI251790 AI522294 AA724341 AW615402
 AI537570 AA470665 AI458375 AW768901 AA447079 T23537 AI783744 R44301 D56621 N91919 AA149749
 426101 26088_1 AL049987 AW362842 T78981 AA247541 AI217018 AW961515 AA632986 AA663108 BE326465 AW872412 AI024689 AA453725
 BE150456 AA229448 AA442638 AA442648 AI916737 AA460220 AA868553 AI827987 AI005467 R31132 AI742087 AA442379
 N56349 AW769479 AI860142 AI917507 AA813604 AI860141 AI459289 AA522837 AI354470 AI921333 BE466760 AW971193
 AW103830 AW277065 AW020895 AI187977 N28268 AI084517 R95914 AA833517 AA563934 AA437299 AA436880 AA447794
 AA812876 AA663178 R31089 AI472712 R64648 AA600372 AA229164 AA703066 AW270324 AI191725 AA551512 AA493776
 426818 272427_1 AA554827 AA701001 AW972954 AL039129 AA385540 AA911663
 429970 31134_1 AK000072 AW840683 AW843764 AW844444 AW844515 AW603469 AW862395 AI860838 AW511708 AF127035 NM_012128
 AK000138
 430378 3170_1 Z29572 AW976377 AA286871 AA633372 AA987627 AA743176 AI865358 AJ006884 AF031845 Z14955
 431958 3394_1 X63629 NM_001793 BE175433 BE153414 BE153425 AW364593 BE315317 AW950190 AA314252 BE142943 AW365220
 AW368405 BE004269 AW366568 AL040609 AI829273 AI591168 BE146183 AI631060 AI830793 W78081 W92295 AI927422
 BE009313 AI371793 AW993031 AI204659 AA535113 AW993030 AI190281 AA555159 AW269637 AW993146 AI149268
 AA425217 AW473194 AI890930 AA551993 AI952106 W92308 AI827275 W45400 AI952328 AW609233 AA774611 AA551779
 AI913967 AI798658 AI537658 AW517535 AA632236 AW339148 AW589522 AA836945 AA961263 AW015821 AW272946
 C00249 W40333 BE143121
 436385 418907_1 BE551618 AI207338 BE220568 AI261568 AW841737 AA714722 AA946891 AI033239
 439608 47438_3 AW864696 AW338889 AI342866 AA084522 AI244150 AI610339 AA425635 AA764930 AA976965 AW805766 AA057765
 AW805845 AW802595 AA262971 AI969620 N75323 BE549060 AW805725 AA025809 N80776 N64595 AW073372 AA025493
 AI819475 AW028879 AW189496 AA442907 AW410368 AI911629 N71276 AW316922 AW805838 AA043880 AW189184
 AA449756 AW748153 AA705608 AI910643 AA279492 BE160119 AW805761 AA026262 AA782207 AW057652 AW805768
 H21998 AW194254 AW275178 AA449040 AA279582 N76314 N54348
 442577 54549_1 AA292998 AW238350 AI676059 AW074092 BE566458 AW078677 AW514801 AW073701 AW170620 AI523736 AI580870
 AI923975 AI393326 AI700229 AW450814 AW628452 AI671457 AA937534 AI889694 AW339423 AW291875 AA551874
 AI682314 AI926227 AA397375
 443162 5613_1 T49951 AA025326 H04839 AA393303 R63101 W57657 W25628 AI961431 R71165 N39940 H01548 H01759 AA641624
 AI634930 AA595296 AW994770 AW994747 BE047247 W38159 AA858133 AI701944 AW386273 AA676625 R24676 R79410
 AA922863 AI151319 H01013 AA024482 W02674 H01456 AI150858 AW135972 AW631167 AI270332 H04750 T49622 AA004543
 R63061 AI093066 AI247539 H01225 H03388 AW472933 AA382448 AI219287 N27194 AW389613 AA649738 AW994764
 AW389614 R25176 AA897262 R71626 AA909471 R71240 AW811917 R76109 AI202312 AI866010 R76162 AL117538 R79411
 T58656 AW994674
 446619 685_1 AU076643 AA594604 AA346866 R18197 AA345192 AA337773 AA089791 R84435 AA337838 AW392167 AA075190 D55416
 AW150360 AW366257 AA579816 H93048 AW385689 AW385697 AI186216 AW581197 AL037509 AB019562 AA232626 R97905
 AW368019 AA242891 AW888502 AI798331 AW385635 AW581221 T96947 H87989 AA369511 AA075191 R80742 AA366406
 W92752 H45586 AI864016 AW888497 BE004992 AI384110 AI624256 AI627593 W92728 AI682719 AA948208 AA171734
 N40517 J04765 AA379957 AA362403 NM_000582 AF052124 AA300290 AA333447 AA343721 AW889543 BE566767 R76601
 R18015 AA100531 AA489963 AA101296 AA363513 AA344088 AA336750 T77505 D56440 AL110351 AL110331 F12195 R20175
 AA336664 H17766 AA363538 AA363590 D28760 AW578517 AA363531 AI814667 AA846899 AA366253 AW951285 AA297992
 AA327756 AW361609 AW815455 AW815427 AW815428 D54182 AW852200 AA171630 W27018 AW815864 AW379995
 AW378222 AW362610 BE566022 AW021023 C17352 D58435 AA345409 AI623991 AW020967 AI924770 AI799443 AW946393
 AA991239 AI571617 AI935181 AI923999 AI826895 AI860319 AW189873 AW270353 AW023584 AI813811 R99929 AW339056
 AA913152 AI636352 AI829394 AW151077 AW192580 AI570119 AI086391 AW021764 AW519154 AI375193 AW268678
 BE465690 AW019983 AW268654 AI573138 AI141809 AI954553 AI559242 AA568945 AA886417 AW338527 AI635881
 BE465666 AI921239 AA968537 AI956027 AA911981 AI827661 AW511046 BE619780 AI922227 AI811870 AW190131
 AW129220 AW512906 AI290757 AI819088 AI623771 AA775616 BE349419 AI126375 H88773 AI241758 AW275157 AI337848
 AI613425 AI631387 AA922631 AI273483 AI982898 AW168957 AI446481 BE501588 BE048264 AI499922 AW023812 BE220523
 AW973846 BE349276 AI141091 AA976060 AW973845 AA101270 AI582472 AW613675 AI139360 AI282627 AI276044 N22345
 AI261875 AA634136 AI824468 AW887693 N27107 R21504 AI042223 N22067 AW196871 AI581019 BE004973 AA252035
 N22087 AA570717 H11250 AI804026 AA368098 AA021512 H08842 N26275 AA176368 AI758758 AA570371 AA232574
 BE221177 AW190221 AW471386 M78225 AI422140 AI624521 AA719775 AA300291 AA568657 AI871430 BE465630 N71862
 T72587 W92721 H88774 D54383 AW103693 AW089986 AI382689 R42363 R44962 T98770 AA357374 AW022074 AI356207
 T29241 AW089431 AI933875 N66267 N67352 AA121786 AA363910 F09824 T95618 N66888 R80550 AI280667 AW196719

		R59299 AW021049 H73469 AI954311 BE439454 AW079450 AW973850 AA348338 AW896006 AW268145 AA853631 H17650
		R39537 N66873 N67240 H06298 AI784199 R44260 AA904118 AA911756 F04544 AA807809 AA665210 AI696448 T29719
		AA837240 T64844 H08926
447033	704603_1	AI357412 AI870708 AI590539 W07459
449032	7945_1	AA045573 AA279920 R20139 AA372783 AW963629 H21473 R78318 W74359 AA022505 AA369091 AW084075 AA503638
		AV660815 AI216262 AA779843 BE219825 AF125534 AW972129 AI919099 AI621283 AI300590 AI953701 AA331415 AW610546
		AW793050 AI953679 AW793047 AW610543 AI671103 AW292105 AW024112 R77947 W76339 AA305111 AA132523 AA227467
		H21401 AW366572 AW024129 AI701886 AI654744 BE042803 AI347173 AW866053 AW662710 R36639 AI469777 AA962733
		AI865366 AA501998 AW866054 BE178974
457407	333252_1	AA505035 AW235098 AI634028

Table 26

Seq ID NO: 1 DNA sequence
Nucleic Acid Accession #: see Table 25 & 25A for complete list

1 11 21 31 41 51
| | | | |
CAATATAGTA CAATAACTAT TTGCATGACA TTTACATCGG ATATTATGAG TGATCTAGAG 60
TTGATATGAA GTATATGGGA GGATGTGCAA AGGTGATGTG CAAATACTAT GTCATTTTAT 120
AGGGGGGACT TGAGTATCCT TTGTTACCCT CAGGAGATCC TGAAACCAGT CCCCCATGGA 180
TACTGAGGGC TGACTGTATA GTCCTATCCT CACGGAACCT TCATTCTAAT GGGGGAAGAC 240
TGACTATAAA CAAAATATAT GTAATAGGTG GTGGTAAGTA CCGTGGAGAA GTAACAAATG 300
GGGCAAAGTG AGTTATACAG CTCCATTCTT AGAAACCTTG GAGTACTTTT CTTAGTTTAT 360
ACTCGTGGTG GTTTCCTTTT GTCCTCTTTA TTACATGGGA CTCTGACATG TGCCCATAGC 420
TAGGGTGACA GTAGGATCTA CCCGATAGTA GGGTGGCAGT AGGATCTACC CAAAAAGCGT 480
CCTGCTGATA CAGGACCAAA GCATCCTGTT GTTCTCGAGC CTATAAAAAAG AGCTAATGGT 540
GTTGCTTCTC TTAACGTGGG CCTCCTACAC TGTGTTTTGG ATGATTGGTG ATGTCTTGGA 600
TATTCTGTTT CTTTGGAAC TTTGAATATAC AACACTTTAC TAGGGAATTA GCAATGGAAG 660
CAGAGCAAAG ATGTACAGAG GAAACAATGC GTAACCTCTG TGGAATTGAA GTCATGAGGC 720
AGCAGAGAGC TTAATTTACA GCTTTAAAAA TTTTATTTT TTAGAGGGAA TTTACTTGGG 780
AGTAACAGCA GTAATAGTTA ACGGAGCCAG AATGCTTGAG TCATATAATT GCAAAGCAGA 840
GTTGGGAGCA ACAGATGCTA AAGAGTAGTT GCTGTAGTTC CTCTTTGGGT CGTAGGAGCA 900
GTTGTCATAT TACTATATAG CTACTGCATG AAGAAGAGTT CTTAGTGAGG CCTGGGTGAA 960
CAGCTCTTCT TAGTATTCTG TGTGACCCCA TTTGACCTTT TAACAAATCC CTAAGTAAAT 1020
AAATAGCCCC TCAGGAAAAAC TAAGTTTTTC TCTGCTGTTT TTTTGCTTGA GAGAGCTATA 1080
ACTGTAATAG ACTTATATTT CTGAACATTT TAGTGCTTGC CAATATTTGG TAATATTTAT 1140
GTTTCCTATA TTTGTAATGA ACATTCTTCT TCCGGTACAT TTTTGTTAA ATTATTGTTT 1200
GATGGATAAA AGTTCACCTT TTATTGTATA AAATTGACTG AGATTAATTT ATACACATTG 1260
ACAATGGGTG AATAGAATTT TTCAGATTAT TAAAAGCTGA AGGATGACCA CGTAAGCAAA 1320
AAAAAAAAAA AAAAAACCAA CAAAAATAAA CCCAAACCCC TCAACAATTC TCGAACACGA 1380
AACATTCTTC TGATGCCGGC ATCCTGCTT GCAGGTGTGA AGGGGGCAGG AATCAGCGAG 1440
GTGTCCTGGG CTGAGTCCCC GGGGAAGAAT ATGAT

Seq ID NO: 2 DNA sequence
Nucleic Acid Accession #: X83301.1

1 11 21 31 41 51
| | | | |
GCAAAGCCAG CTGGGCTCCT GAGTCCGGTG GGTACTTGGA GAACTTACTA CGTCTAGCTG 60
GAGGATTGTA AATGCACCAA TCAGCATGCT GTGTCTAGCT CAAGATTTTC TCCATCCCCT 120
TATTTTGGGC CAGTGGCTGT CATTACATAT GAGATGAGTC TCTTGAAGAC TACAGATGAA 180
CTCAAGCTCC ATGAGGAGAT GTTTCATTGT CGAGAGCAGT CATGATGGCC TGCCTCCAC 240
ACAAATGCAAC AGAGTGAAAG AGCAGGTTCT GCTTCTTTGG TGTAGTCTG AAGCTTCCTA 300
AGAAACTTCA CATCAGGTGA TGGATAGGAG CAACCCTGTA AAACCAGCCT TAGACTATTT 360
TTCAAACAGG CTGGTGAATT ACCAGATCTC CGTCAAGTGC AGTAACCACT TCAAGTTGGA 420
AGTGTGCTT TTGAATGCAG AGAACAAGT CGTGGACAAC CAGGCTGGGA CCCAGGGCCA 480
GCTGAAGGTG CTGGGTGCCA ACCTCTGGTG GCCGTACCTG ATGCACGAAC ACCCGCCTA 540
CCTGTACTTC TGGGAGGATG GTGATTGCTC ACACCAAAGC CTGGGACCCC TCCAGGCCTG 600
TGACCTTTGG GACCAACTCC ACCTACGCAG CAGACAAGGG GGCTCTGTAT GTGGATGTGA 660
TCCGTGTGAA CAGCTACTAC TCTTGGTATC GCAACTACGG GCACCTGGAG TTGATTCCGC 720
TGCAAGTGGC CGCCAGTTT GAGAATTGGT GTGAGACATC ACAATCCCAT TATTCAGAGC 780
GCGTATGGAG TGGAAACGCT TGTAGGGTTT CACCAGGGCT GGTGAATTAC CAGATCTCCG 840
TCAAGTGCAG TAACCAGTTC AAGTTGGAAG TATGTCTTTT GAATGCAGAA AACAAAGTCG 900
TGGACAACCA GGCTGGGACC CAGGGCCAGC TGAAGGTGCT GGTGCCAACC TCTGGTGGCC 960
GTACCTGATG CACGAACACC CCGCTACCT GACTCTGTGG GAGGATGGTG ATTGCTCACA 1020
CCAAAGCCTT GGACCCCTCC CAGCCTGTGA CCTTTGGGAC CAACTCCACC TACGCAGCAG 1080
ACAAAGGGGC TCTGTATGTG GATGTGATCC GTGTGAACAG CTAATACTCT TGGTATCGCA 1140
ACTACGGGCA CCTGGAGTTG ATTCGGCTGC AGGCCCTGCA GCTGGCCGCC CAGTTTGTGA 1200
ATTGGTGTAA GACATCACA TCCATTATT CAGAGCGCGT ATGGAGTGGA AACGCTTGTA 1260
GGGTTTCACC AGTCTTTCCC AGGGAACCTC GATGAAGTGT TCCAACAAA TGAGCGAGTG 1320
AACCAAGAAG AGGATGACAT TAGATCCAGG AGATACAACA GAGGAGATAA TCTCCAGGAT 1380
GCCTGTGAAG AAAGATCCCT GGATCCCAGG ATGATTATAG GACAAGTTGT TCATAATCCA 1440
GCAGGCCAGA AGACTTCCAG GGAAACTCAT TTCAAGATGA AAATGGACCA GCCGCAGTGG 1500
CTCAGCCTG TAATACCAGC ACTTTGGGAG GCTGAGGCGG GCGGATCACT TGAGGTCAAG 1560
AGTTTGAAAC TAGCCTGGCC AACGTGGCAA AACTCCATCT CTATTAAAGA TACAAAAATT 1620
AGCCAGGCAT AGTGGTGCAT GCCTGTAGTC CCAGCTACTT GGGATGCTGA GGCAGGAAGA 1680
ATTGCTTGAA CCTGGGAGGC AGAGTCTGCG GTGACCGAGA TCATGCCACT GCACTCCAGC 1740
CTGGGTGACA GAGCCAGACT CCGTCTCTAC TAAAAAAAAA AAAAAAAAAA AAA

Seq ID NO: 3 Protein sequence:
Protein Accession #: CAA58280.1

1 11 21 31 41 51
| | | | |
MDRSNPVKPA LDYFSNRLVN YQISVKCSNQ FKLEVCLLNA ENKVVDNQAG TQGQLKVLGA 60
NLWWPYLMHE HPAYLYSWED GDCSHQSLGP LPACDLWDQL HLRSRQGGSV CGCDPCEQLL 120
LLVSQRLAPG VDSAAAGRPV

Seq ID NO: 4 DNA sequence
Nucleic Acid Accession #: BC002622.1

1 11 21 31 41 51
| | | | |
GGCACGAGGC TCCGCCCGCG GCCGGGATGC ACTAGGCAAA GCCAGCTGGG CTCCTGAGTC 60

CGGTGGGTAC TTGGAGAACT TACTACGTCT AGCTGGAGGA TTGTAAATGC ACCAATCAGC 120
 ATGCTGTGTC TAGCTCAAGA TTTTCTCCAT CCCCTTATTT TGGGCCAGTG GCTGTCATTA 180
 CATATGAGAA CTCAAGCTCC ATGAGGAGAT GTTTCATTGT CGAGAGCAGT CATGATGGCC 240
 TGCACCTCCAC ACAATGCAAC AGAGTGAAAG AGCAGGTTCT GCTTCTTTGG TGTAAGTCTG 300
 AAGCTTCTTA AGAAACTTCA CATCAGGTGA TGGATAGGAG CAACCTGTGA AAACCAGCCT 360
 TAGACTATTT TTCAAACAGG CTGGTGAATT ACCAGATCTC CGTCAAGTGC AGTAACCAGT 420
 TCAAGTTGGA AGTGTGTCTT TTGAATGCAG AAAACAAAGT CGTGGACAAC CAGGCTGGGA 480
 CCCAGGGCCA GCTGAAGGTG CTGGGTGCCA ACCTCTGGTG GCCGTACCTG ATGCACGAAC 540
 ACCCGCCTA CCTGTACTCG TGGGAGGATG GTGATTGCTC ACACCAAAGC CTTGGACCCC 600
 TCCCAGCCTG TGACCTTTGT GACCAACTCC ACCTACGCAG CAGACAAGGG GGCTCTGTAT 660
 GTGGATGTGA TCCGTGTGAA CAGCTACTAC TCTTGGTATC GCAACTACGG GCACCTGGAG 720
 TTGATTCAGC TGCAGCTGGC CGCCCAGTTT GAGAATTGGT GTAAGACATC ACAATCCCAT 780
 TATTCAGAGC GCGTATGGAG TGGAAACGCT TGTAGGGTTT CACCAGTCTT TCCCAGGGAA 840
 CTCCGATGAA GTGTTCCAAC AAAATGAGCG AGTGAACCAA GAAGAGGATG ACATTAGATC 900
 CAGGAGATAC AACAGAGGAG ATAATCTCCA GGATGCCTGT GAAGAAAGAT CCCTGGATCC 960
 CAGGATGATT ATAGGACAAG TTGTTTATAA TCCAGCAGGC CAGAAGACTT CCAGGGAAAC 1020
 TCATTCAAGG AGGTGAAAAT GATGGATGAC TCCTCCAAGA TGAAAATGGA CCAGCCGCAG 1080
 TGGCTCAGC CTGTAATACC AGCACTTTGG GAGGCTGAGG CAGGCGGATC ACTTGAGGTC 1140
 AGGAGTTTGA AACTAGCCTG GCCAACGTGG CAAAACCTCA TCTCTATTAA AAATACAAAA 1200
 ATTAGCCAAG CATAGTGGTG CATGCCTGTA GTCCAGCTA CTTGGGATGC TGAGGCAGGA 1260
 AGAATTGCTT GAACCTGGGA GGCAGAGTCT ACAGTGAGCC GAGATCATGC CACTGCACTC 1320
 CAGCTGGGC AACACAGTGA GACTCCATCT CAAAAAAAAA AAAAAAAAAA AA

Seq ID NO: 5 Protein sequence:

Protein Accession #: AAH02622.1

1 11 21 31 41 51
 | | | | |
 MDRSNPKPA LDYFSNRLVN YQISVKCSNQ FKLEVCLLNA ENKVVDNQAG TQGQLKVLGA 60
 NLWWPYLMHE HPAYLYSWED GDCSHQSLGP LPACDLCDQL HLRSRQGGSV CGCDPCEQLL 120
 LLVSQLRAPG VDSAAAGRPV

Seq ID NO: 6 DNA sequence

Nucleic Acid Accession #:

see Table 25 & 25A for complete list

1 11 21 31 41 51
 | | | | |
 ACCTGAGATC AGGAGTTCGA GATCAGCCTG ACCAATAGGG TGAAACCCCG TCTCTACTAA 60
 AAATACAAAA AATTAGCTGG ACACGATGGT GGGTGCCTGT GGTCCCGGCT ACTCGGGAGG 120
 CTGAGACAGG AGAATCAGTT GACCTGGGAG TTGGTGGTTG CAGTGAGCTG AGATCACACC 180
 ATTGCATTCC AAGCCTGGGC AACAAGAGTG AAATCCATC GCAAAAAAAAA AAAAGAAGGG 240
 GCATAATTG TGGATGAGGA TTGATATAA GTTAAAGGAT GGGACATTCT TGGACTTACA 300
 GATGGTGTGA TTGCCTGGCT AGAAGAAGAA TTCCCGGTCA AAAAGAAACC ATCAGCTTTC 360
 CAAGTGTGAA AGAGAGATAA ATCTGTGAAG ATTATAGGGA CTACAGGAAA CTTAATCTTT 420
 TTCTTTGAAA AAGCAATTGT AGCAAAAAAAAA AAGAAAATTT CTTACTGTCA TCTAAAATTG 480
 ACATGGACAT CTTAGTGGAC TAGAAGTTAA GGGCATAAAT TCTCCAGTG ATTTTAAATT 540
 TTAGCATTGT GATTAACACC TTCTAAAATT GCCAGAACTT AATAATAAT TGCTTTTCAT 600
 TATTAGTATG CCATCAAAAT TAGTAGCTGT TTCAGGCTTT AATGTGTCAA GCCTAAAATC 660
 CAGATTTTGG AGGATCTTCT CCCTCTTAAA AGAGATTATCA GTTAACTGCC GTAGAAATAC 720
 ACATGTATAC AAGGGCAGTG TATACATCAG TCTAAAAAAT AAAAATATGT ATACGTTCTG 780
 GTGAGTCTAG CACAGCATTG CCAATAGAA ATACCAATGG AGGTCACAAA TGTGGCCCAT 840
 ATAGGTTAAT TGGTAAATTT TCTNATAGNC ACC

Seq ID NO: 7 DNA sequence

Nucleic Acid Accession #:

AK000942

Coding sequence: 1204-1503

1 11 21 31 41 51
 | | | | |
 GTAAAGGAAT GTCTTTTAA TTCAGCTTTT CTTTCTCCA TGCTAGTGTT ATCAGGTTTT 60
 GGTATTTATT TACTTACAGC ATATGTTATG AAGCTGGTTT GAAAATTGGT TTAGATATA 120
 TCTGCAAGTT TACTACTTTG ACTGTAAAAA AAAAAAATGA AAAAGTAGTT GACATCTGTC 180
 CTCAGAAGAA GTTTGCAGGT TGCATATTTG TGTGTAATA CACAGGCTAA AAGGTAATTT 240
 ATGTTCTTGG GGAATTGAAA TGGTCAGTGG CCCGTTACAG AAATTTATCA GTCATATATC 300
 AGCACCAGTT CATTCTTTTG CACCTTAGGG ACCATCTGTC CCCTGAGGTG ACCTGAGAAA 360
 CAACCAGTTG CCCACAGACT GTTATTTCTT CAAGTGAGCC AGGATTTGAT TCACTGCCT 420
 TATATTCTAT TTTTAGTGA CAGTGCTTTG ATTTTGGGA AAAACTAAAT TTTAAACATA 480
 TTTGAAAAAT GTTATAAGAC TTGGACATTA AGTCTGTTGA TAGCCAAAGT CAGTTTACCA 540
 AAGTAAACA AATAAATCT ATGCTTCTTC ATTGTCAAAG AGCAGTCTGC CATCATGTGG 600
 ATATAAATGG ACTATGTAAA GTGACATGGT GCTTACTCTC TACCTAATAA TAGCCTCCCT 660
 CCTGTTCCAA CAAGATAACC AACAGGTATA TTTAATTTAC CAGTTAATAT GTTTTGGATA 720
 ATTGGCTGCC TTGAAATGCT ATATGTTTAA TAGTACATCA TAGCTTAGT TTTCTTCATA 780
 AGGAAATTAC AGTTACATCC TGGCTAACAT GGTGAAATC CATCTCTACT AAAAATACAA 840
 AAAATTAGCC GGGCGTGGTG GCGGGCACTT GTAGTCCAG CTAAGCGGA GGCTGAGGCA 900
 GGAGAATGCC GTGAACCCAG GAGGCGGAGG TTGCACTGAG CCGAGATCGT GCCACTGTAC 960
 TCTGGCCTGG GAGACAGAGC GAGACTCCAT CTCAAAAAA AAAAAAAAAA AAAAAAAGA 1020
 GAGAGAGAGA CCTGGAGTAG AGATTCTGTC AAAGAATTTT TCTTTCTTG AGAAGCATCT 1080
 GAAATGGAAT CTGTTGCTC TTCGAAATAT GTACTGCTGT AACAGTGAAG CAACCTCAG 1140
 AGTATGCCCT CGTGTGGGCT ACTCGTTGTG GTTTTGAAT TGGGGGAAT GTCTGTGTTT 1200
 GGGTCAAGAA TATGCAACTG GCTGGGCACA TTGGCTCACG CCGTGAATCC CAGCAATTTG 1260
 GGAGGCTGAG GCAGGCGGAT CACCTGAGGT CAGGGCTTCA AGACCAGACT GGCCAACATG 1320
 GTGAAACCCC GTCTCTACTG AAAATACAAA AATTAGCTGG GCATGGTGGC AGGTGCCTGT 1380
 AATCCAGCT ACTCGGAGG CTGACGTGAG AGAATCGCTT GAACCCGGA GTTGGAGGTT 1440
 GCAGTGAGCC GAGATTGCAC CATTGCACTC CAGCTTGGGC AACAAGAGTG AAATCTTGT 1500

CTCAG

Seq ID NO: 8 DNA sequence

Nucleic Acid Accession #:

see Table 25 & 25A for complete list

1 11 21 31 41 51
| | | | |
GACTAGGCTG GGCAACATAG TGAGACCTCA TCTCTAAAT TAAAAAATA AAAGOCACCA 60
GAAAAAAACC TAAAAACATG CCAAGTGACA TCAGTCTTTG ATGAAAATGG CAGCAGAAGA 120
GTGATGCCAT GGGTGGGGT GGGAAATGCT ATTTACAGCAG AGAGGGAGCT GTCATGGAAG 180
ACACCATGTG GCTGGGCACG GTGGCTCACA CCTGTAATCC CAGCACTTTG GGAGATAGAG 240
GCAGGTGGAT CCCTTGAGCT TAGGAATTG AGACTAGCCT GGGCAATAAG AGTGAAACTC 300
CATCTCAAAA AAAAAAAAAA AAAAAGGTGC ATGAAACATA TGAAGCAAAA AGTGAAAGTC 360
CCCATTCTTT TCCTTTTCC AGAGGTGATT TTTGTGGCA ATCTGGTTT ATTCCCTCCC 420
AGACACTTTT CTAGGCATCT ATGCGCTCT ATTCACATAT AAACAAAATA GGAGTTTTCC 480
TGTGCTTCCC TTAAATGGCA TATGTATCTT TCACTCTTTT TTTTACCTA GTGGATCTTT 540
AATACCTTAA AAGCTCAACC TGGGCTTGGT GCGGTGGCTC ATACGTGTAA TCCCAGGCCT 600
TTGGGAGGCC AAGGTGGGAG GATCACTTGA GCTCAGGAGT TCCAGACCAT TCCAAAGCAA 660
AAACAAAAGG ATTTTGAGAT CAGTGTGGGC AACTTAGCAA AACACCATCT CTTAAAAAAA 720
AAAAAAAAAA

Seq ID NO: 9 DNA sequence

Nucleic Acid Accession #:

BC010433.1

Coding sequence: 3-335

1 11 21 31 41 51
| | | | |
GGTCGCCCTC CGTCGTGGTC TGGCGTGTAT TCCGAGCCTT GGTGTCTGGC GGTTCGAG 60
CGTTGGTGTG TGGCGGTTTC CGAGCGTTGG TGTCTGGCGG TTTCCGACCG TTGGTGTCTG 120
GCGGTTTCCG ACCGTTGGTG TCTGGCACGC GCCACCCTCT CTGCTTTGG TTGCGCCATG 180
CCGATGTACC AGACAAGAAG ACAAGAAAAT GATTGAGGA CAGCTTCAAT CGCGGTGTGA 240
AGAAGAAAAGC AGCAAAACGA CCACTGAAAA CAACGCCGGT GGCAAAATAT CCAAAGAAAAG 300
GGTCCCAAGC GGTACATCGT CATAGCCGGA AACAGTCAGA GCCACCAGCC AATGATCTTT 360
TCAATGCTGC GAAAGCTGCC AAAAGTGACA TGCAGCACCG AGAAGTCCGC GTGAAGTGCG 420
TGAAGGCTCT GAAAGGGCTG TACGGTAACC GGGACCTGAC CGCAGCCTG GAGCTCTTCA 480
CTGGCCGCTT CAAGGACTGG ATGGTTTCCA TGATCATGGA CAGAGAGTAC AGTGTGGCAG 540
TGGAGGCCGT CAGATTACTG ATACTTATCC TTAAGAACAT GGAAGGGGTG CTGATGGACG 600
TGGACTGTGA GAGCGTCTAC CCCATTGTGT AGGCCTCTAA TTGAGGCCTG GCCTCTGCTG 660
TGGGTGAATT TCTGTACTGG AAATTTTCT ACCCTGAGTG CGAGATAAGA ACGATGGGTG 720
GAAGAGAGCA ACGCCAGAGC CCAGGTGCCC AGAGGACTTT CTTCCAGCTT CTGCTGTCTC 780
TCTTTGTGGA GAGCAAGCTC CACGACCACG CTGCTTACTT AGTAGACAAC CTGTGGGACT 840
GTGCAGGGAC TCAGCTGAAG GACTGGGAGG GTCTGACAAG CCTGCTGCTG GAGAAGGACC 900
AGAGCACGTG CCACATGGAG CCAGGGCCAG GGACCTTCCA CCTCCTAGGG TGAAACCAGG 960
AGAGATTGCT TGCTTCACTT GTACAAGGCA GGAACGGTGG CATGGGGTGG GGGAAACTTG 1020
GAGTTGGAAG GTGGCTAATC TTGATTCTA TGTTTTGTAT CCTCCTGGCA CTCCAGACCT 1080
GGGTGATGTG CAGGAGAGCA CACTGATAGA AATCCTTGTG TCCAGTGCCC AGCAACTCCT 1140
GCCTCAGCCT CCCGAGCAGC TGGGACTACA GCGCGCCGCC ACCACGCTG GCTAACTTTT 1200
TTGTGTTTTT AGTAGAGACG GGTTTTACC GTGTTGGCCA GGATGGTCTT GATCTCTTGA 1260
CCTTGTGATC CACCTGCCTC ATCATCCCAA AGTGCTGGGA TTACAGGCGT GAGCCACTGC 1320
GCCCAGCATG TTAGACAATT TTAATTCAT CCTCTCTGTG CTGTTGTTTT CTCAGCTGTG 1380
AAAGGAATAT TCTGGTGGGG ACAAGGTAC AGAGTTGCTG AGAGGGTCTC ATGACATGAA 1440
GGTACTGGCC TTGGCACAGT GCCTGGGGGG GCGGGGACTC CGCACATGCC TGTGATGTCA 1500
CAGTTACTGT CAGTTCACAG CGAACCTTCC CTCCTTTTCC TGTGACTTT CCCACACTCC 1560
TGTAACCTC CCTCCCTCCC TTCTCTCTCT CTCTCTCTCT CACTCACGCA CACGCACACA 1620
CACACACACA CACACACACA CACACTCC ATTCAGTGC TCCATGACTC TGGAGTAAAC 1680
TAACGTCTCG AGTTGCCATT GGAAGCCCCG TTGCTCTCAT TTAGACTTTC ATGGGTTATA 1740
GGCACTTTTG ACTTCTGGG GTCCTTCTTC AGTTAAAAAA AAAAATTAGA AAATTAGGCC 1800
GGGCGTGGTG GCACATGCCT GTAATCCAG CACCTTGGCC TCCCAAAGTG CTGGGATTAC 1860
AGGAGTGAGC CACCATGCCC AGCCTCCGTT TGCCTCATTT AGACTTTCAT GGGTTATAGG 1920
CACTTTTGAC TTCTGGGGT CCTTCTCAG TTAACAAAAA AAAAAAAAAA

Seq ID NO: 10 DNA sequence

Nucleic Acid Accession #:

see Table 25 & 25A for complete list

1 11 21 31 41 51
| | | | |
AGTGGNTCCC CCGNCTGCA GGAATTCGGC ACGAGATCAT GATGGCTAAT ATTTCTGAG 60
CACCTTTCAT TCAGGCATGA TGCCAGGTGC ACCAACTTAC TTAATCCTCA TAGCCACCAC 120
CTGAGCAAGC TCCTGTTTAA TAAATGGACC AGTTCTTGT GCTGTTGTAC AAGTTATTTT 180
CTTTCTATAA CGTCTCCTT GTCTCTTTC CACATTCTTA AAGAACTTT CCCTTCTTT 240
AAAGTACTCA GGGAGCCCTG CATTGCTTCT TGAAGCCTTC TCCAGCTTCA TCATCTCACA 300
GTGGTCTCTC TTTTCACTAA ATGTCCAATA TGCTGCACAT AAGTACCCCA AAGTTAGCAC 360
AGGAATTGTT CCATGGCTGT CATATATGTT AAAAATCATT AAAAGTTCAT TTTTCTCTC 420
ATTATGGGAA GGATACATGC TCCTACTAGT AAATTTAGTA GGTAGAAAAA AATTATCACT 480
ATCTAGACTG CTTTCCATT AGTCTTTATG CATAGCTTTC GTGTCTGCCT ATTTTACCT 540
TGTGTTTGA ACTTACTATT ATAAAATATG CGTCTCTATG TTCATTGTCA ACGATTATTT 600
ACAATAACAT GGAGTGGATT TACATGTATT CTCTATATTT GGATTAAAGG AGATAGAGTA 660
TGTGAAATTA AATGGGAGAA GTATCTGATA CATAACAGGC AATACAAAATA TTATCACATA 720
GCGTCAATTT ATTTGTGAAT ATTGAAAGCT CCAAAAAAGA AAAAAAGTTT TTTTAAAT 780
CCCGTAATTA CTTATTGCAG TATTGTGTT ATACAACTG CTCAGTCATT TTGGAGAAAT 840
AACAATTTTT TTCCTCATCA TGAAGTAAGG TATGCTCACT GCAAAAAAAA TCTAGAAAAT 900
AAAGAGGAAC ATGCTAAAGA AAAGAATACT CCCATATAAT CTCTGTCTTC ATAAATAATC 960
TTTTGTAACG CTTATACACT GCTGGTGGGA ATGTAAATTA GTTCAGCCAT TGTGAAAAGT 1020

AGCGTAGCAA TTCCTTGAAG AACTTAAAAT AGATTTACCG TTCAACCCAG CAATCCCATT 1080
ATTGGGCATA TACCCAGTGG AATGTAAATC ATCCTGCCAT AAAAACACAT GCACATGTAT 1140
GTTTCATTGCA GCACTATTCA CAATAGCAAA GACATGGAAT CAACCTATAT GCCCATCAAT 1200
AGTAGACTGA ATAAAGAAAA TATGGTACAT ATTCACCACA GAATACTAAG CAGCCATAAA 1260
AAAAAA

Seq ID NO: 11 DNA sequence
Nucleic Acid Accession #: NM_000582.1
Coding sequence: 88-990

1 11 21 31 41 51
| | | | |
GCAGAGCACA GCATCGTCGG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA 60
AACGCCGACC AAGGAAAAC CACTACCATG AGAATTGCAG TGATTGCTT TTGCCTCCTA 120
GGCATCACCT GTGCCATACC AGTTAAACAG GCTGATTCTG GAAGTTCTGA GGAAGAGCAG 180
CTTTACAACA AATACCCAGA TGCTGTGGCC ACATGGCTAA ACCCTGACCC ATCTCAGAAG 240
CAGAATCTCC TAGCCCCACA GACCTTCCA AGTAAGTCCA ACGAAAGCCA TGACCACATG 300
GATGATATGG ATGATGAAGA TGATGATGAC CATGTGGACA GCCAGGACTC CATTGACTCG 360
AACGACTCTG ATGATGTAGA TGACACTGAT GATTCTCACC AGTCTGATGA GTCTCAACCAT 420
TCTGATGAAT CTGATGAACT GGTCACTGAT TTTCCACCGG ACCTGCCAGC AACCGAAGTT 480
TTCCTCCAG TTGTCCCCAC AGTAGACACA TATGATGGCC GAGGTGATAG TGTGGTTTAT 540
GGACTGAGGT CAAAATCTAA GAAGTTTCGC AGACCTGACA TCCAGTACCC TGATGCTACA 600
GACGAGGACA TCACCTCACA CATGGAAAGC GAGGAGTTGA ATGGTGCATA CAAGGCCATC 660
CCCGTTGCCG AGGACCTGAA CGCGCCTTCT GATTGGGACA GCCGTGGGAA GGACAGTTAT 720
GAAACGAGTC AGCTGGATGA CCAGAGTGCT GAAACCCACA GCCACAAGCA GTCCAGATTA 780
TATAAGCGGA AAGCCAATGA TGAGAGCAAT GAGCATTCCG ATGTGATTGA TAGTCAGGAA 840
CTTTCCAAAG TCAGCCGTGA ATTCCACAGC CATGAATTC ACAGCCATGA AGATATGCTG 900
GTTGTAGACC CAAAAGTAA GGAAGAAGAT AAACACCTGA AATTTCTGAT TTCTCATGAA 960
TTAGATAGTG CATCTTCTGA GGTCAATTA AAGGAGAAAA AATACAATTT CTCCTTTGTC 1020
ATTTAGTCAA AAGAAAAAAT GCTTTATAGC AAAATGAAAG AGAATCATGA ATGCTTCTTT 1080
CTCAGTTTAT TGGTTGAATG TGTATCTATT TGAGTCTGGA AATAACTAAT GTGTTTGATA 1140
ATTAGTTTAG TTTGTGGCTT CATGGAAACT CCCTGTAAAC TAAAAGCTTC AGGGTTATGT 1200
CTATGTTTAT TCTATAGAAG AAATGCAAAC TATCACTGTA TTTAATATT TGTATTCTC 1260
TCATGAATAG AAATTTATGT AGAAGCAAAC AAAATACTTT TACCCACTTA AAAAGAGAAT 1320
ATAACATTTT ATGTCACTAT AATCTTTTGT TTTTAAAGTT AGTGTATATT TTGTTGTGAT 1380
TATCTTTTGT TGGTGTGAAT AAATCTTTTA TCTTGAATGT AATAAGAATT TGGTGGTGTC 1440
AATTGCTTAT TTGTTTCCC ACGGTTGTCC AGCAATTAAT AAAACATAAC CTTTTTACT 1500
GCCTAAAAAA AAAAAAAAAA AAAA

Seq ID NO: 12 Protein sequence
Protein Accession #: NP_000573.1

1 11 21 31 41 51
| | | | |
MRIAIVICFL LGITCAIPVK QADSGSSEK QLYNKYPDAV ATWLNPDPSQ KQNLLAPQTL 60
PSKSNESHDDH MDDMDDEDDD DHVDSQDSID SNDSDDVDDT DDSHQSDSH HSDESDELVT 120
DFPTDLPATE VFTPVVPTVD TYDGRGDSVV YGLRSKSKKF RRPDIQYPA TDEDITSHME 180
SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES 240
NEHSDVIDSQ ELSKVSREFH SHEFHSHEM LVVDPKSKEE DKHLKFRISH ELDSASSEVN

Seq ID NO: 13 DNA sequence
Nucleic Acid Accession #: NM_001793
Coding sequence: 71-2560

1 11 21 31 41 51
| | | | |
AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCCGTCGC GGCAGCTGCT TCACCCCTCT 60
CTCTGCAGCC ATGGGGCTCC CTCGTGGACC TCTCGCTCT CTCCTCCTC TCCAGGTTTG 120
CTGGCTGCAG TCGCGGCCT CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC 180
CTTGGAGGCG GGAGGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGGAAAG TATTCATGGG 240
CTGCCCTGGG CAAGAGCCAG CTCTGTTAG CACTGATAAT GATGACTCA CTGTGCGGAA 300
TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGTG GTTGCTCAA TATCTGTCCC 420
TGAAAATGGC AAGGGTCCCT TCCCCAGAG ACTGAATCAG CTCAAGTCTA ATAAAGATAG 480
AGACACCAAG ATTTTCTACA GCATCACGGG GCCGGGGGCA GACAGCCCCC CTGAGGGTGT 540
CTTCGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTGTAAT AAGCCACTGG ACCGGGAGGA 600
GATTGCCAAG TATGAGCTCT TTGCCACGC TGTGTCAGAG AATGGTGCCT CAGTGGAGGA 660
CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCCTACCA GGTACTTCTG TGATGCAGGT 780
GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT 840
CCATAGCCAA GAACCAAAGG ACCCACACGA CCTCATGTT ACCATTACC GGAGCACAGG 900
CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC 960
CATCCAGGCC ACAGACATGG ATGGGGACGG CTCCACCACC ACGGCAGTGG CAGTAGTGGA 1020
GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
GCCTGAGAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCAGTGATC TGGACGCCCC 1140
CAACTACCA GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT 1200
TACCATCACC ACCACCTG AGAGCAACCA GGGCATCTG ACAACCAGGA AGGGTTTGGA 1260
TTTTGAGGCC AAAAACCAGC ACACCCTGTA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT 1320
GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380
ACCTGTGTTT GTCCACCTT CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440
GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGTACCG 1500
CATCCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACAGC 1560
TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTTGTGAGG AACAACATCT ATGAAGTCAT 1620
GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680

ACTGATTGAT GTCAATGACC ATGGCCCCAGT CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
CCAAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC 1800
CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860
GGAAGGTGAC ACAGTGGTCT TGTCCTGAA GAAGTTCCTG AAGCAGGATA CATATGACGT 1920
GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
GTGCGACTGC CATGGCCATG TCGAAACCTG CCTGGACCC TGAAGGGAG GTTTCATCCT 2040
CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCCTG CTGGTGCTGC TTTTGTGGT 2100
GAGAAAGAAG CGGAAGATCA AGGAGCCCTT CCTACTCCCA GAAGATGACA CCCGTGACAA 2160
CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGGTCTC CGCAATGACG TGGCAACCAAC 2280
CATCATCCCG ACACCCATGT ACCGTCTCTG GCCAGCCAAC CCAGATGAAA TCGGCAACTT 2340
TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCACCA GCCCGGCCCT ACGACACCTT 2400
CTTGGTGTTC GACTATGAGG GCAGCGGCTC CGACGCCGCG TCCCTGAGCT CCCTCACCTC 2460
CTCCGCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCCGCTTCAA 2520
GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG CGGCGCTGCC TGCAGGGCTG 2580
GGGACCAAC GTCAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCTCC TTCAGCTGAG 2640
GACTTCGGAG CTTGTCAGGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
ACGTTAGAGT GGTGCTTCC TTAGCCTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760
AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCTCAG AGGCCAAGTT TCCAGAAGCC 2820
TCTTACCTGC CGTAAAATGC TCAACCCTGT GTCCTGGGCC TGGGCTGCT GTGACTGACC 2880
TACAGTGGAC TTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940
TTTTTTAAT GCTATCTCA AACCGTTAGA GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT 3000
GCTGGGCCCA CTGGCCGTCC TGCATTCTG GTTCCAGAC CCAATGCCT CCCATTGCGA 3060
TGGATCTCTG CGTTTTATA CTGAGTGTGC CTAGGTTGCC CTTATTTTT TATTTTCCCT 3120
GTTGCGTTGC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180
TAAAGAACT TTTCCAGAA AAAAA

Seq ID NO: 14 Protein sequence:
Protein Accession #: NP_001784.2

1 11 21 31 41 51
| | | | |
MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
KGPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLN KPLDREELAK 180
YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGLVP GTSVMQVTAT 240
DEDDAIYTYN GVVAYSISQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
TDMGDGSGTT TAVAVVELD ANDNAPMFDQ QKYEAHVPEN AVGHEVQRLT VTDLDAPNSP 360
AWRATYLMG GDDGDHFTIT THPESNQIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480
DPAGWLAMDP DSGQVTAVGT LDREDEQFVR NNTYEVMLA MDNGSPPTTG TGTLTLTID 540
VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600
TVVLSLKKFL KQDQYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILPVL 660
GAVLALLFLL LVLLLVRKK RKIKEPLLP EDDTRDNVYF YGEEGGGEED QDYDITQLHR 720
GLEARPEVVL RNDVAPTIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

Seq ID NO: 15 DNA sequence
Nucleic Acid Accession #: XM_051860.2
Coding sequence: 261-4346

1 11 21 31 41 51
| | | | |
GAGCTAGCGC TCAAGCAGAG CCCAGCGCGG TGCTATCGGA CAGAGCCTGG CGAGCGCAAG 60
CGGCGCGGGG AGCCAGCGGG GCTGAGCGCG GCCAGGGTCT GAACCCAGAT TTCCAGACT 120
AGCTACCACT CCGCTTGCCC ACGCCCCGGG AGCTCGCGGC GCCTGGCGGT CAGCGACCA 180
ACGTCCGGGG CCGCTGCGCT CCTGGCCCCG GAGGCGTGAC ACTGTCTCGG CTACAGACCC 240
AGAGGGAGCA CACTGCCAGG ATGGGAGCTG CTGGGAGGCA GGACTTCCTC TTCAAGGCCA 300
TGCTGACCAT CAGCTGGCTC ACTCTGACCT GCTTCCCTGG GGCCACATCC ACAGTGGCTG 360
CTGGGTGCCC TGACCAGAGC CCTGAGTTGC AACCTGGAA CCCTGGCCAT GACCAAGACC 420
ACCATGTGCA TATCGGCCAG GGCAAGACAC TGCTGCTCAC CTCTTCTGCC ACGGTCTATT 480
CCATCCACAT CTCAGAGGGA GGCAAGCTGG TCATTAAAGA CCACGACGAG CCGATTGTTT 540
TGCGAACCAG GCACATCCTG ATTGACAACG GAGGAGAGCT GCATGCTGGG AGTGCCCTCT 600
GCCCTTTCCA GGGCAATTTC ACCATCATTT TGTATGGAAG GGCTGATGAA GGTATTGAGC 660
CGGATCCTTA CTATGGTCTG AAGTACATTG GGGTTGGTAA AGGAGGCGCT CTTGAGTTGC 720
ATGGACAGAA AAAGCTCTCC TGGACATTTC TGAACAAGAC CCTTCACCCA GGTGGCATGG 780
CAGAAGGAGG CTATTTTTTT GAAAGGAGCT GGGGCCACCG TGGAGTTATT GTTCATGTCA 840
TCGACCCCAA ATCAGGCACA GTCATCCATT CTGACCGGTT TGACACCTAT AGATCCAAGA 900
AAGAGAGTGA ACGTCTGGTC CAGTATTGTA ACGCGGTGCC CGATGGCAGG ATCCTTTCTG 960
TTGCAGTGAA TGATGAAGGT TCTCGAAATC TGGATGACAT GGCCAGGAAG GCGATGACCA 1020
AATTGGGAAG CAAACACTTC CTGCACCTTG GATTAGACA CCCTGGAGT TTTCTAACTG 1080
TGAAAGGAAA TCCATCATCT TCAAGTGAAG ACCATATTGA ATATCATGGA CATCGAGGCT 1140
CTGCTGCTGC CCGGGTATTC AAATTGTTCC AGACAGAGCA TGGCGAATAT TCAATGTTT 1200
CTTTGTCCAG TAGTGGGTG CAAGACGTGG AGTGACGGA GTGGTTCGAT CATGATAAAG 1260
TATCTCAGAC TAAAGGTGGG GAGAAAATT CAGACCTCTG GAAAGCTCAC CCAGGAAAAA 1320
TATGCAATCG TCCCATTGAT ATACAGGCCA CTACAATGGA TGGAGTTAAC CTCAGCACCG 1380
AGGTTGTCTA CAAAAAAGGC CAGGATTATA GGTTTGCTTG CTACGACCGG GGCAGAGCCT 1440
GCCGGAGCTA CCGTGTACGG TTCTCTGTG GGAAGCCTGT GAGGCCCAAA CTCACAGTCA 1500
CCATTGACAC CAATGTGAAC AGCACCATTG TGAACCTGGA GGATAATGTA CAGTCATGGA 1560
AACCTGGAGA TACCTGGTC ATTGCCAGTA CTGATTACTC CATGTACCAG GCAGAAGAGT 1620
TCCAGGTGCT TCCCTGCAGA TCCTGCGCCC CCAACCAGGT CAAAGTGGCA GGGAAACCAA 1680
TGTACCTGCA CATCGGGGAG GAGATAGACG GCGTGGACAT GCGGGCGGAG GTTGGGCTTC 1740
TGAGCCGGAA CATCATAGTG ATGGGGGAGA TGGAGGACAA ATGCTACCCC TACAGAAACC 1800
ACATCTGCAA TTCTTTGAC TTCGATACCT TTGGGGGCCA CATCAAGTTT GCTCTGGGAT 1860

TTAAGGCAGC AACTTTGGAG GGCACGGAGC TGAAGCATAT GGGACAGCAG CTGGTGGGTC 1920
AGTACCCGAT TCACTTCCAC CTGGCCGGTG ATGTAGACGA AAGGGGAGGT TATGACCCAC 1980
CCACATACAT CAGGGACCTC TCCATCCATC ATACATTCTC TCGCTGCGTC ACAGTCCATG 2040
GCTCCAATGG CTGTGTGATC AAGGACGTTG TGGGCTATAA CTCTTTGGGC CACTGCTTCT 2100
TCACGGAAGA TGGGCCGGAG GAACGCAACA CTTTGGACCA CTGTCTTGGC CTCCTTGTC 2160
AGTCTGGAAC CCTCCTCCCC TCGGACCGTG ACAGCAAGAT GTGCAAGATG ATCAGAGAGG 2220
ACTCCTACCC GGGGTACATC CCAAGCCCA GGCAAGACTG CAATGCTGTG TCCACCTTCT 2280
GGATGGCCAA TCCCAACAAC AACCTCATCA ACTGTGCCGC TGCAGGATCT GAGGAACTG 2340
GATTTTGGTT TATTTTTCAC CACGTACCAA CGGGCCCTC CGTGGGAATG TACTCCCCAG 2400
GTTATTGAGA GCACATTCCA CTGGGAAAAT TCTATAACAA CCGAGCACAT TCCAACCTACC 2460
GGGCTGGCAT GATCATAGAC AACGGAGTCA AAACCACCGA GGCTCTGCC AAGGACAAGC 2520
GGCCGTTCTT CTCAATCATC TGTCCAGAT ACAGCCCTCA CCAGGACGCC GACCCGCTGA 2580
AGCCCGGGA GCCGGCCATC ATCAGACACT TCATTGCCTA CAAGAACCAG GACCACGGGG 2640
CCTGGCTGCG CGGGGGGAT GTGTGGCTGG ACAGCTGCCG GTTTGCTGAC AATGGCATTG 2700
GCCTGACCCT GGCCAGTGGT GGAACCTTCC CGTATGACGA CGGCTCCAAG CAAGAGATAA 2760
AGAACAGCTT GTTTGTGGC GAGAGTGGCA ACCTGGGGAC GGAAATGATG GACAATAGGA 2820
TCTGGGGCCC TGGCGGCTTG GACCATAGCG GAAGGACCCT CCCTATAGGC CAGAATTTTC 2880
CAATTAGAGG AATTCAGTTA TATGATGGCC CCATCAACAT CCAAACTGC ACTTTCCGAA 2940
AGTTTGTGGC CCTGGAGGGC CGGCACACCA GCGCCCTGGC CTCCGCTG AATAATGCCT 3000
GGCAGAGCTG CCCCCATAAC AACGTGACCG GCATTGCCTT TGAGGACGTT CCGATTACTT 3060
CCAGAGTGTT CTTCGGAGAG CCTGGGCCCT GGTTCACCA GCTGGACATG GATGGGGATA 3120
AGACATCTGT GTTCCATGAC GTCGACGGCT CCGTGTCCGA GTACCCTGGC TCCTACCTCA 3180
CGAAGAATGA CAACTGGCTG GTCCGGCACC CAGACTGCAT CAATGTCCC GACTGGAGAG 3240
GGGCCATTG CAGTGGGTGC TATGCACAGA GTACATTCA AGCCTACAAG ACCAGTAACC 3300
TGCGAATGAA GATCATCAAG AATGACTTCC CCAGCCACCC TCTTACCTG GAGGGGGCGC 3360
TCACCAGGAG CACCCATTAC CAGCAATACC AACCGGTTGT CACCCTGCAG AAGGGCTACA 3420
CCATCCACTG GGACCAGACG GCGCCCGCG AACTCGCCAT CTGGCTCATC AACTCAACA 3480
AGGGCGACTG GATCCGAGTG GGGCTCTGCT ACCCGCGAGG CACCACATTC TCCATCCTCT 3540
CGGATGTTCA CAATCGCTG CTGAAGCAAA CGTCCAAGAC GGGCGTCTTC GTGAGGACCT 3600
TGCAGATGGA CAAAGTGGAG CAGAGCTACC CTGGCAGGAG CCACTACTAC TGGGACGAGG 3660
ACTCAGGGCT GTTGTTCCTG AAGCTGAAAG CTCAGAACGA GAGAGAGAAG TTTGCTTCT 3720
GCTCCATGAA AGGCTGTGAG AGGATAAAGA TTAAAGCTCT GATTCCAAAG AACGCAGGCG 3780
TCAGTGACTG CACAGCCACA GCTTACCCCA AGTTCACCGA GAGGGCTGTC GTAGACGTGC 3840
CGATGCCCAA GAAGCTCTT GGTTCACG TGAAACAAA GGACCATTTT TTGGAGGTGA 3900
AGATGGAGAG TTCCAAGCAG CACTTCTTCC ACCTCTGGA CGACTTCGCT TACATTGAAG 3960
TGGATGGGAA GAAGTACCC AGTTCGGAGG ATGGCATCCA GGTGGTGGTG ATTGACGGGA 4020
ACCAAGGGCG CGTGGTGAGC CACACGAGCT TCAGGAACTC CATTCTGCAA GGCATACCAT 4080
GGCAGCTTTT CAACTATGTG GCGACCATCC CTGACAATTC CATAGTGCTT ATGGCATCAA 4140
AGGGAAGATA CGTCTCCAGA GGCCCATGGA CCAGAGTGCT GGAAAAGCTT GGGGAGACA 4200
GGGTCTCAA GTTGAAGAG CAAATGGCAT TCGTTGGCTT CAAAGGCAGC TTCCGGCCCA 4260
TCTGGGTGAC ACTGGACACT GAGGATCACA AAGCCAAAAT CTTCAGTT GTGCCATCC 4320
CTGTGGTGAA GAAGAAGAAG TTGTGAGGAC AGCTGCCGCC CGGTGCCACC TCGTGGTAGA 4380
CTATGACGGT GACTCTTGGC AGCAGACCAG TGGGGGATGG CTGGGTCCCC CAGCCCCTGC 4440
CAGCAGCTGC CTGGGAAGGC CGTGTTCAG CCTGTATGGG CCAAGGGAAG GCTATCAGAG 4500
ACCCTGGTGC TGCCACCTGC CCTACTCAA GTGTCTACCT GGAGCCCTG GGGCGGTGCT 4560
GGCCAATGCT GGAAACATTC ACTTTCCTGC AGCCTCTGG GTGCTCTCT CCTATCTGTG 4620
CCTCTTCAGT GGGGGTTTGG GGACCATATC AGGAGACCTG GGTGTGCTG ACAGCAAAGA 4680
TCCACTTTGG CAGGAGCCCT GACCCAGCTA GGAGGTAGTC TGGAGGGCTG GTCAATCACA 4740
GATCCCCATG GTCTTCAGCA GACAAGTGAG GGTGGTAAAT GTAGGAGAAA GAGCCTTGGC 4800
CTTAAGGAAA TCTTACTCC TGTAAGCAAG AGCCAACCTC ACAGGATTAG GAGCTGGGGT 4860
AGAAGTGGCT ATCCTTGGGG AAGAGGCAAG CCCTGCTCT GGGCGTGTCC ACCTTTCAGG 4920
AGACTTTGAG TGGCAGGTTT GGACTTGGAC TAGATGACTC TCAAAGGCCC TTTAGTTCT 4980
GAGATTCCAG AAATCTGCTG CATTTCACAT GGTACCTGGA ACCCAACAGT TCATGGATAT 5040
CCACTGATAT CCATGATGCT GGGTGCCCCA GCGCACACGG GATGGAGAGG TGAGAACTAA 5100
TGCCTAGCTT GAGGGGTCTG CAGTCCAGTA GGGCAGGCAG TCAGGTCCAT GTGACTGCA 5160
ATGCCAGGTG GAGAAATCAC AGAGAGGTAA AATGGAGGCC AGTGCCATT CAGAGGGGAG 5220
GCTCAGGAAG GCTTCTTGCT TACAGGAATG AAGGCTGGGG GCATTTTGCT GGGGGGAGAT 5280
GAGGCAGCCT CTGGAATGGC TCAGGGATTC AGCCCTCCCT GCCGCTGCCT GCTGAAGCTG 5340
GTGACTACGG GGTCCGCCCT TGCTACGTC TCTTGCCCC ACTCATGATG GAGAAGTGTG 5400
GTCAGAGGGG AGCAATGGGC TTTGCTGCTT ATGAGCACAG AGGAATTCAG TCCCAGGCA 5460
GCCCTGCCTC TGACTCCAAG AGGGTGAAGT CCACAGAAGT GAGCTCTGC CTTAGGGCT 5520
CATTTGCTCT TCATCCAGGG AACTGAGCAC AGGGGGCTC CAGGAGACCC TAGATGTGCT 5580
CGTACTCCCT CGGCCTGGGA TTTCAGAGCT GGAAATATAG AAAATATCTA GCCCAAAGCC 5640
TTCATTTTAA CAGATGGGGA AAGTGAGCCC CCAAGATGGG AAAGAACCAC ACAGCTAAGG 5700
GAGGGCCTGG GGAGCCCCAC CTTAGCCCTT GCTGCCACAC CACATTGCCT CAACAACCGG 5760
CCCCAGAGTG CCCAGGCACT CTTGAGGTAG CTCTGGAAA TGGGGACAAG TCCCTCGAA 5820
GGAAAGGAAA TGACTAGAGT AGAATGACAG CTAGCAGATC TCTCCCTCC TGCTCCAGC 5880
GCACACAAAC CCGCCCTCCC CTGGGTGTTG GCGGTCCCTG TGGCCTTCACT TTTGTTCACT 5940
ACCTGTCAGC CCAGCCTGGG TGCACAGTAG CTGCAACTCC CCATTGGTGC TACCTGGCTC 6000
TCCTGTCTCT GCAGCTCTAC AGGTGAGGCC CAGCAGAGGG AGTAGGGCTC GCCATGTTTC 6060
TGGTGAGCCA ATTTGGCTGA TCTTGGGTGT CTGAACAGCT ATTGGGTCCA CCCCAGTCCC 6120
TTTCAGCTGC TGCTTAATGC CCTGCTCTCT CCCTGGCCA CTTATAGAG AGOCCAAAGA 6180
GCTCCTGTAA GAGGGAGAAC TCTATCTGTG GTTTATAATC TTGCACGAGG CACCAGAGTC 6240
TCCCTGGGTC TTGTGATGAA CTACATTTAT CCCCTTCTCT GCCCCAACCA CAACTCTTT 6300
CCTTCAAAGA GGGCCTGCCT GGCTCCCTCC ACCCAACTGC ACCCATGAGA CTCGGTCCAA 6360
GAGTCCATTG CCCAGGTGGG AGCCAACCTG CAGGGAGGTC TTTCCACCA AACATCTTT 6420
AGCTGCTGGG AGGTGACCAT AGGGCTCTGC TTTAAAGAT ATGGCTGCTT CAAAGGCCAG 6480
AGTCACAGGA AGGACTTCTT CCAGGGAGAT TAGTGGTGAT GGAGAGGAGA GTTAAATGA 6540
CCTCATGTCC TCTTGTCCA CGGTTTGTG GAGTTTTCAC TCTTCTAATG CAAGGGTCTC 6600
ACACTGTGAA CCACTTAGGA TGTGATCACT TTCAGGTGGC CAGGAATGTT GAATGTCTT 6660
GGCTCAGTTC ATTTAAAAA GATATCTATT TGAAAGTTCT CAGAGTTGA CATATGTTTC 6720
ACAGTACAGG ATCTGTACAT AAAAGTTTCT TTCTAAACC ATTCACCAAG AGCCAATATC 6780
TAGGCATTTT CTGGTAGCA CAAATTTTCT TATGCTTAG AAAATGTGTC TCCTTGTAT 6840
TTCTGTTTGT AAGACTTAAG TGAGTTAGGT CTTTAAAGGA AGCAACGCTC CTCTGAAATG 6900
CTTGTCTTTT TTCTGTTGCC GAAATAGCTG GTCCTTTTTC GGGAGTTAGA TGTATAGAGT 6960
GTTTGTATGT AAACATTTCT TGTAGGCATC ACCATGAACA AAGATATATT TCTATTTAT 7020

TTATTATATG TGCACCTCAA GAAGTCACTG TCAGAGAAAT AAAGAATTGT CTAAATGTC

Seq ID NO: 16 Protein sequence:
Protein Accession #: XP_051860.2

```

1      11      21      31      41      51
|      |      |      |      |
MGAAGRQDFL FKAMLTISWL TLTCFPGATS TVAAGCPDQS PELQPWNPGH DQDHHVHIGQ 60
GKTLTLLTSSA TVYSIHSEG GKLVIKDHDE PIVLRTRHIL IDNGGELHAG SALCPFQGNF 120
TIILYGRADE GIQDPYGYL KYIGVGKGGG LELHGQKKLS WTFLNKTLP GGMAEGGYFF 180
ERSWGHGRGVI VHVIDPKSGT VIHSDRFDTY RSKKESERLV QYLNAVDPGR ILSVAVNDEG 240
SRNLDDMARK AMTKLGSKHF LHLGFRHPWS FLTVKGNPSS SVEDHIEYHG HRGSAAARVF 300
KLFQTEHGEY FNVLSSEWV QDVEWTEWFD HDKVSQTKGG EKISDLWKAH PGKICNRPID 360
IQATTMDGVN LSTEVVYKKG QDYRFACYDR GRACRSYRVR FLCGKPVVRP LTVTIDTNVN 420
STILNLEDNV QSWKPGDTLV IASTDSMYQ AEEFQVLPGR SCAPNQVKVA GKPMYHIGE 480
EIDGVDMRAE VGLLSRNIV MGEMEDKCYP YRNHICNFFD FDTFGGHIKF ALGFKAHLE 540
GTELKHMGGQ LVGQYPIHFH LAGDVDERGG YDPPTYIRDL SIHHTFSRCV TVHGSNGLLI 600
KDVVGYNSLG HCFETEDGPE ERNTFDHCLG LLVKSGLLP SDRDSKMCKM ITEDSYPGYI 660
PKPRQDCNAV STFWMANPNN NLINCAAAGS EETGFWFIFH HVPTGPSVGM YSPGYSEHIP 720
LGKFYNNRAH SNYRAGMIID NGVKTTEASA KDKRFPLSI SARYSFHQDA DPLKPREPAI 780
IRHFIAKYNQ DHGAWLRGGD VWLDSRFAD NGIGLTLASG GTFPYDDGSK QEIKNSLFVG 840
ESGNVGTEMM DNRIWGPGL DHSGRTLPIG QNFPIRGIQL YDGPINQNC TFRKFVALEG 900
RHTSALAFRL NNAWQSCPHN NVTGLAFEDV PITSRVFFGE PGPWFNQLDM DGDKTSVFHD 960
VDGSVSEYPG SYLTKNNDWL VRHPDCINVP DWRGACISGC YAQMYIQAQY TSNLRMKIHK 1020
NDFPSHPLYL EGALTRSTHY QYQPVVTLQ KGYTIHWDQT APAELAIWLI NFNKGDWIRV 1080
GLCYPGRGTF SILSDVHNR LKQTSKTGVF VRTLQMDKVE QSYPRGRSHYY WDEDSGLLFL 1140
KLKAQNEREK FAFCSMKGCE RIKIKALPK NAGVSDCTAT AYPKFTERAV VDVPMPPKLF 1200
GSQLKTKDHF LEVKMESSKQ HFFHLWDFH YIEVDGKKYP SSEDGIQVVV IDGNQGRVVS 1260
HTSFRNSILQ GIPWQLFNYV ATIPDNSIVL MASKGRYVSR GPWTRVLEKL GADRGLKLKE 1320
QMAFVGFKGS FRPIWVTLDT EDHKAKIFQV VPIPVVKKKK L

```

Seq ID NO: 17 DNA sequence
Nucleic Acid Accession #: NM_015515.1
Coding sequence: 61-1329

```

1      11      21      31      41      51
|      |      |      |      |
AGTTCTGCGG TGCCAGGGAG TGGAGCAGAG CTCAGCCCCG TCCCAAACAC AGATGGGACC 60
ATGAACTCCG GACACAGCTT CAGCCAGACC CCTCGGCCT CCTTCCATGG CGCCGGAGGT 120
GGCTGGGGCC GGCCAGGAG CTTCACAGG GCTCCACCG TCCATGGCGG TGCGGGGGGA 180
GCCCGCATCT CCTGTCTT CACCACCGG AGCTGCCAC CCCCTGGAGG GTCCTGGGGT 240
TCTGGAAGAA GCAGCCCCCT ACTAGGCGGA AATGGGAAGG CCACCATGCA GAATCTCAAC 300
GACCGCCTGG CCTCTACCT GGAGAAGGTT CGCGCCCTGG AGGAGGCCAA CATGAAGCTG 360
GAAAGCCGCA TCCTGAAATG GCACAGCAG AGAGATCCTG GCAGTAAGAA AGATTATTCC 420
CAGTATGAGG AAAACATCAC ACACCTGCAG GAGCAGATAG TGGATGGTAA GATGACCAAT 480
GCTCAGATTA TTCTTCTCAT TGACAATGCC AGGATGGCAG TGGATGACTT CAACCTCAAG 540
TATGAAAATG AACACTCCTT TAAGAAAGAC TTGGAATTTG AAGTCGAGGG CCTCCGAAGG 600
ACCTTAGACA ACCTGACCAT TGTCACAACA GACCTAGAAC AGGAGGTGGA AGGAATGAGG 660
AAAGAGCTCA TTCTCATGAA GGAGCACCAT GAGCAGGAAA TGGAGGAGCA TCATGTGCCA 720
AGTGACTTCA ATGTCAATGT GAAGGTGGAT ACAGGTCCCA GGGAAGATCT GATTAAGGTC 780
CTGGAGGATA TGAGACAAGA ATATGAGCTT ATAATAAAGA AGAAGCATCG AGACTTGGAC 840
ACTTGGTATA AAGAACAGTC TGCAGCCATG TCCAGGAGG CAGCCAGTCC AGCCACTGTG 900
CAGAGCAGAC AAGGTGACAT CCACGAACTG AAGCGCACAT TCCAGGCCCT GGAGATTGAC 960
CTGCAGGCAC AGTACAGCAC GAAATCTGCT TTGAAAAACA TGTTATCCGA GACCCAGTCT 1020
CGGTACTCCT GCAAGCTCCA GGACATGCAA GAGATCATCT CCCACTATGA GGAGGAACTG 1080
ACGCAGCTAC GCCACGAACT GGAGCGGCAG AACAATGAAT ACCAAGTGCT GCTGGGCATC 1140
AAAACCCACC TGGAGAAGGA AATCACCACG TACCGACGGC TCCTGGAGGG AGAGAGTGAA 1200
GGGACACGGG AAGAATCAAA GTCGAGCATG AAAGTGTCTG CAACTCCAAA GATCAAGGCC 1260
ATAACCCAGG AGACCATCAA CGGAAGATTA GTTCTTTGTC AAGTGAATGA AATCCAAAAG 1320
CAGCATGAG ACCAATGAAA GTTCCGCT GTTGTAAGT CTATTTTCCC CCAAGGAAAAG 1380
TCCTTGACA GACACCAGTG AGTGAGTTCT AAAAGATACC CTTGGAATTA TCAGACTCAG 1440
AAACTTTTAT TTTTITTTT CTGTAACAGT CTCACCAGAC TTCTCATAAT GCTCTTAATA 1500
TATTGCACTT TTCTAATCAA AGTGCAGTT TATGAGGGTA AAGCTCTACT TTCTACTGC 1560
AGCCTTCAGA TTCTCATCAT TTTGCATCTA TTTGTAGCC AATAAACTC CGCACTAGC

```

Seq ID NO: 18 Protein sequence:
Protein Accession #: NP_056330.1

```

1      11      21      31      41      51
|      |      |      |      |
MNSGHSFSQT PSASFHAGG GWGRPRSFPR APTVHGGAGG ARISLSFTTR SCPPPGGSWG 60
SGRSSPLLGG NGKATMQNLN DRLASYLEKV RALEEANMKL ESRILKWHQQ RDPGSKKDYS 120
QYEENITHLQ EQIVDGKMTN AQILLIDNA RMAVDDFNK YENEHSFKKD LEIEVEGLRR 180
TLDNLITVTT DLEQEVEGMR KELILMKEHH EQEMEEHVP SDFNVNVKVD TGPREDLIKV 240
LEDMRQYEL IKKKHKRDL TWYKEQSAAM SQEAASPATV QSRQGDHIL KRTFQALEID 300
LQAQYSTKSA LENMLSETQS RYSCKLQDMQ EIISHYEEEL TQLRHELERQ NNEYQVLLGI 360
KTHLEKEITT YRRLLEGESE GTREESKSSM KVSATPKIKA ITQETINGRL VLCQVNEIQK 420
HA

```

Seq ID NO: 19 DNA sequence
Nucleic Acid Accession #: see Table 25 & 25A for complete list

```

1      11      21      31      41      51
|      |      |      |      |

```


TTTTTTTTTT TAAAAAAA GAGGCTTGGT AAGTTTTTGA TACTTAGTTG ACTTTTAGCA 60
TTATCCAGCA TTTGTATTAT GAACCAGTGA GTACTGTAAT TTTTCTTTCC CTTTCAGAAA 120
GACTCAAAGG GAACATATAA ATGTTTCTTA TTTTNNNNNN NNNNNNNNNN NNNNNNNNNN 180
NNNNNACCCAT CGTGCGATGA TCNNNNNNNN NNNNNNNNNN NNNNNNTTGGG ATCCAGTTTC 240
AAATAAGGTA TGGGAAAAAC AGATGTTTTT ATTATCGCCA CTTAATCCTT ACTTCCGATT 300
ATAATTATAC ATGTTTGGCT GTAATACTA TACTAAAGCA TGCTTGTGAA AGTAGACTTC 360
TACAAGGACA GAAAACCCAC AACAACAAAG ATCGATCACG AAAGACAAGG CATATTTCATT 420
CATTAAATTTA CTTCTCTTAG ACCCGGGACA TGTGGGACAA ATACTTTTGT CCTCATGGAT 480
GGCTTGATAA TTTATTTATA TGTCTAGAG TCTGAGGATT TTCTTTCAGT GGCAGACAAC 540
AAAGGATGTT ACAATTTACT TCAAAATAAT ACAATCATGG TTTAATTAC AGTGTAATC 600
CATAACTATT TTATAGAGAT GGATTATCAT ACATGGGATT ATAAAAATAA CTTACCCATA 660
TGCTTGCAAA ATAGACTTTT CCTATTGGGA GGAACATCTT TTAACCTAAA ACGGATTTAT 720
TTCAGATGAA TTAGACAGTA CATTTTTCAG GAGAACCAGC CTTACTGGAT GATCTTTTGT 780
CAGGTTTGA GGCCTCTTCT TTGTCTTTCG AACCATAACC CCTTTTCAGC TGAAGACCAC 840
TGGCCTTCAA CCAAGCCAG GAGTTTGGCT CAAATGA

Seq ID NO: 20 DNA sequence

Nucleic Acid Accession #: D32051.1

Coding sequence: 72-1373

1 11 21 31 41 51
| | | | |
GAATTCGAAC CAGGTGGCCA CCCGGTGTG GTTTCATTTT CCTTTGGAAT TTCTGCTTTA 60
CAGACAGAAC AATGGCAGCC CGAGTACTTA TAATTGGCAG TGGAGGAAGG GAACATACGC 120
TGGCCTGGAA ACTTGACAG TCTCATCATG TCAAACAAGT GTTGGTTGCC CCAGGAAACG 180
CAGGCACTGC CTGCTCTGAA AAGATTTCAA ATACCGCCAT CTCAATCAGT GACCACACTG 240
CCCTTGCTCA ATTCTGCAAA GAGAAGAAAA TTGAATTTGT AGTTGTTGGA CCAGAAGCAC 300
CTCTGGCTGC TGGGATTGTT GGAACCTGA GGTCTGCAGG AGTGCAATGC TTTGGCCCAA 360
CAGCAGAAGC GGCTCAGTTA GAGTCCAGCA AAAGGTTTGC CAAAGAGTTT ATGGACAGAC 420
ATGGAATCCC AACCACACAA TGGAAGGCTT TCACCAAACC TGAAGAAGCC TGCAGCTTCA 480
TTTTGAGTGC AGACTTCCCT GCTTTGGTTG TGAAGGCCAG TGGTCTTGCA GCTGAAAAAG 540
GGGTGATTGT TGCAAAGAGC AAAGAAGAGG CCTGCAAAGC TGTACAAGAG ATCATGCAGG 600
AGAAAGCCTT TGGGGCAGCT GGAGAAACAA TTGTCAATTGA AGAACTTCTT GACGGAGAAG 660
AGGTGTCGTG TCTGTGTTT ACTGATGGCA AGACTGTGGC CCCCATGCCC CCAGCACAGG 720
ACCATAAGCG ATTACTGGAG GGAGATGGTG GCCCTAACAC AGGGGGAATG GGAGCCTATT 780
GTCCAGCCCC TCAGGTTTCT AATGATCTAT TACTAAAAAT TAAAGATACT GTTCTTCAGA 840
GGACAGTGGA TGGCATGCAG CAAGAGGGTA CTCCATATAC AGGTATTCTC TATGCTGGAA 900
TAATGCTGAC CAAGAATGGC CCAAAGTTC TAGAGTTTAA TTGCCGTTT GGTGATCCAG 960
AGTGCCAAGT AATCCTCCCA CTCTTAAAA GTGATCTTTA TGAAGTGATT CAGTCCACCT 1020
TAGATGGACT GCTCTGCACA TCTCTGCCTG TTTGGCTAGA AAACCACACC GCCCTAACTG 1080
TTGTCAATGG AAGTAAAGGT TATCCTGGAG ACTACACCAA GGGTGTAGAG ATAACAGGGT 1140
TTCTTGAGGC TCAAGCTCTA GGACTGGAGG TGTCCCATGC AGGCACTGCC CTCAAAAATG 1200
GCAAAGTAGT AACTCATGGG GGTAGAGTTC TTGCAGTCAC AGCCATCCGG GAAAAATCTCA 1260
TATCAGCCCT TGAGGAAGCC AAGAAAGGAC TAGCTGCTAT AAAGTTTGAG GGAGCAATTT 1320
ATAGGAAAGA CATCGGCTTT CGTGCCATAG CTTTCTCCA GCAGCCCAGG TAAAACTCTA 1380
AGCAAGTTAG CTGTAGTGCC ATTTAGAAAA CTGGCCTAAA TGGCTATGTA GAACATTCCA 1440
TTAACCTAT AAGTCATTCA GTATTCTTT CTCTCTGTGG GAGTGATACA GTCTTGGTTT 1500
GTATTTTGTG TGAATCAAAA CTGGTTATAG CAATACTCAA ATGGAAAAAA CTTCATGATA 1560
GCGTAAGTTT GGAAAGTTTA GCAAAATCAC AGTGGTACTG ATTTTATTT GTTTTCTATT 1620
TTTTTATTT TATATTTTA ATTTTAA CAGGGTCTT CTCTCTGCC CAAGTTCTCA 1680
TGCCTCAGCC TCCCAAATAG CTGGGACTAC AGGCACAGGC CACCACACCT GGCTAATTTT 1740
TTTGTATTT TTGTGGAGAT GGGGTTACAC ATGTTGCCAA GGCCAGTCTG AAAGCCTGGG 1800
CTCAAGTGAT CCTCTGCTT TGGCTCCCA AAATGCTGGG ACTATAGGCA TGAGGCGCTG 1860
CACTTGGCCT GATACTGATT TTTATTCCT CGGTTATCAC ATAGTGTGT ATTTGAAACA 1920
TAGTTCATGG TTTTATCAA GAACTGAAGA TGAGAATACT GGTCACTAA CTTTGTAAAT 1980
TGATTTGATT ATACTGTAAT GTTTGACAGT CCCATTTTAA CTGCGTTTG TATCTATTAC 2040
TAAAATGTAT TTTTGACCT CTTACTGATT CATGGTTGGT ATGTACAAAC TGTTGACTTG 2100
TAAAATCAAT AAAGTCTTAG TTGG

Seq ID NO: 21 Protein sequence

Protein Accession #: BAA06809.1

1 11 21 31 41 51
| | | | |
MAARVLIIGS GGREHTLAWK LAQSHHVQV LVAPGNAGTA CSEKISNTAI SISDHTALAQ 60
FCKEKKIEFV VVGPEAPLAA GIVGNLRSAG VQCFGPTAEA AQLESSKRFA KEFMDRHGIP 120
TAQWKAFKTP EEACSFILSA DFPALVVKAS GLAAGKGVV AKSKEEACKA VQEIMQEKAF 180
GAAGETVIE ELLDGEVSC LCFTDGKTVA PMPPAQDHKR LLEGDGGPNT GGMGAYCPAP 240
QVSNDLLKI KDTVLQRTVD GMQQEGTPYT GILYAGIMLT KNGPKVLEFN CRFGDPECQV 300
ILPLLKSDLY EVIQSTLDGL LCTSLPVWLE NHTALTVMMA SKGYPGDYTK GVEITGFPEA 360
QALGLEVSHA GTALKNGKVV THGGRVLAVT AIRENLISAL EEAKKGLAAI KFEGAIYRKD 420
IGFRAIAFLQ QPR

Seq ID NO: 22 DNA sequence

Nucleic Acid Accession #: EOS cloned

Coding sequence: 1-2424

1 11 21 31 41 51
| | | | |
ATGCCCCCTT TCCTGTTGCT GGAGGCCGTC TGTGTTTTCC TGTTTTCCAG AGTGCCCCCA 60
TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGCC 120
AGCAAAATGA TGTGGTGCTC GGCTGCAGTG GACATCATGT TTCTGTTAGA TGGGTCTAAC 180

AGCGTCGGGA AAGGGAGCTT TGAAAGGTCC AAGCACTTTG CCATCACAGT CTGTGACGGT 240
 CTGGACATCA GCCCCGAGAG GGTCAGAGTG GGAGCATTCC AGTTCAGTTC CACTCCTCAT 300
 CTGGAATTCC CTTGGATTTC ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360
 ATGGTTTTCA AAGGAGGGCG CACGGAGACG GAACTTGCTC TGAAATACCT TCTGCACAGA 420
 GGGTTGCCTG GAGGCAGAAA TGCTTCTGTG CCCCAGATCC TCATCATCGT CACTGATGGG 480
 AAGTCCCAGG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCAGTGTG 540
 TTTGCTGTGG GGGTCAGGTT TCCCAGGTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT 600
 AGAGGGCAGC ACGTGCTGTT GGCTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC 660
 ACCCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC 720
 CCCTGTGAGC ACAGGACGCT GGAGATGGTC CGGGAGTTCG CTGGCAATGC CCCATGCTGG 780
 AGAGGATCGC GCGGACCCCT TGCCTGTCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG 840
 AGAGTGTTC TAACCCACCC TGCCACCTGC TACAGGACCA CCTGCCAGG CCCCTGTGAC 900
 TCGCAGCCCT GCCAGAATGG AGGCACATGT GTTCCAGAAG GACTGGACGG CTACCAAGTGC 960
 CTCTGCCCGC TGGCCTTTGG AGGGGAGGCT AACTGTGCC TGAAGCTGAG CCTGGAATGC 1020
 AGGGTCGACC TCCTCTTCCT GCTGGACAGC TCTGCGGGCA CCACTCTGGA CGGCTTCCTG 1080
 CGGGCCAAAG TCTTCGTGAA GCGGTTTGTG CGGGCCGTGC TGAGCGAGGA CTCTCGGGCC 1140
 CGAGTGGGTG TGGCCACATA CAGCAGGAGC CTGCTGTGG CGTGCCTGT GGGGGAGTAC 1200
 CAGGATGTGC CTGACCTGGT CTGGAGCCTC GATGGCATT CTTCCGTGG TGGCCCCACC 1260
 CTGACGGGCA GTGCCTTGC GAGGCGGCA GAGCGTGGCT TCGGGAGCGC CACCAGGACA 1320
 GGCCAGGACC GGCCACGTAG AGTGTGGTT TTGCTCACTG AGTCACACTC CGAGGATGAG 1380
 GTTGCGGGCC CAGCGCGTCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT 1440
 GAGGCCGTGC GGGCAGAGCT GGAGGAGATC ACAGGCAGCC CAAAGCATGT GATGGTCTAC 1500
 TCGGATCCTC AGGATCTGTT CAACCAAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCCGG 1560
 CAGCGGCCAG GGTGCCGGAC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CACCTCTGCC 1620
 TCAGTAGGGC CCGAGAATTT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG 1680
 TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCCTGGTGG TGTATGGCAG CCAGGTGCAG 1740
 ACTGCCTTCG GGCTGGACAC CAAACCCACC CGGGCTGCGA TGCTGCGGGC CATTAGCCAG 1800
 GCCOCTACC TAGGTGGGT GGGCTCAGCC GGCACCGCC TGCTGCACAT CTATGACAAA 1860
 GTGATGACCG TCCAGAGGGG TGCCCGCCT GGTGTCCCA AAGCTGTGGT GGTGCTCACA 1920
 GCGGGAGAG GCGCAGAGGA TGCAGCGTT CCTGCCAGA AGCTGAGGAA CAATGGCATC 1980
 TCTGTCTTG TCGTGGGCGT GGGGCCTGTC CTAAGTGAGG GTCTGCGGAG GCTTGACAGT 2040
 CCCCAGGATT CCTGATCCA CGTGGCAGCT TACGCCGACC TGCGGTACCA CCAGGACGTG 2100
 CTCATTGAGT GGCTGTGTGG AGAAGCCAAG CAGCCAGTCA ACCTCTGCAA ACCAGCCCG 2160
 TGCATGAATG AGGGCAGCTG CGTCTGCAG AATGGGAGCT ACCGTGCAA GTGTGCGGAT 2220
 GGCTGGGAGG GCGCCACTG CGAGAACCGT GAGTGGAGCT CTTGCTCTGT ATGTGTGAGC 2280
 CAGGGATGGA TTCTTGAGAC GCCCTGAGG CACATGGCTC CCGTGCAGGA GGGCAGCAGC 2340
 CGTACCCCTC CCAGCAACTA CAGAGAAGGC CTGGGCACTG AAATGGTGCC TACCTTCTGG 2400
 AATGTCTGTG CCCCAGGTCC TTAG

Seq ID NO: 23 Protein sequence:

Protein Accession #: EOS cloned

1 11 21 31 41 51
 | | | | |
 MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
 SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFLDLSFST QQEVKARIKR 120
 MVFKGGRTET ELALKYLLHR GLPGGRNASV PQLIIVTDG KSQGDVALPS KQLKERGVTV 180
 FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSAJCSS ATPDCRVEAH 240
 PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD 300
 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
 RAKVVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGPT 420
 LTGSALRQAA ERFGSATTRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLVGS 480
 EAVRAELEEI TGSPKHVMVY SDPQDLFNQI PELQGKLCR QRPGRCTQAL DLVFMLDTS 540
 SVGPENFAQM QSFVRSCALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
 APYLGGVGS A GTALLHIYDK VMTVQRGAR GVPKAVVLT GGRGAEDAAV PAQKLNNNGI 660
 SVLVVGVPV LSEGLRRLAG PRDSLIHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP 720
 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETFLR HMAPVQEGSS 780
 RTPPSNYREG LGTEMVPTFW NVCAFGP

Seq ID NO: 24 DNA sequence

Nucleic Acid Accession #: see Table 25 & 25A for complete list

1 11 21 31 41 51
 | | | | |
 AGGTCGGCTG GTTATCGGGA GTTGGAGGGC TGAGGTCGGG AGGGTGGTGT GTACAGAGCT 60
 CTAGGACTCA CGCACCAGGC CAGTCGCGGG TTTTGGGCGG AGGCCTGGGT TACAAGCAGC 120
 AAGTGC GCGG TTGGGGCCAC TCGAGGCGG TTTTAGAAAA CTGTTTAAAA CAAAGAGCAA 180
 TTGATGGATA AATCAGGAAT AGATTCTCTT GACCATGTGA CATCTGATGC TGTGGAACCT 240
 GCAAATCGAA GTGATAACTC TTCTGATAGC AGCTTATTTA AAACCTCAGTG TATCCCTTAC 300
 TCACCTAAAG GGGAGAAAAA AAACCCCAT CGAAAAATTG TTCGTACACC TGAAGTGTT 360
 CACGCAAGTA TTCATCAAGT GACTCATCTT TTGAACCACT ACCATTGACT ATAAAAGCTA 420
 TTTTGTAAAG ATTCAAGAAC AGGAAAAAGA GATATAAAAA AAAGAAAAAG AGGAGGTACC 480
 AGCCAACAGG AAGACCACGG GGAAGACCAG AAGGAAGGAG AAATCCTATA TACTACTAA 540
 TAGATAAGAA GAAACAATTT AGAAGCAGAG GATCTGGCTT CCCATTTTGA GAATCAGAGA 600
 ATGAAAAAAA CGCACCTTGG AGAAAAATTT TAACGTTTGA GCAAGCTGTT GCAAGAGGAT 660
 TTTTAACTA TATTGAAAAA CTGAAGTATG AACACCACCT GAAAGAATCA TTGAAGCAAA 720
 TGAATGTTGG TGAAGATTGA GAAAATGAAG ATTTTGACAG TCGTAGATAC AAATTTTGG 780
 ATGATGATGG ATCCATTCTT CCTATTGAGG AGTCAACGCT TTTATCTTGA GGACATGGTG 840
 TCTGGAGTTA AAGGTATTGG CATACTCCAC ACATCTGTAC CATTCTTGAG TGATCGCTTA 900
 GGAATGAATG TGATTGGAC TCATTATGTG ATGAGAGTAA GCAATGCTTT TTTTCCAGG 960
 GTGTCAAATT GAGAACCAGG TAGATCCCCA CCACCTACAG TAAAAAGGAC CCTAAAGTAA 1020
 ATTGGTTGAA GAAATTAGAT CCCAAAGATT CTGGTGAAT TTTGAAGTCT TCATCAGTAT 1080
 ATCCATATTA AAACGAGATG ACAGAAGCCA AAGTAATTAT GGGCTGACAG GACAACCTGGA 1140
 TCAGTTTCAT TAAAAAGGGC AAACCTGAAG ATAAATCTTT TGACTCCAGC TCTTAGAGG 1200
 ATCTAAAGTG ACCTTGATGG ACAGTGGAAG AAATCACAAC ATGGAATTCC TCGAATAACA 1260

ATTTATTGAC TTAAATAAT TTTGTCTAAT GCTACATATA CACAATTAAA AAACCTTTAC 1320
ACTATTTCTA GAAAGTCAGC ATGTATTTT GGCTCGAAGT TTCTCTAGTG TTTTCTGTGG 1380
AAGGAATAAA AATTTGAGGT TTCAATACAA AAACAAAACA AACACACGA AACACGAAAA 1440
ACAATCTGTT GTGCGGGCGCC CCTGGGCCCC TTGAGAGAAA ACTTTTITAGA ACCCCTTTTG 1500
CGTTGTGGCG GCCCGGGGGC CCCACAGTTG GGTTTAGGTG GGCACCCTTG TGTCTACAAG 1560
TGGTGTCTCC CCAAGAGAGA GAACACCTCC GGGGTCAAGC GGACAACAAG AGTGCGTCGT 1620
GAGGACTCTT CACCCAAAGT ATATAAAACC CGCCCCGCGG GGAACACCAC GGCCGCTTTT 1680
CTGTAGACAC AACCCCCACA GTGGGAACCT CTGAGGGCGC ACACACAGGG CGAGCCTTAT 1740
CAACAAGGGG TGCCCAACAG AAACCCCGAG TTAATAATCG

Seq ID NO: 25 DNA sequence

Nucleic Acid Accession #:

BC001972.1

Coding sequence: 183-1019

1 11 21 31 41 51
| | | | |
GGTCGGCTGG TTATCGGGAG TTGGAGGGCT GAGGTCGGGA GGGTGGTGTG TACAGAGCTC 60
TAGGACTCAC GCACCGGCC AGTCGCGGGT TTTGGGCCGA GGCCTGGGT ACAAGCAGCA 120
AGTGCGCGGT TGGGGCCACT GCGAGGCCGT TTTAGAAAAC TGTTTAAAAC AAAGAGCAAT 180
TGATGGATAA ATCAGGAATA GATTCTCTG ACCATGTGAC ATCTGATGCT GTGGAACCTG 240
CAAATCGAAG TGATAACTCT TCTGATAGCA GCTTATTAA AACTCAGTGT ATCCCTTACT 300
CACCTAAAGG GGAGAAAAGA AACCCCATTC GAAAAATTGT TCGTACACCT GAAAGTGTTC 360
ACGCAAGTGA TTCATCAAGT GACTCATCTT TTGAACCAAT ACCATTGACT ATAAAAGCTA 420
TTTTTGAAG ATTCAAGAAC AGGAAAAAGA GATATAAAAA AAAGAAAAAG AGGAGGTACC 480
AGCCAACAGG AAGACCACGG GGAAGACCAG AAGGAAGGAG AAATCCTATA TACTACTAA 540
TAGATAAGAA GAAACAATTT AGAAGCAGAG GATCTGGCTT CCCATTTTGA GAATCAGAGA 600
ATGAAAAAAA CGCACCTTGG AGAAAAATTT TAACGTTTGA GCAAGCTGTT GCAAGAGGAT 660
TTTTTAACTA TATTGAAAAA CTGAAGTATG AACACCACCT GAAAGAATCA TTGAAGCAAA 720
TGAATGTTGG TGAAGATTGA GAAAATGAAG ATTTTGACAG TCGTAGATAC AAATTTTGG 780
ATGATGATGG ATCCATTCTT CCTATTGAGG AGTCAACAGC AGAGGATGAG GATGCAACAC 840
ATCTTGAAGA TAACGAATGT GATATCAAAT TGGCAGGGGA TAGTTTCATA GTAAGTTCTG 900
AATCCCTGT AAGACTGAGT GTATACTTAG AAGAAGAGGA TATTACTGAA GAAGCTGCTT 960
TGTCTAAAAA GAGAGCTACA AAAGCCAAAA ATACTGGACA GAGAGGCCTG AAAATGTGAC 1020
AGGATCATGA ATGTCAAAGG CTTTATCTT GAGAACATGG TGTCTGGAGT TAAAGGACTA 1080
TTGTTAGATC TGTGGGAAGG AATTACAAGA CAGTTGCTAA AAGTTTGAAG AAGACGGTTG 1140
CTAAACGTTA TGAAAAACCA GATAATCTAC TTTTACCT TAGGTATTGG CATACTCCAC 1200
ACATCTGTAC CATTCTTGAG TGATCGCTTA GGAATGAATG TGATTGAAC TCATTCTGT 1260
TGAGAGGGTG TCAAATTGAG AACCCAGGTAG ATCCCCACCA CCTACAGTAA AAAGACCCT 1320
AAAGTAAATT GGTGAAGAA ATTAGATCCC AAAGATTCTT GGTGAATTTT GAAGTCTTCA 1380
TCAGTATATC CATATTAATA CGAGATGACA GAAGCCAAAG TAATTATGGG CTGACAGGAC 1440
AACTGGATCA GTTTCATTAA AAAGGGCAAA CTGGAAGATA AATCTTTTGA CTCCAGCTCT 1500
TTAGAGGATC TAAAGTGACC TTGATGGACA GTGGAAGAAA TCACAACATG GAATTCCTCG 1560
AATAACAATT TATTGACTTT AAATAATTTT GTCTAATGCT ACATATACAC AATTAAAAAA 1620
CCTTTACACT AAAAAAAAAA AAAAAA

Seq ID NO: 26 Protein sequence

Protein Accession #: AAH01972.1

1 11 21 31 41 51
| | | | |
MDKSGIDSLD HVTSDAVELA NRSDNSSDSS LFKTQCIPIYS PKGEKRNPIR KfvRTPESVH 60
ASDSSSDSSF EPIPLTIKAI FERFKNRKKR YKKKKKRRYQ PTGRPRGRPE GRNRPYSLI 120
DKKKQFRSRG SGFPFLESEN EKNAPWRKIL TFEQAVARGF FNYIEKLKYE HHLKESLKQM 180
NVGEDLENEF FDSRRYKFLD DDGSISPIEE STAEDEATH LEDNECDIKL AGDSFIVSSE 240
FPVRLSVYLE EEDITBEAAL SKKRATKAKN TGQRGLKM

Seq ID NO: 27 DNA sequence

Nucleic Acid Accession #:

AK027016

Coding sequence: 207-1043

1 11 21 31 41 51
| | | | |
CTTTTCTTCC GCACGGTTGG AGGAGGTCGG CTGGTTATCG GGAGTTGGAG GGCTGAGGTC 60
GGGAGGGTGG TGTGTACAGA GCTCTAGGAC TCACGCACCA GGCCAGTCGC GGATTTTGGG 120
CCGAGGCCTG GGTACAAGC AGCAAGTGCG CGGTTGGGGC CACTGCGAGG CCGTTTITAGA 180
AAACTGTTTA AAACAAAGAG CAATTGATGG ATAAATCAGG AATAGATTCT CTTGACCATG 240
TGACATCTGA TGCTGTGGAA CTTGCAAATC GAAGTGATAA CTCTCTGAT AGCAGCTTAT 300
TTAAACTCA GTGTATCCCT TACTCACCTA AAGGGGAGAA AAGAAACCCC ATTCGAAAAT 360
TTGTTCTGAC ACCTGAAAGT GTTCACGCAA GTGATTATC AAGTGACTCA TCTTTTGAAC 420
CAATACCATT GACTATAAAA GCTATTTTGG AAAGATTCAA GAACAGGAAA AAGAGATATA 480
AAAAAAGAA AAAGAGGAGG TACCAGCCAA CAGGAAGACC ACGGGGAAGA CCAGAAGGAA 540
GGAGAAATCC TATATACTCA CTAATAGATA AGAAGAAACA ATTTAGAAGC AGAGGATCTG 600
GCTTCCCAT TTTAGAATCA GAGAATGAAA AAAACGCACC TTGGAGAAAA ATTTAACGT 660
TTGAGCAAGC TGTGCAAGA GGAATTTTGA ACTATATTGA AAAGCTGAAG TATGAACACC 720
ACCTGAAAGA ATCATTGAAG CAAATGAATG TTGGTGAAGA TTTAGAAAAT GAAGATTTTG 780
ACAGTCGTAG ATACAAATTT TTGGATGATG ATGGATCCAT TTCTCCTATT GAGGAGTCAA 840
CAGCAGAGGA TGAGGATGCA ACACATCTTG AAGATAACGA ATGTGATATC AAATTGGCAG 900
GGGATAGTTT CATAGTAAGT TCTGAATTCC CTGTAAGACT GAGTGTATAC TTAGAAGAA 960
AGGATATTAC TGAAGAAGCT GCTTTGTCTA AAAAGAGAGC TACAAAAGCC AAAAATACTG 1020
GACAGAGAGG CCTGAAAATG TGACAGGATC ATGAATGTCA AAGGCTTTTA TCTTGAGAAC 1080
ATGGTGTCTG GAGTTAAAGG TATTGGCATA CTCCACACAT CTGTACCATT CTTGAGTGAT 1140
CGCTTAGGAA TGAATGTGAT TTGAATCAT TCATGTTGAG AGGGTGTCAA ATTGAGAACC 1200
AGGTAGATCC CCACCACCTA CAGTAAAAAG GACCCTAAAG TAAATTGGTT GAAGAAATTA 1260
GATCCCAAAG ATTCTTGGTG AATTTTGAAG TCTTCATCAG TATATCCATA TAAAACGAG 1320

ATGACAGAAG CCAAAGTAAT TATGGCAAGT AATGGTTTTT ATCTTAACTA TAAGTTATTT 1380
GCTCAAGGGT GTAATGGTCA TTACCAAGGC TTTTAGAATG CAGTTTCTCA TTTGCTGTGG 1440
ACATGACCAT AAAAAAAAAAAT TTCCAGTAG GTTTTCTATC TGCTACGTTG CTAGCAATCA 1500
GCTTATTGGG AACAGTTGAT TAACTGTAAT AGAAATGCAA TACAAATAAA ATGTGAACCA 1560
CATGTGATT TTTTAAAAA TCACTGAGAT TTGAAAATTC TCCTAGATCT CTTGAATCAT 1620
GCAAATTTGC TTTGCCTTTA TATTGTAACC CTTGTGGGTT GCTAATAACC AAGCAGTTTG 1680
TAGTAGAGTT AACTCAGGCT CGTTCTAGGG ACTCATTATG GTTCACTCAC TGTACACTCA 1740
TCTCTGAAAA TGTAATAATT ACTTTTATAC TATTGTTATG TAGGGCTGAC AGGACAACCTG 1800
GATCAGTTTC ATTAATAAGG TATGTATGCA TTAGAAAAGA CATTTGTATG GGTCAATTTCA 1860
AAGAGGGCTT ATGAGGCTGT GAAACCCAGA GCTCTTAACG CTGTGACCAA AGATGGAAGT 1920
TCTCTATAGG AAGCCATAGC ACTCCTAATG TTTGGTGCTA TGTTTTCCTG AGGAGATATA 1980
AAACGTAATA ATCCATGATT GTTGCCATGT GAGAGTTTAA AAGGTTAATC AAAATTCTC 2040
TTCTTCAGGG CAAACTTGAA GATAAATCTT TTGACTCCAG CTCTTTAGAG GATCTAAAGT 2100
GACCTTGATG GACAGTGGAA GAAATCACA CATGGAATTC CTCGAATAAC AATTTATTGA 2160
CTTTAAATAA TTTGTCTAA TGCTACATAT ACACAATTA AAAACCTTTA CACTATTTCT 2220
AGAAAGTCAG CATGTATTTT TGGCTCGAAG TTTCTCTAGT GTTTTCTGTG GAAGGAATAA 2280
AAATTGAGT TTCAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA

Seq ID NO: 28 Protein sequence:

Protein Accession #: BAB15628.1

1 11 21 31 41 51
| | | | |
MDKSGIDSLD HVTSDAVELA NRSDNSSDSS LFKTQCIPYS PKGEKRNPIR KVRTPESVH 60
ASDSSDSSSF EPIPLTIKAI FERFKNRKKR YKKKKRRYQ PTGRPRGRPE GRNPIYSLI 120
DKKKQFRSRG SGFPFLESEN EKNAPWRKIL TFEQAVARGF FNYIEKLKYE HHLKESLKQM 180
NVGEDLENEF FDSRRYKFLD DDGSISPIEE STAEDEDATH LEDNECDIKL AGDSFIVSSE 240
FPVRLSVYLE EEDITEEAL SKKRATKAKN TGQRGLKM

Seq ID NO: 29 DNA sequence

Nucleic Acid Accession #: NM_004289.3

Coding sequence: 493-1695

1 11 21 31 41 51
| | | | |
GCCGCCGCCT CGTCCACCGG AGGAGCCGGC GCCAGCGTGG ACGGCCGCCAG CCAGGCTGTG 60
CAGGGGGGCG GCGGGGACCC CCGAGCGGCT CGGAGTGGCC CTTGGACGC CGGGGAAGAG 120
GAGAAGGCAC CCGCGGAACC GACGGCTCAG GTGCCGGACG CTGGCGGATG TGCGAGCGAG 180
GAGAATGGGG TACTAAGAGA AAAGCACGAA GCTGTGGATC ATAGTTCCCA GCATGAGGAA 240
AATGAAGAAA GGGTGTGACG CCAGAAGGAG AACTCACTTC AGCAGAATGA TGATGATGAA 300
AACAAAATAG CAGAGAAACC TGAAGGGAG GCAGAAAAGA CCACTGAATC TAGAAATGAG 360
AGACATCTGA ATGGGACAGA TACTTCTTTC TCTCTGGAAG ACTTATTCCA GTTGCTTTCA 420
TCACAGCCTG AAAATTCAC TGGAGGGCATC TCATTGGGAG ATATTCTCT TCCAGGCAGT 480
ATCAGTGATG GCATGAATTC TTCAGCACAT TATCATGTAA ACTTCAGCCA GGCTATAAGT 540
CAGGATGTGA ATCTTCATGA GGCCATCTTG CTTTGTCCCA ACAATACATT TAGAAGAGAT 600
CCAACAGCAA GGAATTCACA GTCACAAGAA CCATTCTGC AGTTAAATTC TCATACCACC 660
AATCCTGAGC AAACCTTCC TGGAACCTAAT TTGACAGGAT TTCTTTCACC GGTGACAAT 720
CATATGAGGA ATCTAACAAG CCAAGACCTA CTGTATGACC TTGACATAAA TATATTGAT 780
GAGATAAACT TAATGTCAAT GGCCACAGAA GACAACCTTG ATCCAATCGA TGTTTCTCAG 840
CTTTTGTGATG AACCAGATTC TGATTCTGGC CTTTCTTAG ATTCAAGTCA CAATAATACC 900
TCTGTCAATCA AGTCTAATTC CTCTCACTCT GTGTGTGATG AAGGTGCTAT AGGTTATTGC 960
ACTGACCATG AATCTAGTTC CCATCATGAC TTAGAAGGTG CTGTAGGTGG CTACTACCCA 1020
GAACCCAGTA AGCTTTGTCA CTTGGATCAA AGTGATCTG ATTTCCATGG AGATCTTACA 1080
TTTCAACACG TATTTCAATA CCACACTTAC CACTTACAGC CAACTGCACC AGAATCTACT 1140
TCTGAACCTT TTCCGTGGCC TGGGAAGTCA CAGAAGATAA GGAGTAGATA CCTTGAAGAC 1200
ACAGATAGAA ACTTGAGCCG TGATGAACAG CGTGCTAAAG CTTTGCATAT CCTTTTTTCT 1260
GTAGATGAAA TTGTCGGCAT GCCTGTTGAT TCTTCAATA GCATGTTAAG TAGATATTAT 1320
CTGACAGACC TACAAGTCTC ACTTATCCGT GACATCAGAC GAAGAGGGAA AAATAAAGTT 1380
GCTGCGCAGA ACTGTCTGTA ACGCAAATTC GACATAATTT TGAATTTAGA AGATGATGTA 1440
TGTAACCTTG AAGCAAAGAA GGAACTCTT AAGAGAGAGC AAGCACAATG TAACAAAGCT 1500
ATTAACATAA TGAAACAGAA ACTGCATGAC CTTTATCATG ATATTTTATG TAGATTAAGA 1560
GATGACCAAG GTAGGCCAGT CAATCCCAAC CACTATGCTC TCCAGTGTAC CCATGATGGA 1620
AGTATCTTGA TAGTACCCAA AGAAGTGGT GCCTCAGGCC AAAAAAGGA AACCCAAAAG 1680
GGAAAGAGAA AGTGAGAAGA AACTGAAGAT GGAATCTATT ATGTGAAGTA GTAATGTTCA 1740
GAAACTGATT ATTTGGATCA GAAACCATG AAAGTCTTC AAGAATTGTA TCTTTAAGTA 1800
CTGCTACTTG AATAACTCAG TTAACGCTGT TTGAAGCTT ACATGGACAA ATGTTTAGGA 1860
CTTCAAGATC AACTTGTGG GCAATCTGGG GGAGCCACAA CTTTTCATGA AGTGCATTGT 1920
ATACAAAATT CATAGTTATG TCCAAAGAAT AGGTTAATCAT GAAAACCCAG TAAGACTTTC 1980
CATCTTGGCA GCCATCCTT TTAAGAGTAA GTTGTTACT TCAAAAAGAG CAAACACTGG 2040
GGATCAAATT ATTTAAGAG GTATTTCAGT TTTAAATGCA AAATAGCCTT ATTTTCATT 2100
AGTTTGTAG CACTATAGT AGCTTTTCAA ACATATTTT AATCTTTATA TTTAACTTAT 2160
AAATTTTGCT TTCT

Seq ID NO: 30 Protein sequence:

Protein Accession #: NP_004280

1 11 21 31 41 51
| | | | |
MNSSAHYHVN FSQAISQDVN LHEAILCPN NTFRRDPTAR TSQSQEPFLQ LNSHTTNPEQ 60
TLPGTNLTGF LSPVDNHMRN LTSQDLLYDL DINIFDEINL MSLATEDNFD PIDVSQLFDE 120
PDSDSLGLSLD SSHNNTSVK SNSSHVCDE GAIGYCTDHE SSSHHDLEGA VGGYYPEPSK 180
LCHLDQSDSD FHGDLTFQHV FHNHTYHLQP TAPESTSEPF PWPQKSQKIR SRYLEDTRN 240
LSRDEQRAKA LHIPFSVDEI VGMPVDSFNS MLRYLLTDL QVSLIRDIRR RGKNKVAAQN 300
CRKRKLDIIL NLEDDVCNLQ AKKETLKREQ AQCNKAINIM KQKLHDLYHD IFSRLRDDQG 360

RPVNPNHIAL QCTHDGSILI VPKELVASGH KKETQKGKRR

Seq ID NO: 31 DNA sequence

Nucleic Acid Accession #:

NM_033260.1

Coding sequence: 1-1208

```
1   11   21   31   41   51
|   |   |   |   |
ATGAAGTTGG AGGTGTTTCGT CCTCGCGCG GCGGCGGGG ACAAGCAGGG CAGTGACCTG 60
GAGGGCGCGG GCGGCAGCGA CGCGCCGTCC CCGCTGTCGG GCGGCGGAGA CGACTCCCTG 120
GGCTCAGATG GGGACTGCGC GGCCAAGCCG TCCGCGGGCG GCGGCGCCAG AGATACGCAG 180
GGCGACGGCG AACAGAGTGC GGGAGGCGGG CCGGGCGCGG AGGAGGCGAT CCCGGCAGCA 240
GCTGCTGCAG CCGTGGTGGC GGAGGGCGCG GAGGCCGGGG GCGGCGGGCC AGGCGCGGGC 300
GGCGCGGGGA GCGGCGAGGG TGCACGCAGC AAGCCATATA CGCGGCGGCC CAAGCCCCCC 360
TACTCGTACA TCGCGCTCAT CGCCATGGCC ATCCGCGACT CGGCGGGCGG GCGCTTGACG 420
CTGGCGGAGA TCAACGAGTA CCTCATGGGC AAGTTCCCCT TTTCCGCGG CAGCTACACG 480
GGCTGGCGCA ACTCCGTGCG CCACAACCTT TCGCTCAACG ACTGCTTCGT CAAGGTGCTG 540
CGCGACCCCT CGCGGCCCTG GGGCAAGGAC AACTACTGGA TGCTCAACCC CAACAGCGAG 600
TACACCTTCG CCGACGGGGT CTTCCGCGCG CGCCGCAAGC GCCTCAGCCA CCGCGCGCCG 660
GTCCCCGCGC CCGGGTGTGC GCCCCAGGAG GCCCCGGGCC TCCCCGCCGC CCGCGCGCCC 720
GCGCGCGCGC CCGCGGCTC GCGCGCATG CGCTCGCCCG CCGCGCAGGA GGAGCGCGCC 780
AGCCCCGCGG GCAAGTTCTC CAGCTCCTTC GCCATCGACA GCATCCTGCG CAAGCCCTTC 840
CGCAGCCGTC GCCTCAGGGA CACGCGCCCC GGGACGACGC TTCAAGTGGGG CGCGCGCGCC 900
TGCGCGCGCG TGCGCGGTT CCGCGCGCTC CTCCCCGCGG CGCCCTGCAG GGCCCTGCTG 960
CCGCTCTGCG CGTACGGCGC GGGCGAGCCG GCGCGGCTGG GCGCGCGCGA GGCCGAGGTG 1020
CCACCGACCG CGCGCCCCCT CCGCTTGCA CCTCTCCCG GCGCGGCCCC CGCCAAGCCA 1080
CTCCGAGGCC CGCGGCGCGG CGGCGCGCAC CTGTACTGCC CCTGCGGGCT GCGCGCAGCC 1140
CTGCAGGCGG CCTTAGTCCG NCGTCTGGC CCGCACCTGT CGTACCCGTG GGAGACGCTC 1200
CTAGCTTGA
```

Seq ID NO: 32 Protein sequence

Protein Accession #: NP_150285.1

```
1   11   21   31   41   51
|   |   |   |   |
MKLEVFVPRA AHGDKQGS DL EGAGGSDAPS PLSAAGDDSL GSDGDCAAKP SAGGGARDTQ 60
GDGEQSAGGG PGAEAI PAA AAAAVVAEGA EAGAAGPGAG GAGSGEGARS KPYTRRPKPP 120
YSYIALIAMA IRDSAGGRLT LAINEYLMG KFPFFRGSYT GWRNSVRHNL SLNDCFVKVL 180
RDPSPRPWGD NYWMLNPNSE YTFADGVFRR RRKRLSHRAP VPAPGLRPEE APGLPAAPPP 240
APAAPASPRM RSPARQEERA SPAGKFSSSF AIDSILRKPF RSRRLRDTAP GTTLQWGAAP 300
CPPLPAFPAL LPAAPCRALL PLCAYGAGEP ARLGAREAEV PPTAPPLLLA PLPAAAPAKP 360
LRGPAAGGAH LYCPLRLPAA LQAALVRRPG PHSYPVETL LA
```

Seq ID NO: 33 DNA sequence

Nucleic Acid Accession #:

NM_012128.2

Coding sequence: 43-2796

```
1   11   21   31   41   51
|   |   |   |   |
GAACAAACCA ACATTTGAGC CAGGAATAAC TAGAGAGGAA CAATGGGGTT ATTCAGAGGT 60
TTTGTTCCTC TCTTAGTTCT GTGCTGCTG CACCAGTCAA ATACTTCCTT CATTAGCTG 120
AATAATAATG GCTTTGAAGA TATTGTCATT GTTATAGATC CTAGTGTGCC AGAAGATGAA 180
AAAATAATTG AACAAATAGA GGATATGGTG ACTACAGCTT CTACGTACCT GTTTGAAGCC 240
ACAGAAAAAA GATTTTTTTT CAAAAATGTA TCTATATTAA TTCCTGAGAA TTGGAAGGAA 300
AATCCTCAGT ACAAAGGCC AAAACATGAA AACCATAAAC ATGCTGATGT TATAGTTGCA 360
CCACCTACAC TCCAGGTAG AGATGAACCA TACACCAAGC AGTTCACAGA ATGTGGAGAG 420
AAAGGCGAAT ACATTCATT CACCCCTGAC CTTCTACTTG GAAAAAACA AAATGAATAT 480
GGACCAACAG GCAAACGTT TGTCCATGAG TGGGCTCACC TCCGGTGGGG AGTGTGTTGAT 540
GAGTACAATG AAGATCAGCC TTTCTACCGT GCTAAGTCAA AAAAAATCGA AGCAACAAGG 600
TGTTCCGCAG GTATCTCTGG TAGAAATAGA GTTTATAAGT GTCAAGGAGG CAGCTGTCTT 660
AGTAGAGCAT GCAGAAATTGA TTCTACAACA AAACGTATG GAAAAGATTG TCAATTCCTT 720
CCTGATAAAG TACAAACAGA AAAAGCATCC ATAATGTTA TGCAAAGTAT TGATTCTGTT 780
GTTGAATTTT GTAACGAAAA AACCCATAAT CAAGAAGCTC CAAGCTACA AAACATAAAG 840
TGCAATTTTA GAAGTACATG GGAGGTGATT AGCAATTCTG AGGATTTTAA AAACACCATA 900
CCCATGGTGA CACCACCTCC TCCACCTGTC TTCTCATTGC TGAAGATCCG TCAAAGAATT 960
GTGTGCTTAG TTCTTGATAA GTCTGGAAGC ATGGGGGGTA AGGACCGCCT AAATCGAATG 1020
AATCAAGCAG CAAAACATTT CCGTCTGCAG ACTGTTGAAA ATGGATCCTG GGTGGGGATG 1080
GTTCACTTTG ATAGTACTGC CACTATTGTA AATAAGCTAA TCCAAATAAA AAGCAGTGAT 1140
GAAAGAAACA CACTCATGGC AGGATTACCT ACATATCCTC TGGGAGGAAC TTCCATCTGC 1200
TCTGGAATTA AATATGCATT TCAGGTGATT GGAGAGCTAC ATTCCCACT CGATGGATCC 1260
GAAGTACTGC TGCTGACTGA TGGGAGGAT AACACTGCAA GTTCTTGAT TGATGAAGTG 1320
AAACAAAGTG GGGCCATTGT TCATTTTATT GCTTTGGGAA GAGCTGCTGA TGAAGCAGTA 1380
ATAGAGATGA GCAAGATAAC AGGAGGAAGT CATTTTATG TTTCAGATGA AGCTCAGAAC 1440
AATGGCCTCA TTGATGCTTT TGGGGCTCTT ACATCAGGAA ATACTGATCT CTCCAGAAAG 1500
TCCCTTCAGC TCGAAAGTAA GGGATTAACA CTGAATAGTA ATGCCTGGAT GAACGACACT 1560
GTCATAATTG ATAGTACAGT GGGAAAGGAC ACGTTCTTTC TCATCAGATG GAACAGTCTG 1620
CCTCCAGTA TTTCTCTCTG GGATCCAGT GGAACAATAA TGGAATAATT CACAGTGGAT 1680
GCAACTTCCA AAATGGCTTA TCTCAGTATT CCAGGAAGT CAAAGGTGGG CACTTGGGCA 1740
TACAATCTTC AAGCCAAAGC GAACCCAGAA ACATTAATA TTACAGTAAC TTCTCGAGCA 1800
GCAATTTCTT CTGTGCCTCC AATCAGAGTG AATGCTAAAA TGAATAAGGA CGTAAACAGT 1860
TTCCCCAGCC CAATGATTGT TTACGCAGAA ATTCTACAAG GATATGTACC TGTCTTGA 1920
GCCAATGTGA CTGCTTTTCA TGAATCAGAG AATGGACATA CAGAAGTTT GGAACTTTGT 1980
GATAATGGTG CAGGCGCTGA TCTTTCAAG AATGATGGAG TCTACTCCAG GTATTTTACA 2040
GCATATACAG AAAATGGCAG ATATAGCTTA AAAGTTCGGG CTCATGGAGG AGCAAACACT 2100
GCCAGGCTAA AATTACGGCC TCCACTGAAT AGAGCCGCGT ACATACCAGG CTGGGTAGTG 2160
```

AACGGGGAAA TTGAAGCAAA CCCGCCAAGA CCTGAAATTG ATGAGGATAC TCAGACCACC 2220
 TTGGAGGATT TCAGCCGAAC AGCATCCGGA GGTGCATTG TGGTATCACA AGTCCCAAGC 2280
 CTTCCTTGC CTGACCAATA CCCACCAAGT CAAATCACAG ACCTTGATGC CACAGTTCAT 2340
 GAGGATAAGA TTATTCTTAC ATGGACAGCA CCAGGAGATA ATTTTGATGT TGGAAAAGTT 2400
 CAACGTTATA TCATAAGAAT AAGTGCAAGT ATTCTTGATC TAAGAGACAG TTTTGATGAT 2460
 GCTCTTCAAG TAAATACTAC TGATCTGTCA CCAAAGGAGG CCAACTCCAA GGAAAGCTTT 2520
 GCATTTAAAC CAGAAAATAT CTCAGAAGAA AATGCAACCC ACATATTTAT TGCCATTAATA 2580
 AGTATAGATA AAAGCAATTT GACATCAAAA GTATCCAACA TTGCACAAGT AACTTTGTTT 2640
 ATCCCTCAAG CAAATCCTGA TGACATTGAT CCTACTCCTA CTCCTACTCC TACTCCTGAT 2700
 AAAAGTCATA ATTCTGGAGT TAATATTTCT ACGCTGGTAT TGCTGTGAT TGGGTCTGTT 2760
 GTAATTGTTA ACTTTATTTT AAGTACCACC ATTTGAACCT TAACGAAGAA AAAAATCTTC 2820
 AAGTAGACCT AGAAGAGAGT TTTAAAAAAC AAAACAATGT AAGTAAAGGA TATTTCTGAA 2880
 TCTTAAAAAT CATCCCATGT GTGATCATAA ACTCATAAAA ATAATTTTAA GATGTGCGAA 2940
 AAGGATACTT TGATTAAATA AAAACACTCA TGGATATGTA AAAACTGTCA AGATTAAAAAT 3000
 TTAATAGTTT CATTTATTTG TTATTTTATT TGTAAGAAAT AGTGATGAAC AAAGATCCTT 3060
 TTTCACTG ATACCTGGT GTATATTATT TGATGCAACA GTTTTCTGAA ATGATATTTT 3120
 AAATTGCATC AAGAAATTA AATCATCTAT CTGAGTAGTC AAAATACAAG TAAAGGAGAG 3180
 CAAATAAACA ACATTTGGAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 34 Protein sequence:

Protein Accession #: NP_036260.1

1 11 21 31 41 51
 | | | | |
 MGLFRGFVFL LVLCLLHQSNTSFIKLNNNG FEDIVIVDP SVPEDEKIE QIEDMVTTAS 60
 TYLFEATEKR FFFKNVSILI PENWKENPQY KRPKHENHKH ADVIVAPPTL PGRDEPYTKQ 120
 FTECGEKGEY IHFTPDLLG KKQNEYGPPG KLFVHEWAHL RWGVFDEYNE DQPFYRAKSK 180
 KIEATRCASG ISGRNRVYKC QGGSCLSRAC RIDSTTKLYG KDCQFFPDV QTEKASIMFM 240
 QSIDSVVEFC NEKTHNQEAP SLQNIKCNFR STWEVISNSE DFKNTIPMT PPTPPVFSLL 300
 KIRQRIVCLV LDKSGSMGGK DRLNRMNQAA KHFLQTVEN GSWVGMVHFD STATIVNKLI 360
 QIKSSDERNT LMAGLPTYPL GGTSCSGIK YAFQVIGELH SQLDGEVLL LTDGEDNTAS 420
 SCIDEVKQSG AIVHFIALGR AADEAVIEMS KITGGSHFYV SDEAQNGLI DAFGALTSGN 480
 TDLSQKSLQL ESKGLTLNSN AWMNDTVIID STVGKDTFFL ITWNSLPSI SLWDPSGTM 540
 ENFTVDATSK MAYLSIPGTA KVGWYAYNLQ AKANPETLTI TVTSRAANSS VPPITVNAKM 600
 NKDVNSFPSP MIVYAEILQG YPVLGANVT AFIESQNGHT EVLELLDNGA GADSFKNQDV 660
 YSRYFTAYTE NGRYSLKVRH HGGANTARLK LRPLNRAAY IPGWVVGNEI EANPPRPEID 720
 EDTQTTLEDF SRTASGGAFV VSQVPSLPLP DQYPPSQITD LDATVHEDKI ILTWTFPGDN 780
 FDVGKVQRYI IRISASILDL RDSFDDALQV NTDLSPEKA SKESFAFKP ENISEENATH 840
 IFIAKSIDK SNLTSKVSNI AQVTLFIPQA NPDDIDPTPT PTPTPKSHN SGVNISTLVL 900
 SVIGSVVIVN FILSTTI

Seq ID NO: 35 DNA sequence

Nucleic Acid Accession #: NM_000901.1

Coding sequence: 217-3171

1 11 21 31 41 51
 | | | | |
 CGCGGGAGCC AACTTCAGGC TGCTCAGAGG AAGCCCGTGC AGTCAGTCAC CTGGGTGCAA 60
 GAGCGTTGCT GCCTCGGGCT CTCCCGCTGC AGGGAGAGCG GCACTCGCTG GCCTGGATGT 120
 GGTGGATTG AGGGGGGCTC CGCAGCAGGG GTTCTGTGGC GGTGGCAAGC GCTGCAACAG 180
 GTAGACGGCG AGAGACGGAC CCCGGCCGAG GCAGGGATGG AGACCAAAGG CTACCACAGT 240
 CTCCCTGAAG GTCTAGATAT GGAAAGACGG TGGGGTCAAG TTTCTCAGGC TGTGGAGCGT 300
 TCTTCCCTGG GACCTACAGA GAGGACCGAT GAGAATAACT ACATGGAGAT TGTCACGTA 360
 AGCTGTGTTT CCGGTGCTAT TCCAAACAAC AGTACTCAAG GAAGCAGCAA AGAAAAACAA 420
 GAACTACTCC CTGTCCTTCA GCAAGACAAT AATCGGCCTG GGATTTTAACT ATCTGATATT 480
 AAAACTGAGC TGGAATCTAA GGAACCTTCA GCAACTGTAG CTGAGTCCAT GGGTTTATAT 540
 ATGGATTCTG TAAGAGATGC TGACTATTCC TATGAGCAGC AGAACCAACA AGGAAGCATG 600
 AGTCCAGCTA AGATTTATCA GAATGTTGAA CAGCTGGTGA AATTTTACAA AGGAAATGGC 660
 CATCGTCTTT CCACTCTAAG TTGTGTGAAC ACGCCCTTGA GATCATTAT GTCTGACTCT 720
 GGGAGCTCCG TGAATGGTGG CGTCATGCGC GCCATTGTTA AAAGCCCTAT CATGTGTCT 780
 GAGAAAAGCC CGTCTGTTTG CAGCCCTCTG AACATGACAT CTTGCTTTG CAGCCCTGCT 840
 GGAATCAACT CTGTGCTCTC CACCACAGCC AGCTTTGGCA GTTTTCCAGT GCACAGCCCA 900
 ATCACCAGG GAACTCCTCT GACATGCTCC CTAATGCTG AAAATCGAGG CTCCAGGTCG 960
 CACAGCCCTG CACATGCTAG CAATGTGGGC TCTCCTCTCT CAAGTCCGT AAGTAGCATG 1020
 AAATCCTCAA TTTCCAGCCC TCCAAGTCAC TGCAGTGTA AATCTCCAGT CTCCAGTCCC 1080
 AATAATGTCA CTCTGAGATC CTCTGTGTCT AGCCCTGCAA ATATTAACAA CTCAAGGTGC 1140
 TCTGTTTCCA GCCCTTCGAA CACTAATAAC AGATCCAGC TTTCCAGTCC GGCAGCCAGT 1200
 ACTGTGGGAT CTATCTGTAG CCTGTAAAC AATGCCTTCA GCTACACTGC TTCTGGCACC 1260
 TCTGCTGGAT CCAGTACATT GCGGGATGTG GTTCCAGTC CAGACACGCA GGAGAAAGGT 1320
 GCTCAAGAGG TCCCTTTTCC TAAGACTGAG GAAGTAGAGA GTGCCATCTC AAATGGTGTG 1380
 ACTGGCCAGC TTAATATTGT CCAGTACATA AAACAGAAC CAGATGGAGC TTTAGCAGC 1440
 TCATGTCTAG GAGGAAATAG CAAAATAAAT TCGGATTCTT CATTCTCAGT ACCAATAAAG 1500
 CAAGAAATCAA CCAAGCATT ATGTTCAAGC ACCTCTTTA AAGGGAATCC AACAGTAAAC 1560
 CCGTTTCCAT TTATGGATGG CTCGTATTTT TCCTTTATGG ATGATAAAGA CTATTATTCC 1620
 CTATCAGGAA TTTAGGACC ACCTGTGCCC GGCTTTGATG GTAACGTGTA AGGCAGCGGA 1680
 TTCCAGTGG GTATTAAACA AGAACCAGAT GACGGGAGCT ATTACCCAGA GGCCAGCATC 1740
 CCTTCTCTG CTATTGTTGG GGTGAATTCA GGTGGCAGT CCTTCCACTA CAGGATTGGT 1800
 GCTCAAGGTA CAATATCTTT ATCAGGATCG GCTAGAGACC AATCTTTCCA ACACCTGAGT 1860
 TCCTTCTCTC CTGTCAATAC TTTAGTGGAG TCATGGAAAT CACACGGCGA CCTGTCTGCT 1920
 AGAAGAAGTG ATGGGTATCC GGTCTTAGAA TACATTCCAG AAAATGTATC AAGCTCTACT 1980
 TTACGAAGTG TTTCTACTGG ATCTTCAAGA CCTTCAAAA TATGTTTGGT GTGTGGGGAT 2040
 GAGGCTTCAG GATGCCATTA TGGGGTAGTC ACCTGTGGCA GCTGCAAGT TTTCTTCAA 2100
 AGAGCAGTGG AAGGGCAACA CAACTATTTA TGTGCTGGAA GAAATGATTG CATCATTTGAT 2160
 AAGATTGAC GAAAGAATTG TCCTGCTTGC AGACTTCAGA AATGTCTTCA AGCTGGAATG 2220
 AATTTAGGAG CACGAAAGTC AAAGAAGTTG GAAAGTTAA AAGGGATTCA CGAGGAGCAG 2280
 CCACAGCAGC AGCAGCCCCC ACCCCACCC CCACCCCGC AAAGCCCAGA GGAAGGGACA 2340

ACGTACATCG CTCCTGCAAA AGAACCCCTCG GTCAACACAG CACTGGTTCC TCAGCTCTCC 2400
ACAATCTCAC GAGCGCTCAC ACCTTCCCCC GTTATGGTCC TTGAAAACAT TGAACCTGAA 2460
ATTGTATATG CAGGCTATGA CAGCTCAAAA CCAGATACAG CCGAAAATCT GCTCTCCACG 2520
CTCAACCGCT TAGCAGGCAA ACAGATGATC CAAGTCGTGA AGTGGGCAAA GGTACTTCCA 2580
GGATTTAAAA ACTTGCCTCT TGAGGACCAA ATTACCCTAA TCCAGTATTC TTGGATGTGT 2640
CTATCATCAT TTGCCTTGAG CTGGAGATCG TACAAACATA CGAACAGCCA ATTTCTCTAT 2700
TTTGACCCAG ACCTAGTCTT TAATGAAGAG AAGATGCATC AGTCTGCCAT GTATGAACTA 2760
TGCCAGGGGA TGCACCAAAT CAGCCTTCAG TTCGTTTCGAC TGCAGCTCAC CTTTGAAGAA 2820
TACACCATCA TGAAGTTTT GCTGCTACTA AGCACAATTC CAAAGGATGG CCTCAAAAGC 2880
CAGGCTGCAT TTGAAGAAAT GAGGACAAAT TACATCAAAG AACTGAGGAA GATGGTAACT 2940
AAGTGTCCCA ACAATTCTGG GCAGAGCTGG CAGAGGTTCT ACCAACTGAC CAAGCTGCTG 3000
GACTCCATGC ATGACCTGGT GAGCGACCTG CTGGAATTCT GCTTCTACAC CTTCCGAGAG 3060
TCCCATGCGC TGAAGGTAGA GTTCCCCGCA ATGCTGGTGG AGATCATCAG CGACCAGCTG 3120
CCCAAGGTGG AGTCGGGGAA CGCCAAGCCG CTCTACTTCC ACCGGAAGTG ACTGCCCGCT 3180
GCCCAGAAGA ACTTTGCCCT AAGTTTCCCT GTGTGTGTTCC ACACCCAGAA GGACCCAAGA 3240
AAACCTGTTT TTAACATGTG ATGGTTGATT CACACTTGTT CAACAGTTTC TCAAGTTTAA 3300
AGTCATGTCA GAGGTTTGGG GCCGGGAAAG CTGTTTTTCC GTGGATTTGG CGAGACCAGA 3360
GCAGTCTGAA GGATTTCCCA CCTCCAATCC CCCAGCGCTT AGAAACATGT TCCTGTTCTT 3420
CGGGATGAAA AGCCATATCT AGTCAATAAC TCTGATTTTG ATATTTTCAC AGATGGAAGA 3480
AGTTTAACT ATGCCGTGTA GTTCTGTGTA TCGTTCGCTT GTTTTAAAAG GGTCAAGGA 3540
CTAACGAACG TTTTAAAGCT TACCTTGGT TTGCACATAA AACGTATAGT CAATATGGGG 3600
CATTAAATTT CTTTGTGTTT TAAAAAACA CAAAAAATA AAAAAAAT ATATACAGAT 3660
TCCTGTTGTG TAATAACAGA ACTCGTGGCG TGGGGCAGCA GCTGCCTCTG AGCCCTCGCT 3720
CGTCCACGGT CTTCTGCATC ACTGGTATAC AACTCGTTA GCGTCCATTT CTTATTTAAT 3780
TAGAATGGAT AAGATGATGT TAAATGCCTT GGTGTTGATT CTAGTATCTA TTGTGTTGGC 3840
TTTACAAATA ATTTTTGCA GTCTTTTGCT GTGCTGTACA TACTGTATG TATAAATTAT 3900
GAAGGACCTG AAATAAGGTA TAAGGATCTT TTGTAATGA GACACATACA AAAAAAATCT 3960
TTAATGGTTA ATAGGATGAA TGGGAAAGTA TTTTGAAAG AATTCTATTT TGCTGGAGAC 4020
TATTTAAGTA CTATCTTTGT CTAACAAGG TAATTTTTTT TTGTAAGTG CAATGTCCTG 4080
CATGCATAAT GAACCGTTA CAGTGTATTT AAGAAAGGGA AAGCTGTGCC TTTTGTAGCT 4140
TCATATCTAA TTTACCATA TTTACAGTC TCTGTTGTA ATAACCACAC TGAACCTCT 4200
TCGGTGTCT TGAACCTTT CTACTTTTC TGTACTTTT GTTTTGTCT TGGTCTCCCG 4260
CTTGGGGCAT TTGTGGGACT CCAGCACGTT TTCTGGCTTC TGCTTCATCC TGCTCCATCG 4320
GGGAATGACA CACTGCGGTG TCTGCAGTC CTGGAAGGTG TCATTGACA ACACATGTGG 4380
GAGAGGAGGT CCTTGGAGTG CTGCAGCTTT GGGAAAGCCT GCCTCGTTTC CCTTTTCTC 4440
TAGAAGCAGA ACCAGCTCTA CGAGAGTGAG ACTGGGAACT TGATGGCTCA GAGAGCATCT 4500
TTTCTOCCA TTTTAGAAAA TCAGATTTTC TCCTGTGGGA AAAAAAAT CCATGCACTC 4560
TCTCTGTGTT AAAGATCAGC TATTCCTTC TGATCTTGA AAGAGGTTCT GCACTCCTGG 4620
AACCGGTCAC AGGAACGCAC AGATCATGGC AGGATGCGCT GGGACGGCCC ATCTTGGCAA 4680
GGTTCAGTCT GAATGGCATG GAGACCGGGA GATAGAGGGG TTTAGATTT TAAAAGGTA 4740
GGTTTTAAAA ATAAGTTTAA TACATAACA GTTTTGGAGA AAAATTACAG ATCATATAAG 4800
CAAGACAGTG GCACTAAAAT GTTAAATTCA TTAATCTGTT TGTTTGGCAC TGATGCAATG 4860
TATGGCTTTT CTCTTGCCCC AAATCACAAA CATATGTATC TTTGGGGAAA CTAACAATAT 4920
GATTGCACTA AATAAACTAC TTTGAATAGA GGCCAAATTA ATCTTTTAAA AATGATGATA 4980
ATCATAGGT TTACTCAGTG AAATCATATT AATTATTTT CAAAATCTAA AAGCTGTAGC 5040
TGGAGAAGCC CATGGCCACG AGGAAGCAGC AATTAATTAG ATCAACACTT TTCTCCAGGG 5100
TTCACCATGC AGGCAACATT ACCTTGTCTT TCAAAAGACA CTGCCTTAG TGCAAGGGGA 5160
AACCTGTGAA AGCTGCACTC AGAGGGAGGA GTCTTCTTA CATAATTGC AATTTAGGA 5220
ATTTAATTTA TAGGCAGATC TTTAAATACA GTCAACTTAC GGTGCACAGT AATATGAAAG 5280
CCACACTTTG AAGGTAATAA ATACACAGCA TGCAGACTGG GAGTTGCTAG CAAACAAATG 5340
GCTTACTTAC AAAAGCAGCT TTTAGTTCAG ACTTAGTTTT TATAAAATGA GAATTCTGAC 5400
TTACTTAACC AGGTTTGGGA TGGAGATGGT CTGCATCAGC TTTTGTATT AACAAAGTTA 5460
CTGGCTCTTT GTGTGTCTCC AGGTAACCTT GCTTGATTAA ACAGCAAAGC CATATTCTAA 5520
ATTCAGTGT GAATGCCTGT CCCAGTCCAA ATTGTCTGTC TGCTCTTATT TTTGTACCAT 5580
ATTGCTCTTA AAAATCTTGG TTTGTTACAG TTCATAATTC ACCAAAAAGT TCATATAATT 5640
TAAAGAAACA CTAAATTAGT TTAATAAGAA GCAATTTATA TCTTTATGCA AAAACATATG 5700
TCTGTCTTTG CAAAGGACTG TAAGCAGATT ACAATAAATC CTTTACTTT

Seq ID NO: 36 Protein sequence:

Protein Accession #: NP_000892.1

1 11 21 31 41 51
| | | | |
METKGYHSLP EGLDMERRWG QVSQAVERS LGPTERTDEN NYMEIVNVSC VSGAIPNNST 60
QGSSKEKQEL LPCLQQDNNR PGILTSDIKT ELESKELSAT VAESMGLYMD SVRDADYSYE 120
QQNQQGSMSK AKIYQNVEQL VKFYKGNHR PSTLSCVNTL LRSFMSDSGS SVNGGVMRAI 180
VKSPIMCHEK SPSVCSPLNM TSSVCSPAGI NSVSSTTASF GSFPVHSPIT QGTPLTCSFN 240
AENRGRSHS PAHASNVGSP LSSPLSSMKS SISSPPSHCS VKSPVSSPNN VTLRSSVSSP 300
ANINNSRCSV SSPSNTNRRS TLSSPAASTV GSICSPVNNA FSYTASGTS GSSTLRDVVP 360
SPDTQEKGAQ EVFPKTEEV ESAISNGVTG QLNIVQYIKP EPDGAFFSSC LGGNSKINS 420
SSFSVPKQE STKHSCSGTS FKGNPTVNP PFMDGSYFSF MDDKDYYSL GILGPPVPGF 480
DGNCEGSGFP VGIKQEPDDG SYYPEASIPS SAIVGVNSGG QSFHYRGAQ GTISLSRSAR 540
DQSFQHLSSF PPVNTLVESW KSHGDLSSRR SDGYPVLEYI PENVSSSTLR SVSTGSSRPS 600
KICLVCGDEA SGCHYGVTTC GSCKVFFKRA VEGQHNYLCA GRNDICIDKI RKNCPACRL 660
QKCLQAGMNL GARKSKKLK LKGIHEEQP QQQPPPPPP PQSPPEGTTY IAPAKEPSVN 720
TALVPQLSTI SRALTPSPVM VLENIEPEIV YAGYDSSKPD TAENLLSTLN RLAGKQMIQV 780
VKWAKVLPFG KNLPLEDQIT LIQYSWMCLS SFALSWRSYK HTNSQFLYFA PDLVFNEEKM 840
HQSAMYELCQ GMHQISLQFV RLQLTFFEYT IMKVLLLLST IPKDGLKSQA AFEEMRTNYI 900
KELRKMVTKC PNNSGQSWQR FYQLTKLLDS MHDLVSDLLE FCFYTFRESH ALKVEFPAML 960
VEIISDQLPK VESGNAKPLY FHRK

Seq ID NO: 37 DNA sequence

Nucleic Acid Accession #: see Table 25 & 25A for complete list

1 11 21 31 41 51
| | | | |
CCTACCAGGT TCAAGCAACT CTGCTGCCTC AGCTCCCAAG TAGCTGGGAT TACAGGTGCA 60
TGCCACTACA CCTGGCTTTT TGTATTTTGA GTAGAGATGG TTTTCACTAT GTTGGCCAGG 120
CTGATCTTGA ATTCCTGGCC TGAAGTAATC TGCCTGCCTC AGCCTCCCAA AGTGCTGGGA 180
TTATAGGAGC CACCACACCT GGCATAACTG GTATTTTITA TATGCTTCCT GGGCAACTTA 240
AAAAATTGAT TACTCTGTTG TTTCTTCCTT TTTTITTTT TTTTGGCTTT GACCAATTTG 300
TGAGACCCAA GTATCTCCTA CCTAGAAAAA AAACACACTA AACAGTAAAT GATTACCAAC 360
CTATTTGAAA CAAATCTCAA TTAATTAACA TATACTTCAA GGAGAAGACT TAACAAAATC 420
TTACTTTTCA TTCTTAATAG CTCTTCCAT AAAAAATGTT CACAAGTGTA TCAAATTAGT 480
CCTAACAACT ACTGTTAAGT GATTAATGAA ACAGGAGTGA CAGGAGTGAA TTTAATAATA 540
GCAATAAATA CAGATGGGAC TACATAAATT GTGGAGGTCC TGATGCAAAA CTCTCTCTGT 600
ATTCGATGGC ATCTCAGCTT TCTCATAGAG CTGTTTCACT GTGAGGGTCT TTATCCTTCA 660
TGCAGAGCTT CATTATTTTC TTTCTTCTAG CAATCAGTCC AAAGCACAAT GTCAGAAAGA 720
TCACAACACA TGCAGCAATA ATGGGCTCTA TTGGTACACC CACAGTTTTA TCTTTAACA 780
TC

Seq ID NO: 38 DNA sequence

Nucleic Acid Accession #:

NM_001192.1

Coding sequence: 219-773

1 11 21 31 41 51
| | | | |
AAGACTCAAA CTTAGAAACT TGAATTAGAT GTGGTATTCA AATCCTTACG TGCCGCGAAG 60
ACACAGACAG CCCCCGTAAG AACCCACGAA GCAGGCGAAG TTCATTGTC TCAACATTCT 120
AGCTGCTCTT GCTGCATTG CTCTGGAATT CTTGTAGAGA TATTACTTGT OCTTCCAGGC 180
TGTCTTTCT GTAGCTCCCT TGTTTTCTT TTGTGATCAT GTTGACAGT GCTGGGCAGT 240
GCTCCCAAAA TGAATATTTT GACAGTTTGT TGCATGCTTG CATACCTTGT CAACTTCGAT 300
GTTCTTCTAA TACTCCTCCT CTAACATGTC AGCGTTATTG TAATGCAAGT GTGACCAATT 360
CAGTGAAAGG AACGAATGCG ATTCTCTGGA CCTGTTTGGG ACTGAGCTTA ATAATTTCTT 420
TGGCAGTTTT CGTGCTAATG TTTTGTCTAA GGAAGATAAG CTCTGAACCA TTAAGGACG 480
AGTTAAAAA CACAGGATCA GGTCTCCTGG GCATGGCTAA CATTGACCTG GAAAAGAGCA 540
GGACTGGTGA TGAAATTATT CTTCCGAGAG GCCTCGAGTA CACGGTGGAA GAATGCACCT 600
GTGAAGACTG CATCAAGAGC AAACCGAAGG TCGACTCTGA CCATTGCTTT CCACTCCCAG 660
CTATGGAGGA AGGCGCAACC ATTCTTGTCA CCACGAAAAC GAATGACTAT TGCAAGAGCC 720
TGCCAGCTGC TTGAGTGCT ACGGAGATAG AGAAATCAAT TTCTGCTAGG TAATTAACCA 780
TTTCGACTCG AGCAGTGCCA CTTTAAAAAT CTTTGTGAG AATAGATGAT GTGTGAGATC 840
TCTTTAGGAT GACTGTATTT TTCAGTTGCC GATACAGCTT TTTGCTCTT AACTGTGGAA 900
ACTCTTTATG TTAGATATAT TTCTTAGGT TACTGTTGGG AGCTTAATGG TAGAACTTC 960
CTTGGTTTCA TGATTAAAGT CTTTTTTTTT CCTGA

Seq ID NO: 39 Protein sequence:

Protein Accession #: NP_001183.1

1 11 21 31 41 51
| | | | |
MLQMAGQCSQ NEYFDSLHA CIPQLRCSS NIPPLTCQRY CNASVTNSVK GTNAILWTCL 60
GLSLIISLAV FVLMFLLRKI SSEPLKDEFK NTGSGLLGMA NIDLEKSRGT DEILPRGLE 120
YTVEECTCED CIKSKPKVDS DHCFLPAME EGATILVTK TNDYCKSLPA ALSATEIEKS 180
ISAR

Seq ID NO: 40 DNA sequence

Nucleic Acid Accession #:

NM_025087.1

Coding sequence: 183-2282

1 11 21 31 41 51
| | | | |
ACACTGCCTC GGTTCCGGCA GTGGGTCACT TGGCTGGGGC TCACTTGGCA ACGGGACGCG 60
GGAACGAGGG GCGCGGACGC AGGCCCGGGA GGACGCGGCG GCGGGAACCT GGGGGCGCAG 120
GGCTAGGGCA GCGGGCCCGA CCCGCACGGC TTTCTGGAA AGCGCTGCCC CTCGCCGCGG 180
CGATGACCTC GCTGTGGAGA GAAATCCTCT TGGAGTGGCT GCTGGGATGT GTTCTTGGT 240
CTCTCTACCA TGACCTGGGA CCGATGATCT ATTACTTTCC TTGCAACA CTAGAACTCA 300
CTGGGCTTGA AGGTTTTAGT ATAGCATTTT TTCTCCAAT ATTCCTAACA ATTACTCCTT 360
TCTGGAATTT GGTTAACAAG AAGTGGATGC TAACCCTGCT GAGGATAATC ACTATTGGCA 420
GCATAGCCTC CTTCCAGGCT CCAAATGCCA AACTTCGACT GATGGTTCTT GCGCTTGGGG 480
TGCTTCTCTC ACTGATAGTG CAAGCTGTGA CTTGGTGGTC AGGAAGTCAT TTGCAAAGGT 540
ACCTCAGAAAT TTGGGGATTG ATTTTAGGAC AGATTGTTCT TGTGTTCTA CGCATATGGT 600
ATACTTCACT AAACCCAATC TGGAGTTATC AGATGTCCA CAAAGTGATA CTGACATTAA 660
GTGCCATAGC CACACTTGAT CGTATTGGCA CAGATGGTGA CTGCAGTAAA CCTGAAGAAA 720
AGAAGACTGG TGAGGTAGCC ACGGGGATGG CCTCTAGACC CAACTGGCTG CTGGCAGGGG 780
CTGCTTTTGG TAGCCTTGTG TTCCTCACCC ACTGGGTTTT TGGAGAAGTC TCTCTTGT 840
CCAGATGGGC AGTGAGTGGG CATCCACATC CAGGGCCAGA TCCTAACCCA TTTGGAGGTG 900
CAGTACTGCT GTGCTTGGCA AGTGGATTGA TGCTTCCATC TTGTTTGTGG TTTCGTGGTA 960
CTGGTTTGTG CTGGTGGGTT ACAGGAACAG CTTCACTGTC GGGGCTCCTT TACCTGCACA 1020
CATGGGCAGC TGCTGTGTCT GGCTGTGTCT TCGCCATCTT TACTGCATCC ATGTGGCCCC 1080
AAACACTTGG ACACCTTATT AACTCAGGGA CAAACCCTGG GAAAACCATG ACCATTGCCA 1140
TGATATTTTA TCTTCTAGAA ATATTTTCT GTGCTGGTG CACAGCTTTT AAGTTTGTCC 1200
CAGGAGGTGT CTACGCTAGA GAAAGATCAG ATGTGCTTTT GGGGACAATG ATGTTAATTA 1260
TCGGGCTGAA TATGCTATTT GGTCTAAGA AAAACCTTGA TTGCTTCTT CAAACAAAAA 1320
ACAGTTCTAA AGTGCTTTT AGAAAGAGTG AAAAATACAT GAAACTTTT CTGTGGCTGC 1380
TTGTTGGTGT GGGATTGTTG GGATTAGGAC TACGGCATAA AGCCTATGAG AGAAAACTGO 1440
GCAAAGTGGC ACCAACCAAA GAGGTCTCTG CTGCCATCTG GCCTTTCAGG TTTGGATATG 1500
ACAATGAAGG GTGGTCTAGT CTAGAAAGAT CAGCTCACCT GCTCAATGAA ACAGGTGCAG 1560
ATTCATAAC AATTTTGGAG AGTGATGCTT CTAAGCCCTA TATGGGGAAC AATGACTTAA 1620

CCATGTGGCT AGGGGAAAAG TTGGGTTTCT ATACAGACTT TGGTCCAAGC ACAAGGTATC 1680
 ACACTTGGGG GATTATGGCT TTGTCAAGAT ACCCAATTGT GAAATCTGAG CATCACCTTC 1740
 TTCCGTCACC AGAGGGCGAG ATCGCACCAG CCATCACATT GACCGTTAAC ATTCGGGGCA 1800
 AGCTGGTGGA TTTTGTCTG ACACACTTTG GGAACCACGA AGATGACCTC GACAGGAAAC 1860
 TGCAGGCTAT TGCTGTTTCA AAACACTGA AAAGTAGCTC TAATCAAGTG ATATTTCTGG 1920
 GATATATCAC TTCAGCACCT GGCTCCAGAG ATTATCTACA GCTCACTGAA CATGGCAATG 1980
 TGAAGGATAT CGACAGCACT GATCATGACA GATGGTGTGA ATACATTATG TATCGAGGGC 2040
 TGATCAGGTT GGGTTATGCA AGAATCTCCC ATGCTGAACT GAGTGATTCA GAAATTCAGA 2100
 TGGCAAAATT TAGGATCCCT GATGACCCCA CTAATTATAG AGACAACCAG AAAGTGGTCA 2160
 TAGACCACAG AGAAGTTTCT GAGAAAATTC ATTTAATCC CAGATTGGA TCCTACAAAG 2220
 AAGGACACAA TTATGAAAAC AACCATAATT TTCATATGAA TACTCCCAA TACTTTTAT 2280
 GAAACATTTA AAACAAGAAG TTATTGGCTG GGAAAATCTA AGAAAAAAG TATGTAAGAT 2340
 AAAAAGAAGA GATTAATGAA AGTGGGAAAA TACACATGAA GAACCTCAAC TAAAAAACA 2400
 CATGGTATCT ATGCAGTGGG AAATTACCTC CATTTGTAAT CTATGTTGCT TAATAAAAAAC 2460
 ATTTCTCTAA AAAAAAAAAA AAAAAA

Seq ID NO: 41 Protein sequence:

Protein Accession #: NP_079363.1

1 11 21 31 41 51
 | | | | |
 MTSWREILL ESSLGCVSWS LYHDLGPMIY YFPLQTELT GLEGFSIAFL SPIFLTITPF 60
 WKLVNKKWML TLLRIITIGS IASFQAPNAK LRLMVLALGV SSSLIVQAVT WWSGSHLQRY 120
 LRIWGFILGQ IVLVVLRWY TSLNPIWSYQ MSNKVILTS ALATLDRIGT DGDCKPPEEK 180
 KTGEVATGMA SRPNWLLAGA AFGSLVFLTH WVFGEVSLVS RWAVSGHPPH GPDNPFGGA 240
 VLLCLASGLM LPSCWFRGT GLIWWVTGTA SAAGLLYLHT WAAAVSGCVF AIFTASMWPQ 300
 TLGHLNSGT NPGKMTIAM IFYLLEIFFC AWCTAFKFPV GGVYARERSD VLLGTMMMLI 360
 GLNMLFGPKK NLDLLQTKN SSKVLFRKSE KYMKLFLWLL VGVGLLGLGL RHKAYERKLG 420
 KVAPTKEVSA AIWPFRRGYD NEGWSSLERS AHLLNETGAD FITLESAS KPYMGNNDLT 480
 MWLGEKLGFY TDFGPSTRYH TWGIMALSRY PIVKSEHLL PSPEGEIAPA ITLTVNISGK 540
 LVDFVVTDFG NHEDDLRKL QAIKAVSKLLK SSSNQVIFLG YITSAPGSRD YLQLTEHGNV 600
 KDIDSTDHDR WCEYIMYRGL IRLGYARISH AELSDSEIQM AKFRIPDDPT NYRDNQKVVI 660
 DHREVSEKIH FNPRFGSYKE GHNYENNHNH HMNTPKYFL

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method of detecting a metastatic colorectal cancer-associated
2 transcript in a cell from a patient, the method comprising contacting a biological sample from
3 the patient with a polynucleotide that selectively hybridizes to a sequence at least 80%
4 identical to a sequence as shown in Tables 1-26.
- 1 2. The method of claim 1, wherein the biological sample comprises
2 isolated nucleic acids.
- 1 3. The method of claim 1, wherein the polynucleotide is labeled.
- 1 4. The method of claim 1, wherein the polynucleotide is immobilized on
2 a solid surface.
- 1 5. An isolated nucleic acid molecule consisting of a polynucleotide
2 sequence as shown in Tables 1-26.
- 1 6. An expression vector comprising the nucleic acid of claim 5.
- 1 7. A host cell comprising the expression vector of claim 6.
- 1 8. An isolated polypeptide which is encoded by a nucleic acid molecule
2 having polynucleotide sequence as shown in Tables 1-26.
- 1 9. An antibody that specifically binds a polypeptide of claim 8.
- 1 10. The antibody of claim 10, which is an antibody fragment.
- 1 11. The antibody of claim 10, which is a humanized antibody
- 1 12. A method of detecting a metastatic colorectal cancer cell in a
2 biological sample from a patient, the method comprising contacting the biological sample
3 with an antibody of claim 9.
- 1 13. The method of claim 12, wherein the antibody is labeled.
- 1 14. A method of detecting antibodies specific to metastatic colorectal
2 cancer in a patient, the method comprising contacting a biological sample from the patient
3 with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1-26.

15. A method for identifying a compound that modulates a metastatic colorectal cancer-associated polypeptide, the method comprising the steps of:

(i) contacting the compound with a metastatic colorectal cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.; and

(ii) determining the functional effect of the compound upon the polypeptide.

16. The method of claim 15, wherein the functional effect is determined by measuring ligand binding to the polypeptide.

17. A method of inhibiting proliferation of a metastatic colorectal cancer-associated cell to treat colorectal cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound that modulates a polypeptide encoded by a sequence as shown in Tables 1-26.

18. A drug screening assay comprising the steps of

(i) administering a test compound to a mammal having colorectal cancer or a cell isolated therefrom;

(ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26. in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of colorectal cancer.

19. A pharmaceutical composition for treating a mammal having colorectal cancer, the composition comprising a compound identified by the assay of claim 18 and a physiologically acceptable excipient.

20. A method of detecting a metastatic colorectal cancer-associated polypeptide in a cell from a patient, the method comprising contacting a biological sample from the patient with a antibody that that specifically binds a polypeptide encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

21. The method of claim 21, wherein the antibody is labeled.